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Maximum DB seq length: 2000000000
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Maximum Match 100%
Listing first 45 summaries
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| (gqn2_6/ptodata/2/ina/5A_COMB.seq:*
| (cqn2_6/ptodata/2/ina/5B_COMB.seq:*
| (gqn2_6/ptodata/2/ina/6_COMB.seq:*
| (gqn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
| (gqn2_6/ptodata/2/ina/backfiles1.seq:*
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US-09-058-389A-5
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US-08-762-500-19
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REGISTRATION NUMBER: 30,742
REFERENCE,DOCKET NUMBER: 7853-078-999
REFERENCE,COCKET NUMBER: 7853-078-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)7909090
TELEPAX: (212)8699741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ 1D NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1228 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 08/799,910
FILING DATE: 13-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/011,787
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
                                                                        MOLECULE TYPE: CDNA FEATURE:
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20000

NAME/KEY: Coding Sequence LOCATION: 1...468
OTHER INFORMATION:

TOPOLOGY: STRANDEDNESS: TYPE: nucleic acid

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US/08826246 OMPOSITIONS AND METHODS FOR THE TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE 4 W: S: HOTO OF THE AMERICAS ELLP E of the Americas US/08/826,246 US/08/826,246 US/08/99,910 08/799,910	ALIGNMENTS	US-08-946-666-2 US-08-916-745-2 US-09-042-929-2 US-09-646-661-2 US-09-042-960-2	-09-188-930- -08-458-568A -08-726-214- -08-140-729A	US-09-135-021-1 US-09-135-021-5 US-08-458-568-71 US-08-403-852D-6 US-08-510-6468-6 US-08-926A-6 US-08-926A-6 US-08-926A-6 US-08-926A-6	
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100.0%; Score 1228; ilarity 100.0%; Pred. No. 0; Conservative 0; Mismatches
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                                                                            ; LOCATION: 1...468
; OTHER INFORMATION:
US-08-944-495-9
                                                                                                                                                                                                             REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)7990900
TELEFAX: (212)8699741
TELEFAX: (212)8699741
TELEY: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1228 base pairs
Query Match
Best Local Similarity
Matches 1228; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IDM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944;495
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NAME: Coruzzi, Laura A
                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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                                                                                                                                      MOLECULE TYPE: FEATURE:
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CITY: New York
STATE: NY
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ZIP: 10036-2711
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                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                       NAME/KEY:
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GENERAL INFORMATION:

APPLICANT: FALB, Dean A.

APPLICANT: FALB, Dean A.

ITITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE

TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CARDIOVAS.

FILE REFERENCE: 7853-126.

CURRENT APPLICATION NUMBER: US/09/126,640A

CURRENT FILING DATE: 1998-07-30

EARLIER APPLICATION NUMBER: 08/870,434

EARLIER APPLICATION NUMBER: 08/799,910

EARLIER APPLICATION NUMBER: 08/799,910

EARLIER FILING DATE: 1997-02-13

EARLIER FILING DATE: 1997-02-13

EARLIER FILING DATE: 1996-02-16

NUMBER: FASTED TON NUMBER: 60/011,787

EARLIER FILING DATE: 1996-02-16

NUMBER OF SEQ ID NOS: 44

SOCTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 5

LENGTH: 1228
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NUMBER OF SEQ ID
SOFTWARE: FastSEC
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LENGTH: 1228
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Best Local Similarity
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Patent No. 6099823
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Patent No. 5670367
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                                                                                                                            APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT
NUMBER OF SEQUENCES: 52
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               COUNTRY: USA
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                                                               CITY: Alexandria
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                                                 Sequence 14, Applicat Patent No. 5670367 GENERAL INFORMATION:
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APPLICANT:

DORNER, F. SCHEIFLINGER, FALKNER, F. G.

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Application US/08232463

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US-08-232-463-14
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Best Local Similarity
"hohes 6; Conserva
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                                                                                                                                                                                                                                                                              1179
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IMMEDIATE SOURCE:
                                                                                                                                                                                                          1239
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ATTORNEY/AGENT INFORMATION:
NAME: BENT SCLEPBER A
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA: APPLICATION NUMBER:
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1419 YYYYYYYYYYYY 1431
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                                                                 AATCTGACTTCGGAGCCCTCGGACTACGCTCTGGACCTCAGCACCTTTCCTCCAGCAACAC 456
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899149
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                   1321
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
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MEDIUM TYPE: Floppy disk
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22313-0299
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CITY: Alexandria
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RERERERERERERERATCG 1063
                          AAAAAAAAAAAAAAACTCG 1226
                                                                             CGACTGTCGAGATCGCCTAGTATGTTCTGTGAACACAAATAAAATTGATTTACTGTCAAA 1207
                                                                                                       CAACTCGCCTTTACGGTGGCTGCGAGGTAGAGGGTTGGGGGCTTGGTGGGCCTGTCACGGAG 1147
                                                                                                                                                           ACTIGTIGAGACTTCGGCGGACCATTAGGAATGAGATCCGTGAGATCCTTCCATCTTCTT 1087
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Matches

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Conservative

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Score 42; DB Pred. No. 0.15 0; Mismatches

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DB 1; Length 8438; 165;

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Query Match Best Local Similarity

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LOCATION:
US-07-945-283-1
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 8438 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA RE-BASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 27976
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                      FEATURE:
NAME/KEY:
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MEDIUM TYPE: Floppy
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                                       FEATURE:
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                         NAME/KEY:
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CLASSIFICATION:
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IBM PC compatible
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Ronald D.
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Involving The EPU and LLT Genes
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                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                   TELEFAX: (206) 682-60 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 530 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                     NAME: No. 6114150tenburg Ph.D., Carol REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 390036.402C1
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Baskaran, TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Weissman,
APPLICANT: Baskaran,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                     438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/758,662
FILING DATE: 29-NOV-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: SEED and BERRY LLP
STREET: 701 Fifth Avenue, 6300 Columbia Center
CITY: Seattle
                   95
                                                                                          <u>3</u>5
                                                                                                                                                                                                                                                        STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 98104
                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE:
                   GTCCTGAGATCTTCACCTTCGACCCTCTCCCGGAGCCCGCAGCGGCCCCCTGCCGGGCGCCC 154
                                                                                        CCATCCTGCAGGCCCGACCCGGGCCCCCTCCACCATCCCGGGACCCCGGGGGGGCTCCG 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATCCCTGGCGCCCACCCCTG 373
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                                                     -GACCCTCTCCCGGAGCCCGCAGCGGCCCCTGCCGGGGGCAGCGCCCCAGCGCCCTCTCGCGGGCA 173
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                                                                                                                             Score 41.2; DB 3;
Pred. No. 0.069;
D; Mismatches 73;
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73;
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                                                                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (617)720-2441
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/845,998
                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: LCTELECOMMUNICATION INFORMATION TELEPHONE: (617)720-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                             ANTI-SENSE:
                                                                                                                                                                                                                                                                                                          HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
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NAME: Van Amsterdam, John R
REGISTRATION NUMBER: 40,212
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STREET: υς
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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                           155
                                                                                                             697
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                                                                                                                                                                                                                                                   NAME/KEY:
                                                                                                                                                                 Local Similarity 53.1
                                                                                                                                     COUNTRY: UZIP: 02210
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                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
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CCCGCGCCGCCGCCGGCCATGAGCGCGAGCGACGG 540
                          CCAGCGCCTCTCGCGGGCACCGAAAGCGCAGCCGCAGG 192
                                                     GTCCTGAGATCTTCACCTTCGACCCTCTCCCGGAGCCCGCAGCGGCCCCTGCCGGGCGCCC 154
                                                                                                           17, AF.
NO. 5879892
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De Smet, Charles
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RESULT 10
US-09-128-155-16
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US-09-206-537-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Van Amsterdam, John R.
REGISTRATION NUMBER: 40,212
REFERENCE/DOCKET NUMBER: L0461
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)720-3500
TELEFAX: (617)720-2441
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7, Application US/09206537 Patent No. 6130052
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: LEUKEMIA ASSOCIATED GENES NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: WOJf, Greenfield & Sacks, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                                                                                                             697
                                                                                                                STREET:
CITY: E
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                                                                                                                                               95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/206,537 FILING DATE:
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                                                                                                                                                                                                                                                                                                                                           NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
                                                                                    CCAGCGCCTCTCGCGGGCACCGAAAGCGCAGCCGCAGG 192
                                                                                                                                              GTCCTGAGATCTTCACCTTCGACCCTCTCCCGGAGCCCGCAGCGGCCCCTGCCGGGCCCC 154
                                                                                                                                                                           CCCCCCCCCCCCCCCCCCCATGAGCGCGAGCGACGG 540
                                                                                                                                                                                                                                                   Similarity
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Boon, Thierry
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Pred. No. 0.18;
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Patent No. 5705732
Patent No. 5705732 5684223
GENERAL INFORMATION:

APPLICANT:
APPLICANT:

Bothwell, Alfred I Elliott, Eileen A. Flavell, Richard *I*

Alfred L.M

Sims, Peter J

APPLICANT: APPLICANT: APPLICANT:

APPLICANT: APPLICANT:

Rollins, Scott Bell, Leonard Squinto, Stephen Madri, Joseph Sequence 2,

Application US/08087007

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; LOCATION: (1)...(19331)
; OTHER INFORMATION: n = A,T,C or
US-09-128-155-16
RESULT 11
US-08-087-007-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ 1D NO 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 09404/052001
CURRENT APPLICATION NUMBER: US/
CURRENT FILING DATE: 1998-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL MOLECULES OF
TITLE OF INVENTION: AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EARLIER FILING DATE: 1997-08-04
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                                                                        22291 gcagtacgctataat 22305
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                                                                                                                                                                                                                                                                    265 CTGCTGCTCACCATCGTCTTCTGCCAGATCCTGATGGCTGAAGAGGGGTGTGCCCGGCGCCC 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGGGGCTCCGGTCCTGAGATCTTCACCTTCGACCCTCTCCCGGAGCCCGCAGCGGCCCCT 144
                                                                                                                CTCGAGCCCTTTAAT 399
                                                                                                                                                     CTGCCTCCAGAGGACGCCCTAACGCCGCATCCCTGGCGCCCACCCCTGTGTCCCCCGTC
                                                                                                                                                                                                                                                                                                                                                                                                                           GCCGGGCGCCCCAGCGCCTCTCGCGGGCACCGAAAGCGCAGCCGCAGGGTTCTCTACCCT 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGAGTGGTCCCGGCGCCAGCTGCCAGTCGAGGGAACCGAACCCCAGCCAAAAAGGCTTCTCTTT 264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44.38;
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Pred. No. 1.
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US-08-483-433-2

Sequence 2. Application US/08483433

: Patent No. 6100443

: GENERAL INFORMATION:
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Best Local :
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ORGANISM: Hom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: PADST, PALTER L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
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HYPOTHETICAL:
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LIBRARY: GenBa
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                                                                                                                                                                                                                                                                                                                                STREET: 1100 P
CITY: Atlanta
STATE: Georgia
                                                                                                                         685 CCAA 688
                                                                                                                                                          506 AAAA 509
                                                                                                                                                                                         625 TACTCCACCCGTCTTGTTGTCCCACCCTTGGTGACGCAGAGCCCCAGCCCCAGACCCCGC 684
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Local Similarity 51.1%;
nes 94; Conservarion
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CLONE: Human DAF cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
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TOPOLOGY: linear
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1100 Peachtree Street, Suite 2800
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end of Exon 1, genomic sequence)"
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Pred. No. 0.
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OTHER INFORMATION: end of Exon 1, genomic sequence)"
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Best Local
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION NUMBER: 07/906,
APPLICATION NUMBER: 9, 1992
FILING DATE: June 29, 1992
FILING DATE: June 29, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-873-8794
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                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
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                                                                                                                                                             326 TGCCTCCAGAGGACGCCCCTAACGCCGCGCTCCCTGGGGCCCCACCCCTGTGTCCCCCGTCC 385
625 TACTCCACCCGTCTTGTTTGTCCCACCCTTGGTGACGCAGAGCCCCAGCCCAGACCCCGC
                                                                                        386 TCGAGCCCTTTAATCTGACTTCGGAGCCCTCGGACTACGCTCTGGACCTTCAGCACTTTCC 445
                                                                   565 TAGGGCCCCGGGGTATGACGCCGGAGCCCTCTGACCGCACCTCTGACCACAACAAACCCC
                               446 TCCAGCAACACCCGGCCGCCTTCTAACTGTGACTCCCCGCACTCCCCAAAAAGAATCCGA 505
                                                                                                                                                                                                                                                                                                                                                          LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
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TOPOLOGY: lir
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SYSTEM: PC-DOS/MS-DOS
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SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
Dase pairs
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NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,
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386 TCGAGCCCTTTAATCTGACTTCGGAGCCCTCGGACTACGCTCTGGACCTCAGCACTTTCC 445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                 NAME/KEY: misc_feature LOCATION: 1..819
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                              TGAGTCCAGAGGCTGTTGCCAGGAGCTCCTCCTCCTTCCCCTCCCCACTCTCCCCGAGTC 564
                                                            TGCCTCCAGAGGACCCCCTAACGCCGCATCCCTGGCGCCCCACCCCTGTGTCCCCCGTCC
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(: U.S.
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Human DAF cDNA
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                                                                                            Conservative
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end of Exon 1, genomic sequence)"
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                           302 CCGGCCCCGGCCCCGGCCTCCGACCCGCTCCGGGGCACGGCCCCGGCCCCGGCCCCCAG
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Relaction
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
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Application US/09058389A

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TOPOLOGY: lin

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HYPOTHETICAL: N
US-09-058-389A-5
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Search completed: January 30, 2001, 21:28:30 Job time: 19992 sec
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TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 6354 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                       Query Match 3.1%; Score 38.6; DB 3; Length 6354; Best Local Similarity 65.9%; Pred. No. 1; Matches 56; Conservative 0; Mismatches 29; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/058,389A FILING DATE: April 9, 1998 CLASSIFICATION: 800 ATTORNEY/AGENT INFORMATION: NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742 REFERENCE/DOCKET NUMBER: 1340-1-013N TELECOMMUNICATION INFORMATION: TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS;
ADDRESSE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPI.ICANT: Belt, Judith A.
APPI.ICANT: Crawford, Charles R.
APPILICANT: Patel, Suryen
TITLE OF INVENTION: A NITROBENZYLMERCAPTOPURINERIBOSIDE
TITLE OF INVENTION: (NBMPR)-INSENSITIVE, EQUILIBRATIVE, NUCLEOSIDE TRANSPORT
TITLE OF INVENTION: PROTEIN, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF
TITLE OF INVENTION: USE
                                                                                                             2521 CCTGCGCCCCCTGCCCTCCAGCCCT 2545
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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ZIP: 07601
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STATE: New Jersey
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Minimum DB :
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Maximum Match 100%
Listing first 45 summaries
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Copyright (c) 1993 - 2000 Comp
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5947.064 Million cell updates/sec
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                                                                                                                     Human colon cancer
EST clone 0417. H
EST clone BY66. H
                                                                                                                                                                        Nucleotide sequenc
Human Fchd605 gene
                Human gene express
                                                    Human colon cancer
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Human gene express	217264	20	1312		8	<u>4</u> 5
Human gene express	216153	20	749		8	44
Human DNA demethyl	X61218	20	1804		9.	43
Thermophilus therm	X58429	20	2681		9	42
DNA encoding a hum	X30342	20	954		39.6	41
ш	X02974	20	3198		9.	40
Human ovarian tumo	Z77506	20	2188		9	39
cDNA sequence of f	V60339	19	1120		9	38
Human gene express	217479	20	1523		40	37
Human gene express	217507	20	1523		40	36
	Q77739	15	2232		40.4	35
Alpha 2, 3-sialyl	Q73117	15	2179		40.4	34
Human gene express	214922	20	300		40.4	ω ω
Human gene express	Z17058	20	1017		40.6	32
Mouse DNA demethyl	X61220	20	1966		40.8	3
Human adenosine Al	X53491	20	114955		41	30
	V33912	20	4524		41.2	29
ш	216923	20	1102		41.2	28
Hybrid promoter of	Q03062	11	1345		41.4	27
Expression vector	Q13318	12	1344		41.4	26
Chicken beta-actin	Q01620	11	1275		۲.	25
Human colon cancer	A02539	21	989		41.6	24
Human colon cancer	A02528	21	1459	3.4	$\mathbf{\mu}$	23
Complete nucleotid	Z30163	20	34094		42	22
oding Pseu	Q73500	15	8438		4	21
Cardiac adenylyl c	095540	16	4356			20
adeny.lyl	Q37543	14	4356		2	19
colon cance	A02477	21	1127		2	18
Human adenosine re	A34741	21	4475			17
Human adenosine re	A34740	21	2375			16
Human colon cancer	A02504	21	1593		44.8	15
Human adenosine Al	X53491	20	114955		7.	14
Human cyclic nucle	251683	21	4228		7 .	13

ALIGNMENTS

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RESULT
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CDS
                                                                                                                                                                                                                     fchd605 gene; human; cardiovascular disease; oncogenic disorder; diabetic retinopathy; fibroproliferative disorder; artherosclerosis; TGF-beta signalling pathway; TGF; Transforming growth factor; pancreatic cancer; angiogenesis; inflammation; fibrosis; tumour growth;
        Falb DA;
                                                                                                                                                                                                                                                                          Nucleotide sequence of human fchd605 gene
                                                                                                                                                                                                                                                                                             31-MAY-2000 (first entry)
                                                                                                                                                                                                                                                                                                                   250711;
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                                                30-JUL-1998;
                                                                     30-JUL-1999;
                                                                                                              WO200006206-A1.
                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                            vascularisation; cytostatic; antidiabetic; opthalmological; ds
                          (MILL-) MILLENNIUM PHARM INC
                                                                                          10-FEB-2000
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Matches 1228;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; Y45017
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             GACGCCACCCGGTGCTTGAGGCGGGACCGAGGCGCACAGAGACCGAGGCGCATAGAGACCC
                                                                CGAGAGCGTATCCCCAACTGGGACTTCCGAGGCAACTTGAACTCAGAACACTACAGCGGA
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foam cell; cardiovascular disease; atherosclerosis; ischaemia
reperfusion; hypertension; restenosis; arterial inflammation;
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cccgcactccccaaaaagaatccgaaaaaccacaaagaaacaccaggcgtacctggtgcg
                              CCCGCACTCCCCAAAAAGAATCCGAAAAACCACAAAGAAACACCAGGCGTACCTGCTGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel nucleic acids, used to develop products for the diagnostreatment of disorders involving unwanted cell proliferation particularly cancers, especially colon cancer
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Carroll E,
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Catino TJ,
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AGAACACTACAGCGGAGACGCCACCCGGTGCTTGAGGCGGGACCGAGGCGGACAGAGACCC 6/4 aggcctacgtggtgcgcgagagcglatccccaactgggacltccgaggcaacttgaactc AGGCGTACCTGGTGCGCGAGAGCGTATCCCCAACTGGGACTTCCGAGGCAACTTGAACTC 584

agaacactacagcggagacgccacccggtgcttgaggcgqqaccgagggcgcacagagacc

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Query Match
Best Local Similarity
                                                                                                           This sequence represents an expressed sequence tag (EST), and is a polynucleotide of the invention. The polynucleotides of the invention are all secreted EST sequences isolated from a variety of human tissue sources. The EST sequences and proteins encoded by them are predicted to have useful biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, immune stimulating or suppressing activity, haematopoiesis regulating activity, tissue growth activity, haemostatic activity, cactivity, receptor/ligand activity, anti-inflammatory activity, cadherin/tumour invasion suppressor activity, tumour inhibition activity. The EST sequences are also stated to be useful for gene
                                                                                                                                                                                                                                                                                                                                                                     New polynucleotides encoding human secreted proteins - dee.g. human blood, kidney, foetal lung, placenta, testes, ovary, pituitary, retina and colon cDNA libraries
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Spaulding V,
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                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                The present sequence represents a human expressed sequence tag (EST). The polynucleotide, which is a secreted EST, and the encoded protein are predicted to have useful biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, immune stimulating or suppressing activity, haematopolesis regulating activity, tissue growth activity, haematopolesis regulating chemotactic/chemokinetic activity, acciviny/inhibin activity, chemokinetic activity, and inflammatory activity, cadherin/tumour invasion suppressor activity, tumour inhibition activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; secreted protein; expressed sequence tag; EST; haematopoiesis; tissue growth; activin; inhibin; chemotaxis; chemokinesis; haemostatic; receptor; ligand; thrombolytic; anti-inflammatory; cadherin; anti-tumou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   V89271;
                                                                                                                                                                                                                                                                                                                                                                                                                       New polynucleotides encoding human secreted proteins - derived e.g. human blood, kidney, foetal lung, placenta, testes, brain, ovary, pituitary, retina and colon cDNA libraries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EST clone BY66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                V89271 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Agostino MJ, Jacobs K, Racie LA, Spaulding V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-APR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9845436-A2
                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CEMY ) GENETICS INST INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCCTCTGCTGTAAATGCAGGTCTCTTGGTATTTATTGAGCTTTTGTGGGACTGGTGGAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 therapy; ss.
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                                                          CTCGAGCCCTTTAATCTGACTTCGGAGCCCTCGGACTACGCTCTGGACCTCAGCACTTTC 444
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                                          CTICGAGCCCTTTAATICTGACTTCGGAGCCCTCGGACTACGCTCTGGACCTTCAGCACTTTIC 134
                                                                                                      169;
Similarity
                                                                                                                                                                            193
                                                                                                                                                                                                     The polynucleotide may also be useful for gene therapy
                                                                                                      Conservative
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98.3%;
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                                                                                                                                                                           39 C; 68 G;
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                                                                                                      0; Mismatches
                                                                                                                    Score 167.2; DB : Pred. No. 4.5e-35.
                                                                                                                                                                            51 T; 0 other;
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                                                                                                                                   DB 20;
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Sibson DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q77534;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human nucleic acid fragments, isolated from brain, adrenal the placenta or bone marrow comprise any of: (A) a sequence selected from (Q76401-Q77613), (B) an allelic variation of a sequence as described in (A), or (C) a sequence complemental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Brain; placenta; bone marrow; genetic analysis;
detection; homology; human; adrenal tissue; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleic acid fragment encoding for genetic analysis and \text{mapping}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-JUL-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 297 BP; 66 A; 117 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence known per se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Preferred sequences exhibit no more than 90% homology to a human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to (A) or (B).
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                                           181 CGCAGCCGCAGGGTTCTCTACCCTCGAGTGGTCCGGCGGCCAGCTGCCAGTCGAGGAACCG
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                                                                                            ctcccgaagcccacagcggcccctgccgggcaccccagcltc-ctcgcaggcaccaaaag
                                                                                                                  CTCCCGGAGCCCGCAGCGCCCTGCCGGGGCGCCCCAGCGCCTCTCGCGGGCACCGAAAG
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, Starkey M;
                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                    Score 151; DB 1 pred. No. 1e-30; 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to (A) or (B). Preferred sequences exhibit no more than sequence known per se.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human nucleic acid fragments, isolated from brain, adrenal tissue the placenta or bone marrow comprise any of: (A) a sequence selected from (076401-077613), (B) an allelic variation of a
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                                                                                                                                                                                                                                                                                                                       GCTGCCACCCGACCATGACCATCCTGCAGGCCCCGA----CCCCGGGCCCCCTCCACCATCC 73
                                                                                                                       CAGCGGCCCCTGCCGGGCGCCCAGCGCCTCTCGCGGGCACCGGAAAGCGGCAGCCGCAGGG
                                                                                                                                                                                                                                              CGGGACCCCGGCGGGGCTCCGGTCCTGAGATCTTCACCTTCGACCCTCTCCCGGAGCCCG
                                                                                                                                                                                                                                                                                             gctgcaaccaccccgtggccccctaccagccccaatctccaaaccccgcacgtcgatca
                                                 TITCTCTACCCTCGAGTGCTCCGGCGCCAGCTGCCAGTCGAGGAACCGAACCCAGC 248
                                                                                             caycogocotyc--gaaccotocaactogttcacacgogocgaaagcotattcccagga
                                                                                                                                                                                             tgacyccaccaacayctgcagcccctgagatcttcaccttagaccctctcccgaaycccy
                                                                                                                                                                                                                                                                                                                                                                                                  152;
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Starkey M;
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                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58 A; 117 C; 49 G;
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64.7%;
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                                                                                                                                                                                                                       Score 70.4; DB 13,
Pred. No. 1.9e-09;
""" matches 77;
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drenal tissue; ds.
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15-MAY-1998;
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21-OCT-1998;
27-OCT-1998;
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probe; detection; cancerous state; metastasis; identification;
breast cancer; oestrogen receptor-positive breast cancer; ther
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Lamson G, Drmanac R,
Leshkowitz D, Kita D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-MAY-1999;
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98US-0105234
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98US-0085537
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Randazzo F, Kennedy (
Crkvenjakov R, Dickso
Garcia V, Jones LW,
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R, Dickson M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Garcia PD, Suc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C, Pol D, Kassam
on M, Drmanac S, I
Stache-Crain B;
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Claim 1; Page 994; 1097pp; English

A00010 to A02716 represent polynucleotides isolated from cDNA libraries constructed from human colon cancer cell lines. The present invention also describes a method of detecting differentially expressed genes correlated with a cancerous state of a mammalian cell, comprising confecting at least one differentially expressed gene product in a test sample derived from a cell suspected of being cancerous, where detection of the differentially expressed gene product is correlated with a cancerous state of the cell from which the test sample was derived. The polynucleotides sequences can be used in a method for detecting conferentially expressed genes correlated with a cancerous state of a mammalian cell. The polynucleotides can also be used as probes for cetecting and mapping related genes. They can be used in diagnosis and correlated with a cancer, or responsiveness of cancer to therapy). This is particularly for breast concer, oestrogen receptor-positive breast cancer, oestrogen receptor-positive breast cancer, oestrogen receptorbreast cancer, lung cancer, and colon

Sequence 1000 BP; 21 A; 53 C; 574 G; 22 T; 330 other;

ç Query Match Best Local S Matches 47 CCCCGACCCCGGGCCCTCCACCATCCGGGGGGACCCCGGGGGGGCTCCGGTCCTGAGATCT 106 Similarity Conservative 35.98; Score 57.4; DB 21; pred. No. 9.6e-06; 0; Mismatches 286; DB 21; Length 1000; Indels · 0 Gaps

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밁 812 TCACCTITCGACCCTICITCCCGGAGCCCGCAGCCGCCCCTIGCCGGGCGCGCCCCAGCGCCTICITC 166

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A00010 to A02716 represent polynucleotides isolated from cDNA libraries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  colon cancer cell line polynucleotide sequence SEQ ID NO:2479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; colon cancer; tumour; diagnosis; gene expression product; probe; detection; cancerous state; metastasis; identification; breast cancer; oestrogen receptor-rositive breast cancer; therapy; oestrogen receptor-regative breast cancer; lung cancer; ss.
                                                                                                                  632 NCCCCNNCNNCCCNCCNNCNCCCNCCCNTCCTCNCCGNCCNCNNCNCCCNCNCCCNCNCCNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J, Innis MA, Garcia PD, Sudduth-Klinger
Randazzo F, Kennedy GC, Pot D, Kassam A;
Crkvenjakov R, Dickson M, Drnanac S, Lab
Garcia V, Jones LW, Stache-Crain B.
167 GCGGGCACCGAAAGCGCAGGCAGGGTTCTCTACCCTCGAGTGGTCCGGCGCCAGCTGC
                                                                                                                                            GCCAGATICCTGATGGCTGAAGAGGGTGTGCCGGCGCCCCTGCCTCCAGAGGACGCCCCTA
                                                                                                                                                                     CAGTICGAGGAACCGAACCCAGCCAAAAGGCTTCTCTTTTTTGCTCTCACCATCGTCTTCT
                                                                                                                                                                                                347 ACGCCGCATCCCTGGCGCCCAGCCCTGTGTCCCCCGTCCTCGAGCCCTTTAATCTGACTT
                                                                                                                                                                                                                          512 CCCCNCGCCNCCNCCCCCNNCCCCCNGCGNCCTNNCNCCCNNCGNCCCCCNCGCCTCCNCNC
                                                                                                                                                                                                                                                   407 CGGAGCCCTCGGACTACGCTCTGGACCTCAGCACTTTCCTCCAGCAACACCCGGCCGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to determine cancerous states of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 995-996; 1097pp; English.
                                                                                                                                                                                                                                                                                                                       392 CCCNNCNNCCCCCNCNCNCCCCC 367
                                                                                                                                                                                                                                                                                                        467 TCTAACTGTGACTCCCGGCACTCCCC
                                                                                                                                                                                                                                                                                                                                                                                                     ВР
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98US-0085537.
98US-0085696.
98US-0105234.
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Lamson G, Drmanac R,
Leshkowitz D, Kita D,
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15-MAY-1998;
21-OCT-1998;
27-OCT-1998;
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constructed from human colon cancer cell lines. The present invention also describes a method of detecting differentially expressed genes.

Correlated with a cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample derived from a cell suspected of being cancerous, where detection of the differentially expressed gene product is correlated with a cancerous state of the cell from which the test sample was derived. The polynucleotides sequences can be used in a method for detecting differentially expressed genes correlated with a cancerous state of a mammalian cell. The polynucleotides can also be used as probes for detecting and mapping related genes. They can be used in diagnosis and prognosis of diseases and disorders (e.g. identification of prognosis of diseases and disorders (e.g. identification of responsiveness of cancer to therapy). This is particularly for breast cancer, oestrogen receptor-positive breast cancer, oestrogen receptor-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45 GGCCCCGACCCCGGCCCCTCCACCATCCCGGGACCCCGGCGGGGCTCCGGGCTCCTGAGAT 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    345 TAACGCCGCATCCCTGGCGCCCACCCCTGTGTCCCCCGTCCTCGAGCCCTTTAATCTGAC 404
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detection, mapping, tissue typing, profiling: forensic, cancer,
genetic analysis, colorectal cancer, breast cancer, lung cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               105 CTTCACCTTCGACCTCTCCCGGAGCCCGCAGCGGCCCCTGCCGGGCGCCCCAGCGCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    165 TCGCGGGCACCGAAAGCGCAGCGCAGGGTTCTCTACCCTCGAGTGGTCCGCGCCCAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        580 CCCCNCCCNNCCNNNNCNCNNNNNCNCCCCNNNNANCNNCGNNGNNCGNCCCCCCNNNNN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                405 TTCGGAGCCCTCGGACTACGCTCTGGACCTCAGCACTTTCCTCCAGCAACACCCGGCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1218;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human gene expression product cDNA sequence SEQ 1D NO:4735
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                      Seguence 1218 BP; 9 A; 31 C; 494 G; 37 T; 647 other;
                                                                                                                                                                                                                                                                                                                                                                                                               Score 55.2; DB 21;
Pred. No. 4e-05;
0; Mismatches 343;
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Best Local Similarity 26.9%;
Matches 126; Conservative
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us-08-799-910-9.rng

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The present invention describes a library of human polynucleotides comprising the sequences given in 212512 to 21779. Also described is a method of detecting differentially expressed genes correlated with the cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample from a cell suspenced of being cancerous, where the gene product is encoded by one of the 548 polynucleotide sequences given in 212532 to 21779. The be used for a variety of purpose, e.g. detection of expression levels, mapping, tissue typing or profiling, forensics, genetic analysis and detection of polymorphisms. Polypeptides encoded by the polynucleotides can be used for aising antibodies for experimental, diagnostic and therapeutic purposes. The polynucleotides may also be used to construct encoded protein); and to detect differences in expression levels between two cells (e.g. to identify abnormal or diseased tissue in a human, to cancer); The polynucleotides may also a disease such as cancer). The polynucleotides of the invention are especially used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cancer). The polynucleotides of the invention are especially used in the diagnosis, prognosis and management of colorectal cancer, breast cancer, and lung cancer. The polynucleotides can also be used to screen for
                                                                                                                                                                                                                                                                                                    CINVENJANOV K, DILLADOM K, CONTROLL K, Innis MA;
Escobedo J, Garcia PD, Garcia V, Giese K, Innis MA;
Jones WL, Kassam A, Kennedy GC, Kita D, Labbt 1;
Lamson G, Leshkowitz D, Pot D, Randazzo F, Reinhard C;
Stache-Crain B, Sudduth-Klinger J, Williams LT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel human genes and their expression products which are differentially expressed in different cell types
                                                                                                                                                                                                                                                                                          Drmanac S;
se K, Innis MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1337 BP; 42 A; 577 C; 27 G; 22 T; 669 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 2250-2251; 2479pp; English.
                                                                                                                                                                                                                                                                                  Dickson M, Drmanac R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            peptide analogues and antagonists.
                                                                                                                98US-0080666.
98US-0072910.
98US-0075954.
98US-0080114.
                                                                             99WO-US01619
                                                                                                                                                                                                                                       CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-494092/41.
                                                                                                                                                                                                                                   (CHIR ) CHIRON COR (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                              Crkvenjakov R,
WO9938972-A2
                                                                         28-JAN-1999;
                                                                                                                                                                         31-MAR-1998;
03-APR-1998;
                                      05-AUG-1999
                                                                                                                  03-APR-1998
                                                                                                                                       28-JAN-1998
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67 ACCATICCCGGGACCCCGGGGGGGTCCTGAGATCTTCACCTTCGACCCTCTCCCG 126 813 cecenencencenennenencencecenennnnnenenecennnenen 872 GAGCCCGCAGCGGCCCCTGCCGGGCCCCCCAGCGCCTCTCGCGGGCACCGAAAGCGCAGC 186 7 CACTUTGGCAGCTGCCACCGACCATGACCATCCTGCAGGCCCCGACCCCGGGCCCCTCC 66 187 CGCAGGGTTCTCTACCCTCGAGTGGTCCGGCGCCAGCTGCCAGTCGAGGAACCGA DB 20; Length 1337; Score 52.2; DB 20; Length Pred. No. 0.00026; 0; Mismatches 393; Indels ö Query Match 4.3%; Best Local Similarity 22.5%; Matches 114; Conservative **Ouery Match** 753 127

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933 cภกกกษณกษณกษณกายกากกากกระบากการกระบากกระบากกระบากกระบากกระบากกระบากกระบากกระบากกระบากกระบากกระบากกระบากกระ

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A00010 to A02716 represent polynucleotides isolated from cDNA libraries constructed from human colon cancer cell lines. The present invention also describes a method of detecting differentially expressed genes correlated with a cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample derived from a cell suspected of being cancerous, where detection of the differentially expressed gene product is correlated with a cancerous state of the cell from which the test sample was derived.
                                                                                     247 GCCAAAAGGCTTCTCTTTCTGCTGCTCACCATCGTCTTCTGCCAGATCCTGATGCTGAA 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mamma]jan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sudduth-Klinger 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Human colon cancer cell line polynucleotide sequence SEQ ID NO:2529.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human, colon cancer; tumour; diagnosis; gene expression product; probe; detection; cancerous state; metastasis; identification; breast cancer; oestrogen receptor-positive breast cancer; therapy; oestrogen receptor-negative breast cancer; s.
                                                         GAGGGTGTGCCGGCGCCCCTGCCTCCAGAGGACGCCCCTAACGCCGCATCCCTGGCGCCC
                                                                                                                 367 ACCCTGTGTCCCCGTCCTCGAGCCCTTTAATCTGACTTCGGAGCCCTCGGACTACGCT
                                                                                                                                                                             427 CTGGACCTCAGCACTTTCCTCCAGCAACACCCGGCCTTCTAACTGTGACTCCCCGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Escobedo J, Innis MA, Garcia PD, Sudduth-Klinger Jiese K, Randazzo F, Kennedy GC, Pot D, Kassam A; nanac R, Crkvenjakov R, Dickson M, Drmanac S, Labakita D, Garcia V, Jones LW, Stache-Crain B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polynucleotide library used to determine cancerous states of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ž
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                                                                                                                                                                                                                                                                    1233 cenceenennennennencene 1259
                                                                                                                                                                                                                                     487 CTCCCCAAAAAGAATCCGAAAAACCAC 513
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98US-0085537.
98US-0085696.
98US-0105234.
                                                                                                                                                                                                                                                                                                                                            A02538 standard; cDNA; 1126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORP.
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                                                                  detecting and mapping related genes. They can be used in diagnosis and prognosis of diseases and disorders (e.g. identification of prognosis of pre-metastatic cancerous states, stages of cancer, or responsiveness of cancer to therapy). This is particularly for breast cancer, oestrogen receptor-positive breast cancer, oestrogen receptor-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          429 ---CCANICCCCTGCCTCGTTTCANCCGGTTGCCTCTCGCNNNCCCNCNCCCTNCC 373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73 CCGGGACCCCGGCGGGGTCCTGAGATCTTCACCTTCGACCCTCTCCGGGAGCCC 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          372 CGCCTCCNCCTCTCNCCCNCGGCTACNCCCNCCCACCGCNCCCNCCNCCCTNCGCNTCCC 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      313 GTGCCGGCCCCCTGCCTCCAGAGGACGCCCCTAACGCCGCATCCCTGGCGCCCACCCCT 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     312 CCCCCGGGGNNCCNGCGGCNGCCTAAAACCCCNANNAAAGTNCCCCNCGCCCCCCCCNNG 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       373 GTGTCCCCCCCTCCTCGAGCCCTTTAATCTGACTTCGGAGCCCTCGGACTACGCTCTGGAC 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 252 NCNNNCGCCNCCCNACGCCNCTCCNGCCCCNCNCCCNGNCTNCCCCAAGGTCCNAAAA 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              433 CTCAGCACTTTCCTCCAGCAACACCCGGCCGCCTTCTAACTGTGACTCCCCGCACTCCCC 492
                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                       13 CGCAGCTGCCACCCGACCATGACCATCCTGCAGGCCCCGGACCCCGGGCCCCCTCCACCATC 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The polynucleotides sequences can be used in a method for detecting differentially expressed genes correlated with a cancerous state of mammalian cell. The polynucleotides can also be used as probes for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             193 GTTCTCTACCCTCGAGTGGTCCGGCGCCCAGCTGCCAGTCGAGGAACCGAACCCAGCCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               493 AAAAAGAATCCGAAAAAACCACAAAGAACACCAGGCGTAACCTGGTGCGCGAGAGCGTATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           253 AGGCTTCTCTTTCTGCTGCTCACCATCGTCTTCTGCCAGATCCTGATGGCTGAAGAGGGT
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                                                                                                                                                                                                                                                                                                              DB 21; Length 1126;
                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                      Sequence 1126 BP; 101 A; 102 C; 575 G; 57 T; 291 other;
                                                                                                                                                                                            negative breast cancer, lung cancer, and colon cancer
                                                                                                                                                                                                                                                                                                           Query Match
4.0%; Score 49.6; DB 21;
Best Local Similarity 33.2%; Pred. No. 0.0012;
Matches 192; Conservative * 0; Mismatches 383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          553 CCCAACTGGGACTTCCGAGGCAACTTGAACTCAGAACAC 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72 NNTNCCNNNCNNCCCCTNNNCNCNNNCNNNCNNCNC 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T20789;
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                                                                                                                                                                                                                                                                                                                                                                                                                      A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 783 "GS" sequences given in T19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA which is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(7) as the sole primer. Since the 3'-untranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cyclic nucleotide-associated protein-2; CNAP-2; human; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for
                                                                                                                                                                                                                                                                                            Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1158 GATCGCCTAGTATGTTCTGTGAACACAAAATAAAATTGATTTACTGTCAAAAA 1210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequences) as a means of diagnosing abnormal cell function or recognising different cell types.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human cyclic nucleotide-associated protein-2 (CNAP-2) cDNA.
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94.3%; Pred. No. 0.00069;
iive 0; Mismatches 3
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                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 723; 2245pp; Japanese.
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                                                                                           94WO-JP01916.
                                                                                                                          93JP-0355504.
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Best Local Similarity 94.39
Walches 50; Conservative
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                                                                                                                                                                                                                                                           WPI; 1995-206931/27.
                                                                                                                                                               (MATS/) MATSUBARA K.
                                                                                                                                                                                   OKUB/) OKUBO K.
                                                                                                                                                                                                                        Matsubara K,
                                                                                                                          12-NOV-1993;
               WO9514772-A1
                                                                                         11-NOV-1994;
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                                                    01-JUN-1995
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Homo sapiens

us-08-799-910-9.rng

1087 cctgtgaagcccacatccctggaaaccccctcggcccttgctgagccgclgcgtctcc 1146

GCCGCAGGGTTCTCTACCCTCGAGTGGTCCGGCGCCAGCTGCCAGTCGAGGAACCGAACC 244

1147 atgccaggggacatctcaggct--tgcagggtggcccccgctccgacttcgacatggcct 1204

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305 AAGAGGGTGTGCCGGCCCCCTGCCTCCAGAGGACGCCCCTAACGCCGCATCCCTGGCGC 364

245 CAGCCAAAAGGCTTCTTTTTTGCTGCTCACCATCGTCTTCTGCCAGATCCTGATGGCTG 304

1205 atgagogigycoggaictocogigicocigoaggaagaggocicoggggggicociggoag 1264

365 CCACCCCTGTGTCCCCCGTCCTCGAGCCCTTTAATCTGACTTCGGAGCCCTCGGACTAC 423

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Page 10

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The Las Instance town the management of the state of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated cyclic nucleotide associated proteins useful for preventing, diagnosing and treating cell proliferative, autoimmune/inflammatory, neurological, vision, reproductive and smooth muscle disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is the cDNA encoding human cyclic nucleotide associated protein-2 (CNAP-2), identified in Incyte clone 3149674, that is isolated from ADRENONO4 cDNA library. It is expressed in
                                                                   /poroduct= "Human CNAP-2 protein"
/note= "Shares 24% identity to Aquifex pyrophilus
esterase 28LC"
                                                                                                                                                                                                                                                                                                                                                                /bound_molety= "Primer or Probe"
/note= "Useful for amplification or hybridisation
techniques"
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                                                                                                                                                                                                                                                       /*tag= c
/product= "Mature CNAP-2 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Corley NC,
     Location/Qualifiers
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                                                                                                                                                                                                      /*tag=
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                                                                                                                                                                                                                                                                                                         misc_binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-SEP-1998;
                                                                                                                                                                         sig_peptide
                                                                                                                                                                                                                          mat_peptide
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2 967 accagecetgtgegggetecaagagaatggteageaceteagetacagaegageeagg 1026 73 CCGGGACCCCGGCGGGCTCCGGTCCTGAGATCTTCACCTTCGACCCTCTCCCG----- 126 907 ctcttcagccacgagatccagccctgcgtctgttcccagccccggcclcccaactcgc 966 --GAGCCCGCAGCGCCCCTGCCGGGCGCCCCCAGCGCCTCTCGCGGGCACCGAAAGCGCA 184 13 CGCAGCTGCCACCGGACCATGACCATCCTGCAGGCCCCGACCCCGGGCCCCCTCCACCATC 72 DB 21; Length 4228; Score 47.8; DB 21; Length Pred. No. 0.0063; 0; Mismatches 207; Indels .; 0 3.9%; 202; Conservative Similarity Query Match Local Best Loca Matches 127 ద

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The specification describes antisense oligonuclectides (x52869-x5527) directed against at least 2 mRNAs selected from target genes, coding and non-coding regions of RNAs corresponding to target genes, gene initiation codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'-end and the juxta-section between coding and non-coding regions and all segments of RNAs encoding proteins associated with one or more diseases, conditions or mixtures. The antisense oligonucleotides of specifically X55180-271 can be used for the antisense treatment of diseases and conditions. Typical diseases and conditions are those associated with impaired respiration and inflammation, including lung diseases, pulmonary vasoconstriction, inflammation,
                                                                                                                                                                                   Antisense oligonucleotide; multiple target; antisense treatment; impaired respiration; inflammation; lung disease; pulmonary vasoconstriction; inflammation; allergic rhinitis; acute asthma; allergy; asthma; impeded respiration; respiration; pains; pain; cystic fibrosis; pulmonary distress syndrome; pain; cystic fibrosis; pulmonary bypertension; pulmonary vasoconstriction; emphysema; chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma; colon cancer; breast cancer; lung cancer; pancreatic cancer; hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New antisense oligonucleotides used in treatment of, e.g. pulmonary vasoconstriction
                                                                                                                                                   Human adenosine Al receptor antisense oligonucleotide fragment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 37; 120pp; English.
                                   X53491 standard; DNA; 114955 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98WO-US19419.
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97US-0059160.
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                                                                                                             05-JUL-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                prostate cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-229400/19.
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17-SEP-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
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                                                                         X53491;
RESULT 14
                 x53491/c
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ullergic rhinitis, acute asthma, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary by pulmonary vasconstration, emphysema, chronic obstructive pulmonary visease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g. colon cancer, breast cancer, lung cancer, pancreatic ancer, hepatocallular carcinoma, kidhey cancer, melanoma, hepatic metastases, as well as all types of cancers which may metastasize or have metastasized to the lungs, including breast and prostate cancer.
                                                                                                                                                                                                                                                                             108409 G-GCGCCGCCCCCCCCCCCCCNHNNNSGCGAGCCAGCCGCCCCCCCCCCCCCCCCNHNNNS 108351
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                                                                                                                                                                                                                                                  13 CGCAGCTGCCACCGACCATGACCATCCTGCAGGCCCCGGACCCCGGCCCCTCCACCATC 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human colon cancer cell line polynucleotide sequence SEQ ID NO:2495
                                                                                                                                         Sequence 114955 BP; 6071 A; 29417 C; 36712 G; 21328 T; 21427 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probe; detection; cancerous state; metastasis; identification; breast cancer; oestrogen receptor-positive breast cancer; therapy; oestrogen receptor-negative breast cancer; lung cancer; ss.
                                                                                                                                                                                                                                                                                                                                 GCAGGGGGCCCTGCCGGGGGGCCTTTCGCGGGCACCGGAAAGCG--CAGCCGCA
                                                                                                                                                                                                                                                                                                                                                                                              108469 CCCCCCCCCCCNNHNNNSCGAGCCAGGCCCCCCCCCCCCCCCCCCCANHNNNSGCAGCCA
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                                                                                                                                                                                      Length 114955;
                                                                                                                                                                                                                     21; Mismatches 210; Indels
                                                                                                                                                                                      DB 20;
                                                                                                                                                                                                      Pred. No. 0.041;
                                                                                                                                                                                      3.8%; Score 47.2;
38.9%; Pred. No. 0.0
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98US-0085537.
98US-0085696.
98US-0105234.
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                                                                                                                                                                                                                   149; Conservative
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15-MAY-1998;
21-OCT-1998;
27-OCT-1998;
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A00010 to A02716 represent polynucleotides isolated from cDNA libraries constructed from human colon cancer cell lines. The present invention also describes a method of detecting differentially expressed genes correlated with a cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample derived from a cell suspected of being cancerous, where detection of the differentially expressed gene product is correlated with a cancerous state of the cell from which the test sample was derived. The polynucleotides sequences can be used in a method for detecting differentially expressed genes correlated with a cancerous state of the polynucleotides can also be used as probes for mammalian cell. The polynucleotides can also be used as probes for
                                                                          J, Innis MA, Garcia PD, Sudduth-Klinyer J;
Randazzo F, Kennedy GC, Pot D, Kassam A;
Crkvenjakov R, Dickson M, Drmanac S, Labat I;
Garcia V, Jones LW, Stache-Crain B;
                                                                                                                                                                                                                 Polynucleotide library used to determine cancerous states of mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    detecting and mapping related genes. They can be used in diagnosis and prognosis of diseases and disorders (e.g. identification of pre-metastatic cancerons states, stages of cancer, or responsiveness of cancer to therapy). This is particularly for breast cancer, oestrogen receptor-positive breast cancer, oestrogen receptor-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               099
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          negative breast cancer, lung cancer, and colon cancer.
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d C, Giese K, R?
G, Drmanac R, C
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                  CHIRON CORP
HYSEQ INC.
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Best Local Similarity
Matches 155; Conserv
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                                                                                             Reinhard C
Lamson G,
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                  (CHIR ) (HYSE-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          homo
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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EMBL; AF039067; AAC32558.1; -.
EMBL; AF071596; AAC72344.1; -.
SEQUENCE 193 AA; 21028 MW; 7927D9D3FFBC7C57 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1998 (TrEMBLrel. 08, 01-NOV-1998 (TrEMBLrel. 08, 01-MAY-1999 (TrEMBLrel. 10;
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Best Local Similarity 100.
Matches 86; Conservative
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IEX-1L.
075353
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075353
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Q69138 human herpe
Q9ymx0 lymantria d
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caenorhabdi
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O94878 homo sapien
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Q9xy65 euplotes cr
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                                                                                                                                                                                                                                     442
1 VRROLPVEEPNPAKRLLFLL......EPSDYALDLSTFLQQHPAAF
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Copyright (c) 1993 - 2000 Compugen Ltd
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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NCBI_TaxID=5936;
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**REDLINE-94150718; PubMed-7906398;

**MEDLINE-94150718; PubMed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nagase T., Ishikawa K., Suyama M., Kikuno R., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; Prediction of the coding Sequences of unidentified human genes. XI. The complete Sequences of 100 new cDNA clones from brain which code for large proteins in vitro."; For large proteins in vitro."; EMBL: AB018324: BAA34501.1; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 VEEPNPAKRLLFL----LLTIVFCQILMAEEGVP-----APLPPEDAPNAASLAP---- 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 637;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   637 AA; 70516 MW; DEBFB005BA9B9CDD CRC64;
01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 84.5; DB 4;
Pred. No. 0.41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          102 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
19.1%; Score 84.5; D
Best Local Similarity 33.3%; Pred. No. 0.41
Matches 30; Conservative 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53 TPVSPVLEPFNLTSEPSDYALDLSTFLQQH 82
                                                                                                                                                                                                              TISSUE-BRAIN;
MEDLINE-99087487; PubMed-9872452;
                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR01217; PRICHEXTENSN.
                                                       KIAA0781 PROTEIN (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, R160.5 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 368:32-38(1994).
                                                                                                Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                            IPR002965
                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                         NCBI_TaxID-9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                               K1AA0781.
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11. NPAKRILETL-----LTIVFCQILMAEEGVPAPLPPEDAPNAASLAPTPVSPVLEPFN-- 63
                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-ST9, ST11;
MEDLINE-97206572; PubMed-9172827;
Ling Z., Ghosh S., Jacobs M.E., Klobutcher L.A.;
Conjugation-specific genes in the ciliate Euplotes crassus: gene expression from the old macronucleus.";
J. Eukaryot. Microbiol. 44:1-11(1997).
                                                                                                                                                                                                                                                                                            11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 452;
                                                                                                                                                                                                                                                                                     28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30; Indels
Nelson J., Gattung S.;
"The sequence of C. elegans cosmid R160.";
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                              to the EMBL/GenBank/DDBJ databases
                                                                                                                    Waterston R.;
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ database
EMBL; AF099001; AAC68734.1; -
SEQUENCE 102 AA; 11426 MW; AFD366C3932EB26C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               452 AA; 49763 MW; A5C13C49ECA998EA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
05-MAY-2000 (TrEMBLrel. 13, Last annotation update)
CONDAB.
EUPlotes crassus.
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Best Local Similarity 34.5%; Pred. No. 0.61;
Matches 30; Conservative 10; Mismatches 30;
                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity 24.7%; Pred. No. 0.13;
Matches 19; Conservative 19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            368 SAPSLEPSSTLASEPRDIIPDPSAALK 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55 VSPVLEPFN-LTSEPSDYALDLSTFLQ 80
                                                                                                                                                                                                                                                                                                                                                                                                                               66 QVV(KIDPTESDVDMTS 82
                                                                                                                                                                                                                                                                                                                                                                                                    64 ---LTSEPSDYALDLST 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                            SEQUENCE FROM N.A. STRAIN=BRISTOL N2;
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Q9XY65
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4299 LKQESPAPEPPTQHRYTYNVSNLDVRQL-----SAPPPEEPSPPFSPLAPSPAFF 4351
                                     "Structure and expression pattern of human ALR, a novel gene with strong homology to ALL-1 involved in acute leukemia and to Drosophila trithorax.";
                    RRQLPVEEPNPAKRLLFLLLTIVFCQILMAEEGVPAPLP-----PEDAPNA-SLAPT 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 VRROLPVEEPNPAKRLLFLLTIVFCQILMAEEGVPAPLPPEDAPNAASLAPTPVSPVLE 60
                                                                                                                                                                                                                                                                                                                                                                   Prasad R., Zhadanov A.B., Sedkov Y., Bullrich F., Druck T.,
Rallapalli R., Yano T., Alder H., Croce C.M., Huebner K., Mazo A.,
                                                                                                                                                                                                                                                                                       Futeleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Sukaryota, Metazoa, Chordata, Cranlata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17.6%; Score 78; DB 4; Length 4957; 30.4%; Pred. No. 17; tive 12; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PRO1217; PRICHEXTENSN, PROSITE; PS00398; RECOMBINASES_2; UNKNOWN_1. SEQUENCE 4957 AA; 531848 MW; 1026562E1419CEBD CRC64;
                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                           PRT; 4957 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5262 AA
                                                                                           54 PVSPVLEPFNLTSEPSDYALDLSTFLQQHPA 84
                                                                                                                                                                                                      Created)
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                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE-97308; MEDLINE-97308;
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EMBL: AF010404; AAC51735.1; ...
INTERPRO; IPR001214; ...
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                                                                                                                                                                          PRELIMINARY;
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                                                                                                                                                                                                   01-JAN-1998 (TrEMBLrel. 01-JAN-1998 (TrEMBLrel. 01-OCT-2000 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PFAM; PF00628; PHD; 3.
                                                                                                                                                                                                                                                                    Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4352 PLVELPTEP 4360
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Best Local Similarity
Matches 21; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 PF-NLTSEP 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                              NCBI_TaxID-9606;
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01-JAN-1998 (
01-JAN-1998 (
01-OCT-2000 (
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014687
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                                                                                                           Gaps
                                                                                                                                                                             STRAIN=G1;
BDD.IRE=29206572; PubMed=9172827;
Ling 2., Ghosh S., Jacobs M.E., Klobutcher L.A.;
Conjugation-specific genes in the ciliate Euplotes crassus: gene expression from the old macronucleus.";
J. Eukaryot. Microbiol. 44:1-11(1997).
                                                                                                                                                                                                                                                                                                                 Klobutcher L.A., Gygax S.E., Podoloff J.D., Vermeesch J.R., Price C.M., Tebeau C.M., Jahn C.L.;
Price C.M., Tebeau C.M., Jahn C.L.;
Conserved DNA sequences adjacent to chromosome fragmentation and telomere addition sites in Euplotes crassus.";
Nucleic Acids Res. 26:4230-4240(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Aviadenovirus.
NCBI_TaxID=66295;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 302;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 468;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=G1;
Ling 2., Klobutcher L.A.;
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF061334; AAD31724.1; -.
SEQUENCE 468 AA; 51457 MW; 70996125317C592A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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Ojkic D., Nagy E.;
"The DNA scquence of fowl adenovirus B.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL: AF083975; AAD50348.1; -.
SEQUENCE 302 AA; 34763 MW; BF34DF42FF026CCC CRC64;
                          Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
10-MAY-2000 (TrEMBLrel. 13, Last annotation update)
13 KDA PROTEIN 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18.2%; Score 80.5; DB 12; 26.4%; Pred. No. 0.51; Live 26; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18.4%; Score 81.5; DB 5; 34.5%; Pred. No. 0.63; iive 10; Mismatches 30;
  468 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          384 SAPSLEPSSTLASEPRDIIPDPSAALK 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55 VSPVLEPFN-LTSEPSDYALDLSTFLQ 80
                                                                                                                                                                                                                                                                                                    MEDLINE*98391748; PubMed*9722644;
                        01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-MAY-2000 (TrEMBLrel. 13, CONZAB PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30; Conservative
PRELIMINARY;
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Matches 24, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Rest Local Similarity
                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                              Euplotes crassus
                                                                                                                                     NCBI_TaxID=5936;
                                                                                                                        Euplotes
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Burkhart-Schultz K., Gordon L., Dias J., Ramirez M., Stilwagen S.,
Phan H., Velasco N., Do L., Regala W., Terry A., Garnes J.,
Danganan L., Erler A., Christensen M., Georgescu A., Avila J., Liu S.,
Attix C., Andreise T., Trankheim M., Amico-Keller G., Coefield J.,
Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Kronmiller B.,
Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,
                                                                         "Structure and expression pattern of human ALR, a novel gene with strong homology to ALL-1 involved in acute leukemia and to Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 VRROLPVEEPNPAKRLIFILLTIVFCQILMAEEGVPAPLPPEDAPNAASLAPTPVSPVLE 60
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Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,
Burkhart-Schultz K., Gordon L., Dias J., Brower A., Ramirez M.,
Stilwagen S., Phan H., Velasco N., Do L., Regala W., Terry A.,
Garnes J., Danganan L., Erler A., Christensen M., Georgescu A.,
Avila J., Liu S., Attix C., Andreise T., Trankheim M.,
Ganco-Keller G., Coefield J., Duarte S., Lucas S., Bruce R.,
Thomas P., Quan G., Kronmiller B., Arellano A., Sanders C., Ow D.,
Nolam M., Trong S., Kobayashi A., Olsen A.S., Carrano A.V.;
"Sequence analysis of an -1.5 Mb contig in 19913:1 between OLFR and
                   Prasad R., Zhadanov A.B., Sedkov Y., Bullrich F., Druck T.,
Rallapalli R., Yano T., Alder H., Croce C.M., Huebner K., Mazo A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence analysis of a 3.5 Mb region in 19p13.1 between OLFR and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     U1-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
HUMAN HOWOLOG OF MUS MUSCULUS WIZL PROTEIN (HUMAN HOMOLOG OF MUS
MUSCULUS WIZZ PROTEIN) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                          17.6%; Score 78; DB 4; Length 5262; 30.4%; Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                               28; Indels
                                                                                                                                                                                                                                                                                                                 RECOMBINASES_2; UNKNOWN_1.
\(\text{A}\); 564181 MW; 26B7C74CAD417E44 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                             21; Conservative 12; Mismatches
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01-MAY-1999 (TrEMBLrel. 10, Last seq
01-JUN-2000 (TrEMBLrel. 14, Last anno
MEDL.INE=97388474; Pubmed=9247308;
                                                                                                                           Oncogene 15:549-560(1997).
EMBL: AF010403; AAC51734.1; -.
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PROSITE; PSO0398; RECOMBINASES
SEQUENCE 5262 AA; 564181 MW
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                                                                                                                                                                                                                    INTERPRO; IPR001965; -
INTERPRO; IPR002965; -
PFAM; PF00628; PHD; 5.
PFAM; PF00856; SET; 1.
                                                                                                                                                                                                       IPR001841; -.
                                                                                                                                                                INTERPRO; IPRO01214;
INTERPRO; IPR001822;
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                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
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                                                                                                              trithorax.
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RA Manniez-2019006; Pubmed=10731132;
RA Admans M.D., Celniker S.E., Liplk R.N. Evans C.A., Gocayne J.D.,
Radams M.D., Celniker S.E., Richards S., Abburner M., Henderson S.N.,
Suction G.G., Worthan J.R., Yandell M.D., Zahang O., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Maril J.F., Agbayani A., An H. J., Andrews-Pfannkoch C., Baldwin D.,
RA Abril J.F., Agbayani A., An H. J., Andrews-Pfannkoch C., Baldwin D.,
RA Abril J.F., Agbayani A., An H. J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Baytaktargqlu L., Beasley E.M.,
RA Borkova D., Botchan M.R., Bouck J., Baytaktargqlu L., Beasley E.M.,
RA Borkova D., Botchan M.R., Bouck J., Baytaktargqlu L., Dashakov S.,
RA Glerty J.M., Cawley S., Dalike C., Davenport L.B., Davfes P. C.,
RA Glerty J.M., Cawley S., Dalike C., Davenport L.B., Davfes P.,
RA Glodek M., Delother A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Borkova D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Well M., Ilasser K.,
Alali M., Kallush F., Karpen G.H., Kee Z., Kennison J.A., Ketchum K.A.,
RA Hostin D., Houston K.A., Howland T.J., Wall M., Ilashy D., Lai Z.,
RA Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Barko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Rattei B. Mcntosh T.C., McLeod M.P., Mchherson D.,
RA Balati M., Mulshina N.V., Mobarry C., Morris J., Moshrefi A.,
Ralnert K., Remington K.A., Nixon K., Weiseker D.R., Smith T.,
Spier E., Spradling A.C., Stapleton M., Stupski M.P., Smith T.,
Wallams S.M., Woodage T., Worley G.M., Weissenbach J.,
Walliams S.M., Woodage T., Worley K.C., Will D., Yang S., Yao Q., Zhon G.,
Rabang C., Yen R., Reinstond M., Zhong S., Zhu X., Zhu X., Zhu X., Zhun G., Zhan R., Zhong Y., Zhong W., Zhong W., Zhong X., Zhu X., Zhung C., Zhan R., Zhong Y., Zhong W., Zhong W., Zhong X., Zhu X., Zhong Y., Zhong Y., Zhong W., Zhong X., Zhu X., Zhong Y., Zhong Y., Zhong Y., Zhon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera: Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                   Gaps
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80
                                                                                                                                                                                                                                                               DB 4; Length 1568;
                                                                                                                                                                                  1568 AA; 170077 MW; 74F0D34D45F565D0 CRC64;
                                                                                                                                                                                                                                                                                                           17; Indels
                                                                                                                                                                                                                                                                                                                                                                            30 MAEEGVPAPLPPEDAPNAASLAPTPVSPVLE-----PFNLTSEP 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
01.MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
                                                                                                                                                                                                                                                          17.4%; Score 77; DB 4 40.4%; Pred. No. 6.6; ive 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2424 AA
                                                                          PFAM; PF00096; Zf-C2H2; 10.
PROSITE; PS00028; ZINC_FINGER_C2H2; 8.
Zinc-finger; Metal-binding; DNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=20196006; Pubmed=10731132;
EMBL; AC007059; AAD19818.1; -. EMBL; AC006128; AAC97985.1; -. EMBL; AC007059; AAD19817.1; -.
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Best Local Similarity 40.41
Matches 19, Conservative
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                                                                  INTERPRO, IPRO00822;
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NCBI_TaxID=7227
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01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
                                  CG2258 PROTEIN.
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TT 267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neisseria meningitidis (serogroup B)
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
NCBL_Tax(D=491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                28 ILMAEEGVPAPLPPEDAPNAASLAPTPVSPVLEPFNLTSEPS-DYALDLSTFLQQHPAAF 86
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0
                                                                                                                                                                                                                                                                                                                                                             Score 77; DB 5; Length 2424;
Pred. No. 10;
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                                                                                                                                                                                                                                                                                            267616 MW; 8AD62AA33F9AA5D0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               148 AA; 16332 MW; 28E9B40D502D80B4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2000 (TrEMBLrel. 15, Last sequence update) 01-OCT-2000 (TrEMBLrel. 15, Last annotation update) ACYL COA THIOESTER HYDROLASE FAMILY PROTEIN.
Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
"The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
EMBL, RE003484; AAF47980.1; -.
HSSP: P08799; IMND.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 FLLLTIVFCQILMAEEGVPAPLPPEDAPNAASLAPTP 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           148 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                801 AA.
                                                                                                                                                                                                                                                                                                                                                                                                      7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                      Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-0CT 2000 (TFMBLrel. 15, Created) 01-0CT-2000 (TFMBLrel. 15, Last seq 01-0CT-2000 (TFMBLrel. 15, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-MC58 / SEROGROUP B;
MEDLINE-20175755; Pubmed-10710307;
                                                                                                                                                                                             PFAM; PF00063; myosin_head; 1.
PFAM; PF00612; IQ; 3.
                                                                                                                                                                                                                                              PFAM; PF00784; MYTH4; 1.
PRINTS; PR00193; MYOSINHEAVY.
SEQUENCE 2424 AA; 267616 M
                                                                                                                 FLYBASE; FBgn0030252; CG2174.
                                                                                                                                                                                                                                                                                                                                                          17.4%;
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TICR; NMB0925; -.
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                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 36.70
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                   INTERPRO; IPR000048; -. INTERPRO; IPR001609; -. INTERPRO; IPR001609; -.
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les 15; Conserv
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09JZR7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09W3K6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09W3K6
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Q9W3K6
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Adding M.D., Celoliker S.E., Lip P.W., Hoskins R.A., Gocayne J.D., R.A. Adding M.D., Celoliker S.E., Lip P.W., Hoskins R.A., Golle R.F., George R.A., Lewis S.E., Richards S., Ashburner M. Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X., Button G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X., Brandon R.C., Rogers Y.H.C., Blazel R.G., Champe M., Petelifer B.D., RA Man K.H., Doyle C., Batton G.R., Miklos G.L.G., Ballew R.M., Basus A., Barandale J., Bayarktaroglu L., Heasley E.M., Ballew R.M., Basus A., Barandale J., Bayarktaroglu L., Heasley E.M., Ballew R.M., Basus A., Barandale J., Bayarktaroglu L., Heasley E.M., Ballew R.M., Basus D.A., Buttler H., Cadieu E., Center A., Changra A., Cabley S., Dahlke C., Davreport L.B., Davies P., R. Durtls K.C., Busam D.A., Buttler H., Cadieu E., Center A., Changra A., Cabler S., Dahlke C., Devenport L.B., Davies P., R. Dodon M., Duletz S.M., Doup L.E., Downes M., Dugan Rocha S., Dunkov B.C., Dunn P., Rodon K., Doup L.E., Downes M., Dugan Rocha S., Dunkov B.C., Dunn P., Rodon K., Doup L.E., Downes M., Dugan R.S., Gelbart M.M., Glasser K., Gabriellan A., Remander C., Gabriellan A., Kareft C., Rerfaz C., Ferraz C., Radill M., Kalush F., Karpen G.H., Re. Z., Kennison J.A., Ketchum K.A., Jakok P., Lei Y., Levitsky A.A., Li J., Marnison J.A., Mcchum S.M., Moy M., Murphy B., Murphy L., Mushrison J.A., Mcchum S.M., Moy M., Murphy B., Murphy L., Mushrison J.A., Relang Y., Lin X., Maller B.W., Millans N.V., Mobarry C., Morley K.C., Mu D., Yang S., Yao O.A., Spier E., Spradling A.C., Stapleton M., Strong R., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Smith T., Sheng X.H., Zhong F.N., Zaveri J.S., Zhao G., Zhao G.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26 CQILMAEEGVPAPLPPEDA--PNAASLAPTPVS-----PVLEPFNLTSEPSDYALDL 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17.2%; Score 76; DB 5; Length 801; 33.9%; Pred. No. 4.2; tive 8; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A0F5C824663DC391 CRC64;
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3; 1.
; SH3; 1.
89233 MW; ?
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HSSP; P06241; 1SHF.
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Matches 21; Conservative
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PROSITE; PS50002; SH
SEQUENCE 801 AA;
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Search completed: January 30, 2001, 23:11:30
Job time: 3995 sec
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TISSUE=BRAIN;
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                                    000805;
01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
P-GLYCOPROTEIN E.
Leishmania Lropica.
Eukaryota: Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32 EEGVPAPLP-----PEDAPNAA-SLAPTPVSPVLEPFNLTSEPSDYALDLSTFLQQHP 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37 APLP-----PEDAPNAASLAPTPVSPVLEPFN-----LTSEPSDYALDLST 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fowl adenovirus 8.
Viruses; dSDNA viruses, no RNA stage; Adenoviridae; Aviadenovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17.2%; Score 76; DB 5; Length 1677; 33.9%; Pred. No. 9; Live 6; Mismatches 15; Indels 18;
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Best Local Similarity 31.1%; Pred. No. 0.94;
Matches 19; Conservative 17; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PFAM: PF00005; AHC_tran; 2.
PFAM: PF00664; AHC_tran; 2.
PROSTIE; PS00030; RNP_1; UNKNOWN_1.
PROSTIE: PS009211; ABC_TRNSPORTER; UNKNOWN_1.
PROSTIE: PS00962; RIBGSOMAL_S2_1; UNKNOWN_1.
SEQUENCE 1677 AA; 183006 MW; C49208921B71563A CRC64;
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J. Gen. Virol. 79:2507-2516(1998).
EMBL: AF021254; AAC71673.1;
SEQUENCE 114 AA; 13266 MW; 866UEEC6636EABA6 CRC64;
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
LATE 33 K PROTEIN HOMOLOG.
                1677 AA
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Lafuente E., Castanys S., Gamarro F.;
Submitted (APR-1996) to the EMBL/GenB:
EMBL: U55381; AAB51191.1;
HSSP; P13569; 1NBD.
            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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MEDLINE=98451338; PubMed=9780058;
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Matches 20; Conservative
        PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INTERPRO; IPRO00504; -. INTERPRO; IPRO01140; -. INTERPRO; IPR001617; -.
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Caps
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Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID+10090.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
16.7%; Score 74; DB 11; Length 955;
Best Local Similarity 41.9%; Pred. No. 8.3;
Matches 18; Conservative 2; Mismatches 15; Indels
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PRINTS: PR00048; ZINCFINGER.
PROSTIE: PS00028; ZINC_FINGER_C2H2; 5.
Zinc_finger: Metal-binding; DNA-binding.
SEQUENCE 955 AA: 102777 MW: D4DD03A02BECCAAC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        300 GSPTPKNPEDKSPQLSLSPRPTSPRACCPQSEDEGPLNLTSGP 342
                                      01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34 GVPAPLPPEDAPNAASLAPTPVSPVLE-----PFNLTSEP
955 AA.
PRT;
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Sequence 168, Appl Sequence 168, Appl Sequence 169, App Sequence 170, App Sequence 170, App Sequence 3936, Ap Sequence 2936, Ap Sequence 2, Appl Sequence 3126, Appl Sequence 3126, Appl Sequence 3126, Appl Sequence 3126, Appl Sequence 2050, A Sequence 2050, A Sequence 2051, Appl Sequence 22507, A Sequence 23, Appl Sequence 23, Appl

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Run on:

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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: THE TREATMENT AND DIAGNOSIS CHITLE OF INVENTION: CARDIOVASCULAR DISEASE NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS: ADDRESSE: PENNIE & EDMONDS LLP STREET: 1155 AVENUE of the Americas CITY: New York STATE: NY
                                                                                                                                                                    PCT-USO0-1518-170

2 US-60-196-718-170

2 US-60-198-986-170

2 US-60-198-986-170

2 US-60-198-986-170

9 US-60-229-524-80

9 US-60-229-524-80

9 US-60-279-181-2

10 US-60-191-681-2750

10 US-60-191-681-2750

10 US-60-191-681-2750

10 US-60-191-681-2750

10 US-60-191-681-2750

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10 US-60-191-681-30574

10 US-60-191-681-3055

10 US-60-191-681-3055
                                                             PCT-USOO-15136-168
PCT-USOO-15136-96
PCT-USOO-15136-167
US-60-196-718-4945
PCT-USOO-15136-169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/799,910
FILING DATE: 13-FEB-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION UMBER: 60/011,787
FILING DATE: 16-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-799-910-10; Sequence 10, Application US/08799910; GENERAL INFORMATION:
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ZIP: 10018-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
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20102
20102
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APPLICANT:
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                                         RESULT
                                                                                                                                                  ; Search time 57.93 Seconds
(without alignments)
401.549 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 10, Sequence 10, Sequence 10, Sequence 11, Sequence 11, Sequence 10,
                                                                                                                                                                                                                                  US-08-799-910-10
823
1 MCHSRSCHPIMTILQAPTPA......EPSDYALDLSTFLQQHPAAF 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cgn2_6/ptodata//paa//S09_COMB.pep:

Cgn2_6/ptodata//Ppaa//S091_COMB.pep:

Cgn2_6/ptodata//Ppaa//S092_COMB.pep:

Cgn2_6/ptodata//Ppaa//S094_COMB.pep:

Cgn2_6/ptodata//Ppaa//S094_COMB.pep:

Cgn2_6/ptodata//Ppaa//S095_COMB.pep:

Cgn2_6/ptodata//Ppaa//S097_COMB.pep:

Cgn2_6/ptodata//Ppaa//S097_COMB.pep:

Cgn2_6/ptodata//Ppaa//S097_COMB.pep:

Cgn2_6/ptodata//Ppaa//S06_NEW_COMB.pep:

Cgn2_6/ptodata//Ppaa//S06_NEW_COMB.pep:

Cgn2_6/ptodata//Ppaa//S06_NEW_COMB.pep:

Cgn2_6/ptodata//Ppaa//S06_NEW_COMB.pep:

Cgn2_6/ptodata//Ppaa//S06_NEW_COMB.pep:

Cgn2_6/ptodata//Ppaa//S09_NEW_COMB.pep:

Cgn2_6/ptodata//Ppaa//S09_NEW_COMB.pep:

Cgn2_6/ptodata//Ppaa//S09_NEW_COMB.pep:

Cgn2_6/ptodata//Ppaa//S09_NEW_COMB.pep:
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1: /cgn2_6/ptodata/2/paa/PCTUS_COMB.pep:*

2: /cgn2_6/ptodata/2/paa/USO6_COMB.pep:*

3: /cgn2_6/ptodata/2/paa/USO8_COMB.pep:*

4: /cgn2_6/ptodata/2/paa/USO8_COMB.pep:*

5: /cgn2_6/ptodata/2/paa/USO8_COMB.pep:*

7: /cgn2_6/ptodata/2/paa/USO8_COMB.pep:*

7: /cgn2_6/ptodata/2/paa/USO8_COMB.pep:*

10: /cgn2_6/ptodata/2/paa/USO8_COMB.pep:*

11: /cgn2_6/ptodata/2/paa/USO8_COMB.pep:*

12: /cgn2_6/ptodata/2/paa/USO8_COMB.pep:*

13: /cgn2_6/ptodata/2/paa/USO8_COMB.pep:*

14: /cgn2_6/ptodata/2/paa/USO8_COMB.pep:*

14: /cgn2_6/ptodata/2/paa/USO8_COMB.pep:*

14: /cgn2_6/ptodata/2/paa/USO8_COMB.pep:*

14: /cgn2_6/ptodata/2/paa/USO8_COMB.pep:*
                    GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-799-910-10
US-08-825-486-10
US-08-826-248-10
US-08-870-434-11
US-08-925-588-10
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                                                                                                                                                  January 30, 2001, 21:29:34
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Match Length
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Sequence 49, Appl Sequence 37506, A

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Sequence 10, Application US/08826248 GENERAL INFORMATION:
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REGISTRATION NUMBER: 30,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 76
'FELECOMMUNICATION INFORMATION'
'TELEPHONE: (212)7909090
                                                                                             TOPOLOGY: unknown

MOLECULE TYPE: protein

FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                             156 amino acids
                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0
Matches 156; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  156 amino acids
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Diskette
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
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                                                                                amino acid
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ZIP: 10036-2711
                                                                       TYPE: amino ac
STRANDEDNESS:
TOPOLOGY: unki
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US-08-826-248-10
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STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 823; DB 11;
100.0%; Pred. No. 3.2e-60;
ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 APTPVSPVLEPFNLTSEPSDYALDLSTFLQQHPAAF 156
                             NAME: Coruzzi, Laura A
RECISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-067-999
TELECOMMUNICATION INFORMATION:
TELEFAX: (212)7909090
TELEFAX: (212)8699741
TELEFX: 66141 PENNIE
INFORMATION FOR SED 1D NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: Nr
COUNTR: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
COMPUTER: TBM COMPUTER: TBM COMPATIBLE
COMPUTER: TBM COMPATIBLE
COMPUTER: TBM COMPATIBLE
COMPUTER: TBM COMPUTER: TBM COMPATIBLE
COMPUTER:
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: 1155 Avenue of the Americas
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 10, Application US/08825486
GENERAL INFORMATION:
APPLICANT: Falb, Dean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08/799,910 FILING DATE: 13-FEB-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 78
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: 10:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                LENGTH: 156 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (212)7909090
(212)8699741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.
Matches 156; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
FRAGMENT TYPE: internal
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APPLICATION NUMBER: 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                          unknown
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                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
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61 RSRRVLYPRVVRRQLPVEEPNPAKRLLFLLLTIVFCQILMAEEGVPAPLPPEDAPNAASL 120
                                                 0; Gaps
                                                                                                                  1. MCHSRSCHPTWT1LQAPTPAPST1PGPRRGSGPEIFTFDPLPEPAAAPAGRPSASRGHRK 60
; Score 823; DB 12; Length 156;
; Pred. No. 3.2e-60;
0; Mismatches 0; Indels 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Falb, Dean
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: THE TREATMENT AND DIAGNOSIS OF
TITLE OF INVENTION: THE TREATMENT AND DIAGNOSIS OF
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                  121 APTPVSPVLEPFNLTSEPSDYALDI CTFLQQHPAAF 156
                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DOS
SOFTWARE: FASLSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/826,248
FILING DATE: 28-MAR-1997
CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA.
APPLICATION NUMBER: 08/799,910
FILING DATE: 13-FEB-1997
PRIOR APPLICATION NUMBER: 60/011,787
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
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61 RSRRVLYPRVVRRQLPVEEDNPAKRLLFILLTIVFCQILMAGEGUPALLPPEDAPNAASI, 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 RSRRVLYPRVVRRQLPVEEPNPAKRLLFLLLTIVFCQILMAEEGVPAPLPPEDAPNAASL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 156;
                                                                                                                                                                                                                                               Sequence 10, Application US/08925588
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Falb, Dean
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
THE OF INVENTION: CARDIOVASCULAR DISEASE
CARDIOVASCULAR DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 100.0%; Score 823; DB 13; Best Local Similarity 100.0%; Pred. No. 3.2e-60; Matches 156; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: COTUZZI, LAUTA A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-067-999
                                                                                                      121 APTPVSPVLEPFNLTSEPSDYALDLSTFLQQHPAAF 156
                                                                                                                            121 APTPVSPVLEPFNLTSEPSDYALDLSTFLQQHPAAF 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: 1BM Compatible
OMPRATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/925,588
FILING DATE: 08-SEP-1997
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: PENNIE & EDMONDS LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; SEQUENCE DESCRIPTION: SEQ ID NO: 10: US-08-925-588-10
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APPLICATION NUMBER: 08/799,910

FILING DATE: <UNKNOWN>

ATTORNEY/AGENT INFORMATION:
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TELEFAX: (212)869741
TELEX: 6614 PENNIE
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: unknown
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                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: NY
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GENERAL INFORMATION:
APPLICANT: Falb, Dean
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                            RSRRVLYPRVVRRQLPVEEPNPAKRLLFLLLTIVFCQILMAEEGVPAPLPPEDAPNAASL 120
                                                                                                                            Gaps
                                                                                                                                                                                         1 MCHSRSCHPTMTILQAPTPAPSTIPGPRRGSGPEIFTFDPLPEPAAAPAGRPSASRGHRK 60
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                                                                                Length 156;
                                                                                                                            Indels
                                                                              Score 823; DB 12;
Pred. No. 3.2e-60;
Mismatches 0;
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MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION NUMBER: US/08/870,434
FILING DATE: 06-JUN-1997
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENE/DOORET NUMBER: 7853-084
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: 08/799,910
FILING DATE: 13-FEB-1997
ATTORNEY/AGENT INFORMATION:
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TELEFAX: 212-869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 11:
                                                                              Ouery Match
Best Local Similarity 100.0%;
Matches 156; Conservative C
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FYPE: amino acid
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Matches 156; Conservative
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    internal
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; FRAGMENT TYPE:
US-08-826-248-10
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TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: NUCLBIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AN
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CLOO0456
CURRENT APPLICATION NUMBER: US/60/196,718
CURRENT FILING DATE: 2000-04-13
NUMBER OF SEQ ID NOS: 7494
SOFTWARE: FastSEQ for Windows version 4 0
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Pred. No. 7.4e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICART: Human Genome Sciences, Inc.
TITLE OF INVENTION: 50 Human Secreted Proteins
FILE REPERENCE: PS551PCT
CURRENT APPLICATION NUMBER: PCT/US00/15136
CURRENT FILING DATE: 2000-06-01
EARLIER APPLICATION NUMBER: 60/138,629
EARLIER OF FILING DATE: 1999-06-11
NUMBER: OF SEQ ID NOS: 198
SOFTWARE: Patentin Ver. 2.0
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93.5%; Pred. No. /...
3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         125 VSPVLEPFNLTSEPSDYALDLSTFLQQHPAAF 156
121 APTPVSPVLEPFNLTSEPSDYALDLSTFLQQ 151
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; Sequence 168, Application PC/TUS0015136
; GENERAL INFORMATION;
                                                                                                                Sequence 6102, Application US/60196718 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCT-US00-15136-96 Sequence 96, Application PC/TUS0015136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 93,59
Matches 86; Conservative
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Best Local Similarity 100.0
Matches 83; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: HUMAN
US-60-196-718-6102
                                                                                              US-60-196-718-6102
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                                                                                                                                                                                                                                                                                                                           SEQ ID NO 6102
LENGTH: 123
                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MCHSRSCHPTMTILQAPTPAPSTIPGPRRGSGPEIFTFDPLPEPAAAPAGRPSASRGHRK 60
                                                         Sequence 10, Application US/09372044A
GENERAL INFORMATION:
APPLICANT: Deen FALB et al.
TITLE OF INVENTION: Treatment and Diagnosis of Cardiovascular Disease
TITLE OF INVENTION: Treatment and Diagnosis of Cardiovascular Disease
CURRENT APPLICATION UNMBER: US/09/372,044A
CURRENT FILING DATE: 1999-08-11
NUMBER OF SEQ ID NOS: 44
SOFTWARE: FASTEEQ for Mindows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MCHSRSCHPTWT11,QAPTPAPST1PGPRRGSGPE1FTFDP1.PEPAAAPAGRPSASRGHRK 60
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Best Local Similarity 100.0%; Pred. No. 3.2e-60;
Matches 156; Conservative 0; Mismatches 0; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 794; DB 22;
Pred. No. 7.5e-58;
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100.0%; Pred. No. /...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : Sequence 17386, Application US/60197873
; GENERAL INFORMATION:
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APPLICANT: Tanaka, Hiroaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 151; Conservative
                                                                                                                                                                                                                                                                                            ; TYPE: PRT
CORGANISM: Homo sapiens
US-09-372-044-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OKCANISM: Homo sapiens
US-60-197-873-17386
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                      RESULT 6
US-09-372-044-10
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LENGTH: 151
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LENCTH: 156
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us-08-799-910-10.rap

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APPLICANT: BORGAZI, VIVIEN
TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CLOO0456
CURRENT APPLICATION UNMBER: US/60/196,718
CURRENT FILING DATE: 2000-04-13
NUMBER OF SEQ ID NOS: 7494
      NUCLEIC ACTO MOLECULES ENCODING HUMAN SECRETED PROPERNS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MCHSRSCHPTMTILQAPTPAPSTIPGPRRGSGPEIFTFDPLPEPAAAPAGRPSASRGHRK 60
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100.0%; Pred. No. 3.7e-24;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 169, Application PC/TUS0015136
GENERAL INFORMATION:
APPLICANT HUMBN GENOME SCIENCES, INC.
TITLE OF INVENTION: 50 Human Secreted Protelius
FILE REFERENCE: PS551PCT
CURRENT APPLICATION NUMBER: PCT/US00/15136
CURRENT FILING DATE: 2000-06-01
EARLIER APPLICATION NUMBER: 60/138,629
EARLIER FILING DATE: 1999-06-11
NUMBER OF EQ ID NOS: 198
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13.5%; Score 358; DH 1; All 1; Score 358; DH 1; Conservative 0; Mismatches 2
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TITLE OF INVENTION: NUCLEIC ACID MOLECULE
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CLOOO456
CURRENT APPLICATION NUMBER: US/60/196,718
CURRENT FILING DATE: 2000-04-13
NUMBER OF SEQ ID NOS: 7494
SOFTWARE: FastSEO for Windows Version 4.00
SEQ ID NO 4945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 5439, Application US/60196718 ; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                             46.3%
Best Local Similarity 100.0
Matches 70; Conservative
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Best Local Similarity
Matches 66; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 RSRRVLYPRV 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RSRRVSLP 68
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                                                                                                                                                                                                                            ; ORGANISM: HUMAN
US-60-196-718-4945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: HOMO PCT-US00-15136-169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCT-US00-15136-169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-60-196-718-5439
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                                                                                                                                                                                  LENGIH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Xaa equals any of the twenty naturally ocurring PCT-US00-15136-96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51.4%; Score 423; DB 1; Length 83; 100.0%; Pred. No. 1.2e-27; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51.3%; Score 422; DB 1; Length 83; 98.8%; Pred. No. 1.4e-27;
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             APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: 50 Human Secreted Proteins
FILE REFERENCE: PSSIPCT
CURRENT APPLICATION NUMBER: PCT/USOO/15136
CURRENT FILING DATE: 2000-06-01
EARLIER APPLICATION NUMBER: 60/138,629
EARLIER FILING DATE: 1999-06-11
NUMBER: OF SEQ. ID NOS: 198
SOFTWARE: PATENTIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: 50 Human Secreted Proteins
FILE REFERENCE: PSSSIPCT
CURRENT APPLICATION NUMBER: PCT/US00/15136
CURRENT FILING DATE: 2000-06-01
EARLIER APPLICATION NUMBER: 60/138,629
EARLIER FILING DATE: 1999-06-11
NUMBER: OF SEQ ID NOS: 198
SOFTWAKE: PALENTIN Ver. 2.0
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GENERAL INFORMATION:
APPLICANT: Bonazzi, Vivien
TIFLE OF INVENTION: ISÔLATED HUMAN SI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        130 EPFNLTSEPSDYALDLSTFLOQH 152
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Best Local Similarity 100.
Matches 82; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82; Conservative
                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Homo sapiens
PCT-US00-15136-167
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  GENERAL INFORMATION:
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US-60-196-718-4945
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                                                                                                                                                                                                                       SEQ ID NO 96
                                                                                                                                                                                                                                            LENGTH: 83
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                                                                                                                                                                                                                                                                                                                                                         LOCATION:
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43.5%; Score 358; DB 22; Length 92;
Best Local Similarity 100.0%; Pred. No. 2.9e-22;
Matches 66; Conservative 0; Mismatches 0; Indels
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41.3%; Score 340; DB 1; Length 72;
Best Local Similarity 100.0%; Pred. No. 6.8e-21;
Matches 62; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: 50 Human Secreted Proteins
FILE REFERENCE: PSS1PCT
CURRENT APPLICATION NUMBER: PCT/US00/15136
CURRENT FILING DATE: 2000-06-01
FEARLIER APPLICATION NUMBER: 60/138,629
EARLIER FILING DATE: 1999-06-11
NUMBER OF SEQ ID NOS: 198
SOFTWARE: PALENTIN Ver. 2.0
                                                                                                                                                                                                                                                                                                    RESULT 15
PCT-US00-15136-170
: Sequence 170, Application PC/TUS0015136
: GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
OKGANISM: Homo sapiens
PCT-US00-15136-170
; SEO ID NO 5439
; LENGTH: 92
; TYPE: PRT
; ORCANISM: HUMAN
US-60-196-718-5439
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LENGTH: 72
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Search completed: January 30, 2001, 23:10:11 Job time: 6037 sec

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48, Appl 48, Appl 66, Appli 6, Appli 6, Appli 6, Appli 52, Appl 52, Appl 52, Appl

Sequence

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APPLICANT: Falb, Dean
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: THE TREATMENT AND DIAGNOSIS OF
TITLE OF INVENTION: CARDIOVASCULAR DISEASE
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
US-08-231-193A-50
US-08-486-273A-50
US-08-480-474-50
US-08-231-193A-48
US-08-231-193A-48
US-08-486-273A-48
US-08-231-193A-6
US-08-231-193A-6
US-08-486-273A-6
US-08-486-273A-6
US-08-486-273A-6
US-08-486-273A-6
                                                                                                                                           US-08-480-474-52
US-08-940-086A-52
US-08-231-193A-46
                                                                                                                                                                                              ALIGNMENTS
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CONTROLLEN.

OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/826,246

FILLING DATE: 28-MAR-1997

CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 28-MAR 1997
CLASSIFICATION: 800
PRIOR APPLICATION NOBER: 08/799,910
FILING DATE: 13-FEB-1997
FILING DATE: 13-FEB-1997
PRIOR APPLICATION NUMBER: 60/011,787
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: COFUZZI, Laura A
REGISTRATION NUMBER: 30,72
REFERENCE/DOCKET NUMBER: 7853-076
TELECOMMUNICATION: THORMATION:
                                                                                                                                                                                                                                              Sequence 10, Application US/08826246 Patent No. 6048709 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
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INFORMATION FOR SEQ ID NO: 10:
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TELEFAX: (212)8699741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 156 amino acids
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FRAGMENT TYPE: internal
US-08-826-246-10
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  STRANDEDNESS:
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                                                                       January 30, 2001, 19:24:41 ; Search time 36.91 Seconds (without alignments) 75.895 Million cell updates/sec
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Sequence 10, Appl
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                                                                                                                                  1 MCHSRSCHPTMTILQAPTPA......EPSDYALDLSTFLQQHPAAF 156
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Sequence 42,
Sequence 42,
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Sequence 7,
Sequence 4,
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Sequence 4
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                                                                                                                                                                                                                                                                                                 Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
            GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-126-640-11

US-09-356-548-24

US-09-356-9548-3

US-08-574-959A-7

US-08-674-959A-7

US-08-465-713-7

US-08-465-713-7

US-08-320-000A-7

US-08-320-000A-7

US-08-320-000A-7

US-08-320-000A-7

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US-08-320-000A-7

US-08-320-000A-7

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US-08-321-19-6

US-08-321-19-6

US-08-135-929A-11

US-08-135-929A-11

US-08-135-929A-11

US-08-234-193A-42

US-08-34-193A-42

US-08-480-474-42

US-08-480-474-42

US-08-940-086A-42

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US-08-940-086A-42
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-08-940-086A-54
                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                     174772 seqs, 17957048 residues
                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                     - protein search, using sw model
                                                                                                                                                       BLOSUM62 *Gapox 10.0 , Gapoxt 0.5
                                                                                                              US-08-799-910-10
823
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Maximum DB seq length: 200000000
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Match Length DB
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Perfect score:
                                                                                                                                                        Scoring table:
                                                     OM protein
                                                                                                                                    Sequence:
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                                                                         Run on:
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Length 156;

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APPLICANT: Shyjan, Audrew W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: DIAGNOSIS, PREVENTION, AND TREATMENT OF NEOPLASTIC CELL
TITLE OF INVENTION: 24
NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                        GENERAL INFORMATION.

APPLICANT: FALB.

APPLICANT: FALB.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE

TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE:

FILE REFERENCE: 7853-126

CURRENT APPLICATION NUMBER: US/09/126,640A

CURRENT FILING DATE: 1998-07-30

EARLIER PLING DATE: 1997-06-06

EARLIER FILING DATE: 1997-06-06

EARLIER FILING DATE: 1997-02-13

EARLIER FILING DATE: 1996-02-16

NUMBER OF SEQ ID NUMBER: 60/011,787

EARLIER FILING DATE: 1996-02-16

NUMBER OF SEQ ID NOS: 44

SOFTWARE: FRASESEQ for Windows Version 4.0

SEQ ID NO 11
       61 RSRRVLYPRVVRRQLPVEEPNPAKRLLFLLTIVFCQIIMAEEGVPAPLPPEDAPNAASL 120
                               61 RSRRVLYPRVVRRQLPVEEPNPAKRLLFLLTIVFCQILMAEEGVPAPLPPEDAPNAASL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MCHSRSCHPTMTILQAPTPAPSTIPGPRRGSGPEIFTFDPLPEPAAAPAGRPSASRGHRK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 156;
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3. 4e-75;
0;
                                                                                 121 APTPVSPVLEPFNLTSEPSDYALDLSTFLQQHPAAF 156
                                                                                                     121 APTPVSPVLEPFNLTSEPSDYALDLSTFLQQHPAAF 156
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100.0%; Pred. No. 40
live 0; Mismatches
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ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                               Sequence 11, Application US/09126640A
Patent No. 6099823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 24, Application US/09035648; Patent No. 6100031
; GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 156; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo saplens
US-09-126-640-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02110-2804
                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Boston
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                                            Gaps
                                                                                             J MCHSKSCHPTMTTLOAPTPAAPSTIPGPRRGSGPEIFTFDPLPEPAAAPAGRPSASRGHRK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MCHSRSCHPTMT11,QAPTPAPSTİPGPRRGSGPEJFTFUPI,PEPAAAPAGRPSASRGHRK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: THE TREATMENT AND DIAGNOSIS TITLE OF INVENTION: CARDIOVASCULAR DISEASE NUMBER OF SEQUENCES: 44
100.0%; Score 823; DB 3; 100.0%; Pred. No. 4e-75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 823; DB.3
100.0%; Pred. No. 4e-75;
live 0; Mismatches (
                                                                                                                                                                                                                     121 APTPVSPVLEPFNLTSEPSDYALDLSTFLQQHPAAF 156
                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-067-999
TFLECOMMUNICATION INFORMATION:
TELEPHONE: (212)790990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US/08/944,495
                                                                                                                                                                                                                                                                                                                                                Sequence 10, Application US/08944495
Patent No. 6087477
GENERAL INFORMATION:
APPLICANT: Falb, Dean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/799,910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (212)8699741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Diskette
IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 156 amino acids
TYPE: amino acid
                                    Matches 156; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM COMPONERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unknown
                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity
Matches 156; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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                                                                                                                                                                                                                                                                                                                 RESULT 2
US-08-944-495-10
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STATE:
 Query Match
Best Local (
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ZIP: 02109-1875
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                 1520 PAIY 1523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56 RG----
                                                                                                                                                                                                                              153 PAAF 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                      JS-08-574-959A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 264 APPPYSAVTPPPDAFSRGVSSPIAGPAQPPWPQPAPWSOPAFYDSSERIASRDERISVP 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 324 AKRTGILQEAKRRSTTKPMFTFKEPKVSPNP--ELLSLLQNSEGKRGTGAGGDSGPEEDY 38]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Margarit, S. M.
APPLICANT: Margarit, S. M.
APPLICANT: Boriack Sjodin, Ann
APPLICANT: Boriack Spodin, Ann
APPLICANT: Gole, Philip
APPLICANT: Cole, Philip
TITLE OF INVENTION: A CRYSTAL OF A RAS-SOS COMPLEX AND METHODS OF USE
TITLE OF INVENTION: THEREOF
FLE REFERENCE: 6001-1228M
CURRENT APPLICATION NUMBER: US/09/356,952
CURRENT FILING DATE: 1999-07-19
EARLIER APPLICATION UNMER: 60/093,631
EMALIER RELING DATE: 1998-07-21
NUMBER OF SEO ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----TIVFCOILMAEEGVPAPLPPEDAPNAASLAP-TPVSPVLEPFNLTSEP 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   382 LSLGAEACNFMQSSSAKQKTPPPVAPKKSSSQQVTPVSPVWSPCVAPTQP 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1596;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16 APTPAPSTIPGP----RRGSGPEIFTFDPLPEPAAAPAGRPS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 95.5; DB 3;
Pred. No. 0.089;
4; Mismatches 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 3;
SOFTWARE: FastSEO for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/035,648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.6%; Score 95.5; D
28.3%; Pred. No. 0.22
:ive 19; Mismatches
                                                                                                                                                                NAME: Maiklejohn, Ph.D., Anita L. REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/003001
TELECHNUNICATION INFORMATION: TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
                                                                                            PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/818,829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/09356952
Patent No. 6117663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Drosophila melanogaster
US-09-356-952-3
                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 2 SEQUENCE CHARACTERISTICS: LENGTH: 739 amino acids TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 27.0°
Matches 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                            protein
internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52; Conservative
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Best Local Similarity
                                                        FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
FRAGMENT TYPE:
US-09-035-648-24
                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 3
LENGTH: 1596
                                                                                                                                                                                                                                                                                                                                                                           TOPULOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-356-952-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
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                                                                                                      62 SRRV----LYPR----VVRRQLPVE-----EPNPAKRLLFLLLTIVFCQILMAEEGV 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----RVVRRQLPVEEPNPAKRLLFLLTIVFCQILMAEEGVPAPLPPEDAPNAASLAPT 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ETFGGRVPRPAFVHYDKEEASDVEISLESDSDOSVVIVPEGLP-PLPP---PPPSGATPP 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 400 HPRVPPLOPMGPTCPTPAPVPLLRPHRPSGPHRSILRAPCPOWAPCPOOAPCPSAGPMPS 459
4 SRSCHPTMTILQAPTPAPSTIPGPRG--SGPETFTFDPLPEDAAAPAGRPSASKGHKKR 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 HPTMTILQ-----APTPAPSTIPGPRRGSGPE-----IFTFDPLPEPAAAPAGRPSAS 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----HRKRSRR--VLYP------ 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Jackyoon Shin, Insil Joung, Ratna K. Vadlamudi APPLICANT: and Jack L. Strominger TITLE OF INVENTION: p62 POLYPEPTIDES, RELATED POLYPEPTIDES TITLE OF INVENTION: AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 905;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/574,959A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: LAHIVE & COCKFIELD
60 State Street, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UMBER: US/08/574,959A
19-DEC-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: 18M PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 9, Application US/08574959A Patent No. 5962224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Mandragouras, Amy E. REGISTRATION NUMBER: 36,207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: DF
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 23.19
Matches 45; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
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11.2%; Score 92; DB 22.1%; Pred. No. 0.42 tive 17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15 QAPTPAPSTIPGPRRGSGPEIFTFDPLPE------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P: Arnold, White & Durkee
P. O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Arnold, White & Durkee P. O. Box 4433
                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                  FILING DATE: 19930617
CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: PATKET, DAVID L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: ARCD:
TELECPHONICATION INFORMATION:
TELEPHONE: (512) 474-7577
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) MOLECULE TYPE: DNA (genomic) US-08-080-255-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   112 EDAPNAA---SLAPTPVSPV 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1400 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 22.18
Matches 31, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            single
                                                                                                                                                                                                                    COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: AMINO ACID
STRANDEDNESS: Sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                               Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Houston
                                                                                                                                                                    Texas
                                                                                                                                                                                                 77210
                                                                                                            ADDRESSER:
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                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-465-713-7
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                                                                                                                                                              STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69 -----RVVRROLPVEEPNPAKRLLFILLTIVFCQ1LMAEEGVPAPI.PPEDAPNAASLAPT 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1135;
                                                                                                                                                                       APPLICANT: Jackyoon Shin, Insil Joung, Ratna K. Vadlamudi APPLICANT: and Jack L. Strominger TITLE OF INVENTION: p62 POLYPEPTIDES, RELATED POLYPEPTIDES NUMBER OF SEQUENCES: 22 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----HRKRSRR--VLYP----
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                                                                                                                                                                                                                                                                                                                                                                ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.4%; Score 93.5; 23.1%; Pred No. 0.
                                                                                                                                                                                                                                                                                  E: LAHIVE & COCKFIELD 60 State Street, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/574,959A
FILING DATE: 19-DEC-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Mandragouras, Amy E. REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: DFN-008
TELECOMMUNICATION INFORMATION: (617)227-7400
TELEFRHOME: (617)227-541
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                       Sequence 7, Application US/08574959A
Patent No. 5962224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-080-255-7; Sequence 7, Application US/08080255; Patent No. 5487970; GENERAL INFORMATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A'TTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
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Best Local Similarity 23.1'
Matches 45; Conservative
 124 PVSPVLEPFNLTSEP 138
                       124 PVSPVLEPFNLTSEP 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                   Boston
                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                     US-08-574-959A-7
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63 RRVLYPRVV-------RRQLPVEEPNPAKRLLFLLLTIVFCQTLMAEEGVPAPLPP 111
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: DETECTING GENE REARRANGEMENTS AND TITLE OF INVENTION: TRANSLOCATIONS NUMBER OF SEQUENCES: 8 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7, Application US/08465713
Patent NO. 6121419
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT:
Diaz, Manuel O.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION:
TITLE OF INVENTION:
TRANSLOCATIONS
TITLE OF INVENTION:
TRANSLOCATIONS
                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
BLLICATION NUMBER: US/08/080,255
FILING DATE: 19930617
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us-08-799-910-10.rai

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63 RRVLYPRVV------RRQLPVEEPNPAKRLLFLLLTIVFCOILMAEEGVPAPLPP 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              15 QAPTPAPSTIPGPRRGSCPEIFTFDPLPE-----PAAAPAGRPSASKGHRKKS 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                40; Indels
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APPLICANT: Barton, Kenneth A
TITLE OF INVENTION: Immobilized Proteins in Cotton Fiber
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles and Brady
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/217,327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17; Mismatches
                                                                                                         ARCD: 072/PAR
                                                                                                                                                                                                                                                                                                                                                                                      11.2%; Score 92; 22.1%; Pred. No.
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/812,233
FILING DATE: 19-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J
REGISTRATION NUMBER: 27,386
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
    07/900,689
                                                         NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFRENCE/DOCKET NUMHER: ARCD:
TELECOMMUNICATION INFORMATION:
TELEPAN: (512) 320-7200
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1400 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78-08-217-327-4

5 Sequence 4, Application US/08217327

Patent No. 5474925
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P.O. Box 2113
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; MOLECULE TYPE: DNA (genomic)
PCT-US93-05857-7
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TELECOMMUNICATION INFORMATION:
                     FILING DATE: 17/06/92
ATTORNEY/AGENT INFORMATION:
NAME: Parker, David L.
                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 22,19
Matches 31, Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                  single
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APPLICATION NUMBER:
                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: sir
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ZIP: 53701-2113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Board of Regents
APPLICANT: The University of Texas System
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING
TITLE OF INVENTION: GENE REARRANGEMENTS AND TRANSLOCATIONS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Annold, White & Durkee
STREET: P. O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Hest Local Similarity 22.1%; Pred. No. 0.42;
Matches 31; Conservative 17; Mismatches 40; Indels
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SOFTWARE: Patentin Release #1.0, Version #1.25
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SOFTWARR: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/05857
FILING DATE: 19930617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17; Mismatches
                                                                                                                                                                                                                                                             NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: ARCD:072/PAR
TELECOMMUNICATION INFORMATION:
                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,713
FILING DATE: 06-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/080,255
FILING DATE: 17 JUNE 1993
ATTORNEY/AGENT INFOHMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 7, Application PC/rus9305857 GENERAL INFORMATION:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                              (512) 320-7200
                                                                                                                                                                                                                                                                                                                                                                                                                                1400 amino acids
                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy of
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                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Houston
STATE: Texas
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JS-08-465-713-7
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COUNTRY: Us.
77210
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Gaps

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TITLE OF INVENTION: CDNA encoding the rat Dl dopamine
TITLE OF INVENTION: receptor linked to admylyl cyclase activation and
TITLE OF INVENTION: expression of the receptor protein in plasmid-transfection
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                | 11: | 11: 372 PDFRKAFQGLLCCARRAARRRHATHGDRPRASGCLARPGP-PP--SFGAASDDDDDDVVG 428
                                                                312 KALKTLGIIMGVFTLCWLPFFLANVVKAFHRELVPDRLFVFFNWLGYANSAFNPIIYCRS 371
                                                                                                                                                                                                                                                                                                                                                                                                                          Mahan, Lawrence C.
McVittle, Loris D.
EVEVION: CDMA encoding the rat DJ dopamine
VEWION: receptor linked to admylyl cyclase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Knobbe, Martens, Olson and Hear
620 Newport Center Drive, Sixteenth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/029,917
FILING DATE: 03-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/548,714
FILING DATE: 06-JUL-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/444,734A
                                                                                                                                                                                  122 PTPVSPVLEPF----NLTSEPSDYALD 144
                                                                                                                                                                                                             429 ATPPARLLEPWAGCNGGAAAUSDSSLD 455
                                   -- LPVEEPNPAKRI,-
                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/08444734A Patent No. 5610282
                                                                                                                                                                                                                                                                                                                                                                                                         Frederick J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: 1BM PC Compatible OPERATING SYSTEM: PC DOS/MS-SOFTWARE: Patentin Release #
                                                                                                         --ILMAEEGV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (714) 760-0404
TELEFAX: (714) 760-9502
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                       David R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                       Sibley,
Monsma,
                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Sibley,
APPLICANT: MONSMA,
APPLICANT: MOUTELICA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; FRAGMENT TYPE:
US-08-444-734A-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92660
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STATE:
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                                                                                                                                                                                                                                        63 RRVLYPRVVRROLPVEEPNPAKÄLLELLTIVFCOILMAEEGVPAPLPPEDAPNAASLAP 122
                                                                                                                                                                                                                                                                                                                                     9 PPPPATPPPATPPPAT 149
                                                                                                                                                                                    Gaps
                                                                                                                                                                                                               9 PTMTILQAP/PPAPSTIPGPRRGSGPEIF/FPDP-----I.PEPAAAPAGRPSASRCHRKRS 62
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                                                                                                                                                                                  33;
                                                                                                                                  Ouery Match
Best Local Similarity 27.5%; Pred. No. 0.066;
Matches 38; Conservative 8; Mismatches 59; Indels 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Sealfon, Stuart C.
TITLE OF INVENTION: Cloning and Expression of
TITLE OF INVENTION: Clonding and Expression of
TITLE OF INVENTION: Gonadotropin-Releasing Hormone Receptor
NUMBER OF SEQUENCES: 8
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,0.066;
,nes 59; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC Compartable
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/390,000A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEE: Pennie & Edmonds LLP: 1155 Avenue of the Americas New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7, Application US/08390000A
Patent No. 5985583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: MASTOCK, S. Leslie
REGISTRATION UNUBER: 18,872
REFERENCE/DOCKET UNMER: 6923
TELECOMMUNICATION INFORMATION:
TELEFAN: 212 790-9090
TELEFAX: 6141 PENNIE
                                                                                                                                                                                                                                                                                                                                 114 PPASPPPATP---PPATPPPA--
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SEQUENCE CHARACTERISTICS:
LENGTH: 468 amino acids
                                                                                                                                                                                                                                                                                                                                                                                               150 VPAISPVQTP--LTSPPA 165
                                                                                                                                                                                                                                                                                                                                                                        123 TP-VSPVLEPFNLTSEPS 139
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ATTORNEY/AGENT INFORMATION:
214 amino acids
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                                                     ; MOLECULE TYPE: protein US-08-217-327-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
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                  TYPE: amino acid
TOPOLOGY: linear
                                       linear
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Matches 50; Conserva
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US-08-390-000A-7
LENGTH:
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2 Gaps . 46 DB 1; Length 477; Indels 44; 19; Mismatches REFERENCE/DOCKET NUMBER: 34,115
REFERENCE/DOCKET NUMBER: NIH065.001FW1
TELECOMMUNICATION: Query Match 10.7%; Score 88; Best Local Similarity 24.2%; Pred. No. (Matches 50; Conservative 19; Mismatch

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Score 87; DB 1;
Pred. No. 2.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           933 PPOPATPLSOPAVSIEGOVSNPPSTSSTEVNS 964
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                                                                                         122 PTPVSPVLEPF----NLTSEPSDYALD 144
                                                                                                                 438 ATPPARLLEPWAGCNGGAAADSDSSLD 464
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14-APR-1994
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Patent No. 5658784
GENERAL INFORMATION:
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REFERENCE/DOCKET NUMBER: DF
TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO: 2:
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Best Local Similarity 22.4%
Matches 34; Consérvative
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APPLICANT: Emorine, Jean L.
APPLICANT: Emorine, Jean L.
APPLICANT: Emorine, Jean L.
APPLICANT: Strosberg, Donny A.
TITLE OF INVENTION: Nacleotide Sequences Encoding the Murine
TITLE OF INVENTION: Beta3-Adrenergic Receptor and Their Applications
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bell, Seltzer, Park & Gibson
STREET: Post Office Drawer 34009
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| PDFRKAFQGLLCCARRAARRHATHGDRPRASGCLARPGP-PP--SPGAASDDDDDDVVG 437
                                321 KALKTLG1IMGVFTLCWIPFFLANVVKAFHRELVPDRLFVFFNWLGYANSAFNPIIYCRS 380
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PTPAPSTIPCPREGSCPEIFTFDPLPEPAAAPAGRPSAS--RCHRKRSRRVLYPRVVRRQ 74
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                                                                                -----LPVEEPNPAKRL-----LFLLLI,"----
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/087,772A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10.7%; Score 88; DB 24.2%; Pred. No. 0.3; tive 19; Mismatches
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Post Office Drawer 34009
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NAME: Linker, Raymond O.
REO/STRATHON NUMBER: 26,419
REFERENCE/DOCKET NUMBER: 3339-195
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
                                                                                                                                                                                                                                                122 PTPVSPVLEPF----NLTSEPSDYALD 144
                                                                                                                                                                                                                                                                               438 ATPPARLLEPWAGCNGGAAADSDSSLD 464
                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 16, Application US/08087772A; Patent No. 5691155
; GENERAL INFORMATION:
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STATE: No. 5691155th Carolina
COUNTRY: USA
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INFORMATION FOR SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 477 amino acids
TYPE: amino acid
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: peptide US-08-087-772A-16
                                                                                                                                                               98 --- ILMAEEGV----
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Best Local Similarity
Matches 50; Conserv
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US-08-087-772A-16
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| :| :| 1| | :| 381 PDFRKAFQGLLCCARRAARRHATHGDRPRASGCLARPGP-PP--SPGAASDDDDDVVG 437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65 VLYPRVVRRQLP----VEEPNPAKRLLFLLLTIVFCQILMAEEGVPAPLPPEDAPNAASL 120
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--PAPLPPEDAPNAAS---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: Weingarten, Schurgin, Gagnebin & Hayes
Ten Post Office Square
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: ECKNEY, Richard
APPLICANT: Ewen, Mark
APPLICANT: Ewen, Mark
APPLICANT: Livingston, David
TITLE OF INVENTION: NUCLEIC ACID, ENCODING TRANSC
TITLE OF INVENTION: FACTOR P300 AND USES OF P300
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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Page 8

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January 30, 2001, 18:47:31 ; Search Lime 54.97 Seconds (without alignments) 97.039 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                  1 MCHSRSCHPTMTILQAPTPA.......EPSDYALDLSTFLQQHPAAF 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /cqn2_2/gcgdata/geneseq/geneseqp/AA1980.DAT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'gcgdata/geneseq/geneseqp/AA1994.DAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gcgdata/geneseg/genesegp/AA1989.DAT
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/cgn2_2/gcgdata/geneseq/geneseqp/AA1986.DAT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               268485
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       268485 segs, 34193795 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gcgdata/geneseg/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                         OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                         BLOSUM62 *Gapext 0.5
                                                                                                                                                                                                                                                                US-08-799-910-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Minimum DB seq length: 0
Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cgn2_2/cgn2_2
                                                                                                                                                                                                                                                                Title:
Perfect score:
Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Searched:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

50mm
183 1
787 1
168 2

Gene 036 product d Amino acid sequenc Protein sequence o Human Per gene pro Human PER protein Protein encoded by Streptococcus pineu Human p160 polypep Mycobacterium tube Mycobacterium tube Mycobacterium tube Streptococcus pineu	MLL amino acid seq MLL cDNA clone 14-ALL-1 procein. Ho ALL-1 (acute 1ymph lluman atrophin-1 r Cotton fiber speci T. gondii immunoge T. gondii immunoge T. gondii immunoge Mycobacterium tube Amino acid sequenc Amino acid sequenc Amino acid sequenc Protein encoded by Mouse Per gene pro al encoded by	GNMENTS r disease; oncogenic disorder; rative disorder; rative disorder; rative forming growth factor; nflammation; fibrosis; tumour growth; labotic; opthalmological.	g symptoms of fibroproliferative
25790 68821 78185 06809 32216 01687 14566 31186 31185 31855 31855	RA4517 R844517 R84467 R84470 R84647 R86913 R729034 Y729034 Y729031 W729011 W72	A	17394. 26640. RM INC. for ameliorating related disorders
888880100118	0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	otein; 156 Au entry) fchd605 gene ; cardiovascu y; flbroprol pathway; TGi angiogenesis,	394. 640. 1NC. or ame
15996 15996 12990 12990 1291 1985 1135 763	1400 1900 3910 3910 1012 214 171 171 171 171 171 171 171 171 171 1	idard; Protein; (first entry) coded by fchd605 tinopathy; fibr tinopathy; fibr gnalling pathwa cancer; angloge	iens. 206-Al. 000. 999; 99WC-US17394 998; 98US-0126640 MILLENNIUM PHARM IN 0-205414/18. 250711. ing substances for or oncogenic relat.
		standard; Prot 2000 (first e encoded by fc gene; human; c fetinopathy; c fetinopathy; tic cancer; an risation; cyto	A1. ENN 541. 11.
9999 99999 884 888999 9999 99 88084448888888		7 1 7 45017 stand Y45017; 31-MAY-2000 Protein encodiabetic febera fe pancreatic ovascularisa	sap 006 006 B-2 L-1 L-1 L-1 C-1 Ses
2222 2222 2222 2232 2232		SUL 501	XX HOMO XX HOMO XX HOMO XX YX XX XX YX XX YX XX YX YX YX YX YX

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This prolein is encoded by the novel human fchd605 gene (ser-19447) that is up-regulated in monocytes treated with oxidiscut low density lipoproteins that simulate the conditions under which foam cells develop during atherogenesis. The protein has sequence similarity to the mouse gly96 gene and to EST T49532. Novel fchd510, fchd540, fchd602 and fchd605 genes (see T94467-71) provide a lingerprint for the study of cardiovascular diseases, including atherosclerosis, ischemia/reperfusion, hypertension restends and arterial inflammation, Methods are provided for the
                                                                                                                                                                                                                                                                                                                                                                                                                        RSRRVI.YPRVVRRQI.PVEEPNPAKRI.I.FLLI.T1VFCQ1LMAEEGVPAPLPPEDAPNAASL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MCHSRSCHPTMTILQAPTPAPST1PGPRRGSGPE1FTFDPLPEPAAAPAGRPSASKGHRK
        e.g. atherosclerosis, restenosis, hypertension, etc
                                                                                                                                                                                            diagnosis, monitoring in clinical trials, screening for
therapeuLically effective compounds; and treatment of
cardiovascular diseases based on discoveries regarding the
expression patterns of these novel genes.
                                                                                                                                                                                                                                                                                                          99.1%; Score 816; DB 18; 99.4%; Pred. No. 3.3e-68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 6; Fig 5; 163pp; English.
                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UABR-) UAB RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1997-202002/18.
                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 155; Conserv
                                                                                                                                                                                                                                                                  156 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-OCT-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  McDaniel LS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             meningitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Briles DE,
                                                                                                                                                                                                                                                                Sequence
           disease,
                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PspA;
                                                                                                                                                                                                                                                                                                                                                                                                                        6.1
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W14574
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The patent discloses methods for the treatment and diagnosis of cardiovascular diseases by novel human genes which are differentially expressed in different cardiovascular disease states. Compositions which can modify ToF-beta signalling pathway are identified by screening.

These are used therapeutically to treat fibroproliferative and oncogenic disorders, especially TGF (Transforming growth factor)-beta related disorders, including diabetic retinopathy, artheroscierosis, pancreatic cancer, anglogenesis, inflammation, fibrosis, tumour growth and cancer, anglogenesis, inflammation, fibrosis, tumour growth and cancer, unjoquenesis, inflammation, fibrosis, tumour growth and density lipoprotein) can be used to design cardiovascular disease treatment strategies. Depending on whether the up-regulation has a pathogenic or protective effect treatment methods can be designed to increase or decrease the activity of the protein product of the gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                             RSRKVLYPRVVRRQI.PVEEPNPAKRLLF1.L1.F1VFCQ1LMAEEGVPAPI.PPEDAPNAASI, 120
                                                                                                                                                                                                                                                                                                                                                                    New genes differentially expressed in cardiovascular disease - used for diagnosis, drug screening and treatment of cardiovascular
                                                                                                                                                                                                                                                                                                                                                       MCHSRSCHPTWT1LQAPTPAPSTIPGPRRGSGPETFTFUPLPEPAAAPAGRPSASRGHRK
                                                                                                                                                                                                                                                                                                                                .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fchd605 gene; differential expression; monocyte; human; foam cell; cardiovascular disease; atherosclerosis; ischaemia; reperfusion; hypertension; restenosis; arterial inflammation; therapy; diagnosis; drug screening; marker.
                                                                                                                                                                                                                                                                                                    Length 156;
                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                    DB 21;
                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                              100.0%; Score 823; DB 21;
100.0%; Pred. No. 7.4e-69;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 APTPVSPVLEPFNLTSEPSDYALDLSTFLQQHPAAF 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W36006 standard; Protein; 156 AA
           Example; Fig 5; 214pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MILL-) MILLENNIUM PHARM INC
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96US-0011787.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human Fchd605 gene product.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 156; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI: 1997-424966/39
                                                                                                                                                                                                                                                       156 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; T94471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9730065-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-FEB-1996;
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                                                                                                                                                                                                                                                       Seguence
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W36006
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0; Gaps 9

Indels

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0; Mismatches

Length 156;

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Streptococcus pneumoniae surface protein PspC and truncated PspA
                                                                                                                                                                                             pneumococcal surface protein; vaccine; otitis media; itis; bacteraemia; pneumonia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Crain MJ, Hollingshead
R, Yother J;
                                                                                                                                                                                                                                                                                                                                                                      /note= "unidentified amino acid"
                                                                                                                                            Streptococcus pneumoniae PspA central region.
                                                                                                                                                                                                                                                                       Streptococcus pneumoniae strain Db15.
                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
W14574 Standard; Protein; 206
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, Swiatlo E, Tart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96WO-US14819.
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                                                                                                 (first entry)
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6
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                                                 This sequence shows the central portion, including the C-terminus of the alpha-helix region and some of the proline-rich region, of strand but a surface protein A (PspA) of Streptococcus pneumoniae Strain Dbl5. Comparison of the N-terminal and central regions (W1453-57 and W1452-91) of PspA polypeptides from different pneumococcal strains can be used to divide the strains into several families based on sequence homologies. PspA polypeptides, or fragments of them, can be used in vaccines to protect animals against S. pneumoniae infection and hence for the prevention of diseases such as ottlis media, manipolitis, bacteraemia and pneumonia. The sequence of the 3' half of the PspA alpha-helical region and the immediate 5' tip of the coding sequence are likely to be the critical sequences for predicting PspA cross-reactions and vaccine
                                                                                                                                                                                                                                                                                                                    100 tpapapapapapaptpeapapapapkpapapkpapapk-----papapkpapa 147
                                                                                                                                                                                                                                                                                               18 TPAPSTIPGPRRGSGPEIFTFDPLPEPAAAPAGRPSASRGHRKRSRRVLYPKVVRRQLPV 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus pneumoniae surface protein PspC and truncated PspA used in vaccines for protecting animals against S.pncumoniae infection
                                                                                                                                                                                                                                                                                                                                           78 EEPNPAKRILFLLITIVFCQTLMAEEGVPAPLP-PEDAPNAASLAPTPVSPVLEP 131
                                                                                                                                                                                                                                                                                                                                                        used in vaccines for protecting animals against S.pneumoniae
                                                                                                                                                                                                                                                    Score 107; DB 18; Length 206; Pred. No. 0.01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pneumococcal surface protein; vaccine; otitis media;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hollingshead S;
J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "unidentified amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus pneumoniae PspA central region.
                                                                                                                                                                                                                                                               Pred. No. 0.018; Mismatches
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R, Yother
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus pneumoniae strain Ef6796.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       meningitis; bacteraemia; pneumonia.
                                Example 6; Fig 13; 296pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                      W14573 standard; Protein; 129 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Briles DE, Brooks-Walter A,
McDaniel LS, Swiatlo E, Tart
                                                                                                                                                                                                                                                     13.0%;
29.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 29.6
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UABR-) UAB RES FOUND.
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                                                                                                                                                                                                                      206 AA;
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                                                                                                                                                                                                composition.
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          infection
                                                                                                                                                                                                                      Sequence
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diseases such as otitis media, meningitis, bacteraemia and pneumonia. The sequence of the 3' half of the PspA alpha Helical region and the immediate 5' tip of the coding sequence are likely to be the critical sequences for predicting PspA cross-reactions and vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16 APTPAPSTIPGPRRGSGPEIFTFUPLPEPAAAPAGRPSASRGHRKRSKRVLYPRVVRKQL 75
                                          This sequence shows the central portion, including the C-terminus of the alpha-helix region and some of the proline-rich region, of pneumococcal surface protein A (195A) of Stroptococcus pneumoniae Strain Ef6796. Comparison of the N-terminal and central regions (W14533-57 and W14562-91) of PspA polypeptides from different pneumococcal strains can be used to divide the strains into several families based on sequence homologies. PspA polypeptides, or families based on sequence homologies. PspA polypeptides, or fragments of them, can be used in vaccines to protect animals against S, pneumoniae infection and hence for the prevention of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PVEEPNPAKRLLFLLTIVFCQILMAEEGVPAPLP-PEDAPNAASLAPTPVSP 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PspA; pneumococcal surface protein; vaccine; otitis media;
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J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 104; DB 18;
Pred. No. 0.012;
8; Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "unidentified amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "unidentified amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "unidentified amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus pneumoniae PspA central region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Briles DE, Brooks-Walter A, Crain MJ,
McDaniel LS, Swiatlo E, Tart R, Yother
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus pneumoniae strain Bg8743.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    meningitis; bacteraemia; pneumonia.
Example 6; Fig 13; 296pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12.6%;
26.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 12.6
Best Local Similarity 26.5
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  129 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                  composition.
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Briles DE,
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                                                                                                                                                                                   This sequence shows the central portion, including the C-terminus of the alpha-helix region and some of the proline-rich region, of pneumococcal surface protein A (PspA) of Streptococcus pneumoniae strain Bg9163. Comparison of the N-terminal and central regions (W14533-57 and W14562-91) of PspA polypeptides from different pneumococcal strains can be used to divide the strains into several families based on sequence homologies. PspA polypeptides, or Iragments of them, can be used in vaccines to protect animals against 5. pneumoniae infection and hence for the prevention of discases such as otitis media, meninglis, bacteraemia and pneumonia. The sequence of the 3' half of the PspA alpha-helical region and the immediate 5' tip of the coding sequence are likely to be the critical manner::...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  111 apapapapapapa-----papapapapapapa-----pkpapapa 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76 PVEEPNPAKRIJELLTTVFCOILMAEEGVPAPLP-PEDAPNAASLAPTPVSPVLEP 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus pneumoniae surface protein PspC and truncated PspA used in vaccines for protecting animals against S pneumoniae
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used in Vaccines for protecting animals against S.pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pneumococcal surface protein; vaccine; otitis media;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hollingshead S;
J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12.3%; Score 101.5; DB 18; 27.4%; Pred. No. 0.031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus pneumoniae PspA central region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus pneumoniae strain 0922134c.
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R, Yother
                                                                                                                                               Example 6; Fig 13; 296pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            meningitis; bacteraemia; pneumonia
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Swiatlo E, Tart
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Best Local Similarity 27.41
Matches 32; Conservative
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                    WP1; 1997-202002/18.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 190 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        composition.
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                                                                                                         infection
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This sequence shows the central portion, including the C-terminus of the alpha-helix region and some of the proline-rich region, of pneumooccal surface protein A (PspA) of Streptococcus pneumoniae strain 0922134c. Comparison of the N-terminal and central regions (M1453-57 and W14562-91) of PspA polypeptides from different pneumooccal strains can be used to divide the strains into several fragments of them, can be used to divide the strains into several fragments of them, can be used in vaccines to protect animals against S. pncumoniae infection and hence for the prevention of diseases such as ottism medial of the PspA alpha-helical region and the immediate 5' tip of the coding sequence are likely to be the critical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98 etpapapapapapek----paekpapapapapekpapapek----paekpae 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15 QAPTPAPSTIPGPRRGSGPEIFTFDPLPEPAAAPAGRPSASRGHRKRSRRVLYPRVVRKQ 74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75 LPVEEPNPAKRLLFLLLTIVFCQ1LMAEEGVPAPLPPEDAPNAASLAPTPVSP 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12.3%; Score 101; DB 18; Length 180; 27.4%; Pred. No. 0.032; Live 8; Mismatches 34; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pneumococcal surface protein; vaccine; otitis media;
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J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus pneumoniae strain Bg9739.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             meningitis; bacteraemia; pneumonia.
Example 6; Fig 13; 296pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    180 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              composition.
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strain Bg9739. Comparison of the N-terminal and central regions. (W14533-57 and W14562-91) of PspA polypeptides from different pneumococcal strains can be used to divide the strains into several families based on sequence homologies. PspA polypeptides, or fragments of them, can be used in vaccines to protect animals against S. pneumoniae infection and hence for the prevention of diseases such as ottis media, meningitis, bacteraamia and pneumonia. The sequence of the 3' half of the Coling sequence are likely to be the critical sequences for predicting PspA cross-reactions and vaccine
                                                                                                                                                                                                                                                                                                                                                       101 tpapapapapapaptpe----apapapapapkpapa-----pkpapapkpa 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Detection of modulators of Mena and Ena-VASP-like genes and proteins - used in control of cytoskeletal dynamic events in mormal and abnormal cell morphology, adhesion, motility, growth and differentiation
                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                       18 TPAPSTIPCPRKGSCPETFTFDPLPEPAAAPAGRPSASKGHRKRSRRVLYPRVVRRQLPV 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neural Mena+ protein; mammalian Ena; Enabled protein; Ev1 protein; cytoskeleton; cell morphology; cell adhesion; cell differentiation; cell growth; cell motility; mouse.
                                                                                                                                                                                                                                                                                                                                                                                                            78 EEPNPAKKLLFILITIVFCQILMAEEGVPAPI.P---PEDAPNAASI.APTPVSPVI.EP 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This protein comprises novel murine neural Mena+. Its amino sequence was deduced from a cDNA clone (see V02998) obtained
                                                                                                                                                                                                                                                   12.3%; Score 101; DB 18; Length 183; 28.2%; Pred. No. 0.033; tive 8; Mismatches 32; Indels 44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W37151 standard; Protein; 783 AA.
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                                                                                                                                                                                                                                                                                      33; Conservative
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                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                      183 AA;
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a mouse brain cDNA library. Neural Menai contains an exou that introduces 244 amino acids between amino acids 238 and 239 of mammalian Ena (Mena, see W37148). Two other isoforms, neural Mena++ (see W37152), are also disclosed. Unlike Mena, neural Mena isoforms exhibit neural tissue-specific distribution. Based on the disclosed Mena and Ev! genes (see also V02996-97) and proteins (see also W37148-49), a variety of methods and compositions are provided for screening, isolating and characterising endogenous and exogenous factors, drugs and therapeutic agents useful to evaluate and/or control cytoskeletal dynamic events involved in normal and abnormal cell morphology, adhesion, mothlity, growth and/or differentiation. A method of detecting a modulator of Mena activity/expression is
                                                                                                                                                                                                                                                                                                                                                                                                                                                57 GHRKRSRRYLLYPRVVRRQLPVEEPNPAKRLLFLLLTIVFCQILMAEEGVPAPLPPEDAPN 116
                                                                                                                                                                                                                                                                                                                                                                                                 -----pglqaasqpaesptpqylvl------gppapppppppp 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Detection of modulators of Mena and Ena-VASP-Like genes and proteins - used in control of cytoskeletal dynamic events in normal and abnormal cell morphology, adhesion, motility, growth and
                                                                                                                                                                                                                                                                                                                                                                             2 CHSRSCHPTMT-ILQAPTPAPSTIPGPRRGSGPEIFTFDPLPEPAAAP----AGRPSASR 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neural Mena++ protein; mammalian Ena; Enabled protein; Evl protein; cytoskeleton; cell morphology; cell adhesion; cell differentiation; cell growth; cell motility; mouse.
                                                                                                                                                                                                                                                                                                                                            46;
                                                                                                                                                                                                                                                                                                Score 100; DB 19; Length 78 Pred. No. 0.21; ... wismatches 51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Soriano P, Wehland J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GBFB ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH. (HUTC-) HUTCHINSON CANCER RES CENT FRED.
                                                                                                                                                                                                                                                                                                                                            11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 4; Page 60-63; 77pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  117 ----AASLAPTPVSPVLEPFNLTSEP 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     535 gpayasalppppppppppppstgpp 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W37152 standard; Protein; 787
                                                                                                                                                                                                                                                                                                          12.2%;
26.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mena++ protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97WO-US11669
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 26.08
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Niebuhr K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1998-101197/09
                                                                                                                                                                                                                                                          783 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse neural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-JUL-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gertler FB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-JUL-1998
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                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W37152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
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This protein comprises novel murine neural Mena++. Its amino acid sequence was deduced from a CDNA clone obtained from a mouse brain cDNA library. Two other isoforms, neural Mena+ (see W37151) and neural Mena+ (see W37152), are also disclosed. Unlike mammalian Ena (Mena, see W37148), neural Mena isoforms exhibit neural isoforms can expecific distribution. Based on the disclosed Mena and Evlagenes (see also W02996-98) and proteins (see also W37148-49), a variety of methods and compositions are provided for screening,
                                                                                                                                                                     isolating and characterising endogenous and exogenous factors, drugs and therapeutic agents useful to evaluate and/or control cytoskeletal dynamic events involved in normal and abnormal cell morphology, adhesion, motility, growth and/or differentiation method of detecting a modulator of Mena activity/expression is
                                                                                                                                                                                                                                                                                                                     802 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ₩O200001717-A2.
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                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11
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9
This protein comprises novel murine neural Mena++. Its amino acid sequence was deduced from a cDNA clone obtained from a mouse brain contained from a mouse brain to contain forary. Two other isoforms, neural mena+ (see W37151) and neural Mena+ (see W37151) and neural Mena+ (see W37153), are also disclosed. Unlike mammalian through see W37148), neural Mena isoforms exhibit neural classue-specific distribution. Based on the disclosed Mena and Evl genes (see also V02996-98) and proteins (see also W37148-49), a sizelaty of methods and compositions are provided for screening, variety of methods and compositions are provided for screening, cluds and therapeutic agents useful to evaluate and/or control cytoskeletal dynamic events involved in normal and abnormal cell morphology, adhesion, motility, growth and/or differentiation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         506 -----gppaasqpaesptpqqlvl-----gppapppplps 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57 CHRKRSRRVLYPRVVRRQLPVEEPNPAKRLI,FLIJ.TIVFCQ1LMAEEGVPAPI,PPEDAPN 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 CHSRSCHPTMT-ILQAPTPAPSTIPGPRRGSGPE1FTFDPLPEPAAAP----AGRPSASR 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Detection of modulators of Mena and Ena-VASP-like genes and proteins - used in control of cytoskeletal dynamic events in normal and abnormal cell morphology, adhasion, motility, growth and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neural Mona+++ protein; mammalian Ena; Enabled protein; Evl protein; cytoskeleton; cell morphology; cell adhesion; cell differentiation; cell growth; cell motility; mouse.
                                                                                                                                                                                                                                                                                                                                                                          Score 100; DB 19; Length 787; Pred. No. 0.21;
                                                                                                                                                                                                                                                                                                                                                                                                                  51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wehland J;
                                                                                                                                                                                                                                                                                                                                                     12.2%; Scot.
26.0%; Pred. No. v.z.
'''o 11; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HUTC-) HUTCHINSON CANCER RES CENT FRED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sertler FB, Niebuhr K, Soriano P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117 ---- AASLAPTPVSPVLEPFNLTSEP 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            539 gpayasalpppppppppppppppp 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W37153 standard; Protein; 802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse neural Mena+++ protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97WO-US11669.
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                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 26.0%
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4P1; 1998-101197/09.
                                                                                                                                                                                                                                                                                                             787 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-JUL-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W09801755-A1
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                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                         claimed.
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The present sequence represents a high mobility group (HMG)-Y/R protein.
HMG sequences that interact with retinoic acid receptors (RARs) in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying modulators of nuclear receptors, useful e.g. as anticancer and anti-inflammatory agents, according to their effect on binding between the receptor and high-mobility group protein
                                                                                                            471 cgsqaspppgtplastpsskpsvlpspsaga...--pasaetplnpelgdssase 520
                                                                                                                                                     GHRKRSRRVLYPRVVRRQLPVEEPNPAKRLLFLLI.TIVFCQ.II.MAEEGVPAPL.PPEDAPN 116
                                                                                                                                                                                      .....pglqaasqpaesptpqqlvl----gppappppppppppppp
                                                                             2 CHSRSCHPTMT-ILQAPTPAPSTIPGPRKGSGPEIFTFDPLPEPAAAP----AGRPSASR 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Retinoic acid receptor; RAR; high mobility group protein; HMG protein; nuclear receptor; antiproliferative; anti-inflammatory; antipsoriasis; anticancer.
                                            46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Amino acid sequence of high mobility group (HMG)-Y/R protein.
Ouery Match 12.2%; Score 100; DB 19; Length 802; Best Local Similarity 26.0%; Pred. No. 0.21; Matches 38; Conservative 11; Mismatches 51; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chandraratna RA, Ghosn C;
                                                                                                                                                                                                                              ----AASLAPTPVSPVLEPFNLTSEP 138
                                                                                                                                                                                                                                                                   gpayasalppppppppppppstgpp 579
                                                                                                                                                                                                                                                                                                                                                        Y68732 standard; Protein; 168 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-0108298
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Example 4; Paye 63-65; 77pp; English

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ligand dependent manner to induce gene expression can be identified using the method of the invention. The specification describes a method for identifying compounds that modulate a nuclear receptor. The method comprises incubating a polypeptide containing a ligand-binding region of nuclear receptor with test compound in presence of second polypeptide containing the nuclear receptor-binding part of a IMG protein, and detecting any alteration in binding between the two polypeptides. The method is useful for identifying potential antiproliferative, anti-inflammatory, antipsoriasis and anticancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence represents a high mobility group (HMG)-R protein. HMG sequences that interact with retinoic acid receptors (RARs) in a ligand dependent manner to induce gene expression can be identified using the method of the invention. The specification describes a method for identifying compounds that modulate a nuclear receptor. The method comprises incubating a polypeptide containing a
                                                                                                                                                                                                                                                                                                                                                                                     76 -PVEEPNPAKKILETLETIVFCQIIMAEEGVPAPLPPEDAPNAASLAPTPVSPVLEPFNL 134
                                                                                                                                                                                                                                                                                                                                                                                                                           ----aplpp-----ppplpgahhhrl 113
                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Retinoic acid receptor; RAR; high mobility group protein; IMG protein; nuclear receptor; antiproliferative; anti-inflammatory; antipsoriasis; anticancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Identifying modulators of nuclear receptors, useful e.g. as antican and anti-inflammatory agents, according to their effect on binding between the receptor and high-mobility group protein
                                                                                                                                                                                                                                                                                                                   17 PTPAPSTIPGPRRGSGPEIFTFDPLPEPAAAPAGRPSASRGHRKRSRRVLYPRVVRRQL-
                                                                                                                                                                                                                                                                                                                                                   33 ppkepsevptpkr------prgrpkyskknwrrrkrrasrrsprrrss
                                                                                                                                                                                                                                                                                   41;
                                                                                                                                                                                                                                                 Length 168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Amino acid sequence of high mobility group (HMG)-R protein.
                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                 52;
                                                                                                                                                                                                                                                 DB 21;
                                                                                                                                                                                                                                             Score 98.5; DB
Pred. No. 0.05;
                                                                                                                                                                                                                                                                                 9; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Y68731 standard; Protein; 179 AA
                                                                                                                                                                                                                                                                                                                                                                                                                       dpcvppaphwrssfllgldsf----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         135 TSEPSDYALDLSTFILOOHPAA 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12.08; 27.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                 39; Conservative
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                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                             168 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200001717-A2.
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                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Y68731;
                                                                                                                                                               agents.
                                                                                                                                                                                                                                                                               Matches
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ligand-binding region of nuclear receptor with test compound in presence of second polypeptide containing the nuclear receptor-binding part of a HMG protein, and detecting any alteration in binding between the two polypeptides. The method is useful for identifying potential antiproliferative, anti-inflammatory, antipsoriasis and anticancer
                                                                                                                                                                                                                                                                                                                                 81 rrrssdpcvppaphwrssfllgldsf-----aplpp----ppplpqah 119
                                                                                                                                                                                                                                                                                                  RROL--PVEEPNPAKRLLFLLLIIVFCQILMAEEGVPAPLPPEDAPNAASLAPTPVSPVL 129
                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                   TILQAPTPAPSTIPGPRRGSGPETFTEDPLPEPAAAPAGRPSASRCHRKRSKKVLYPRVV 71
                                                                                                                                                                                                                                                      This protein is encoded by gene 036 (see T91708), which was identified by differential display analysis as being expressed at a ligher level in normal colon tissues than in cancerous colon tissues. Gene 036 is a candidate tumour suppressor gene. A correlation was found between an increase in the expression level of gene 036 and a decrease in a colon cell's tumour potential. Hence, methods that increase the level of expression of gene 036 may inhibit or slow the progression to tumours and cancer, e.g. colon cancer. The 036 protein is used in claimed methods for treating a patient suffering from a disorder associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gene 036 product differentially expressed in colon tumour cells.
                                                                                                                                                                                                     41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               colon cancer; differential expression; gene 036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene 036 with reduced or amplified expression in tumour cells used, optionally with genes 097, 030 and 056 or their protein products, for diagnosis and treatment of colonic cancer
                                                                                                                                                                   DB 21; Length 179;
                                                                                                                                                                                                     Indels
                                                                                                                                                                 Score 96.5; DB 21;
Pred. No. 0.083;
9; Mismatches 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diagnosis; gene therapy; tumour suppressor
                                                                                                                                                                                                                                                                                                                                                                                                 120 hhhrlwppppsstcalttlhstpaa 145
                                                                                                                                                                                                                                                                                                                                                                 EPFNLTSEPSDYALDUSTFLQQHPAA 155
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                                                                                                                                                                 11.78; 27.48;
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                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fig 2; 117pp;
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                                                                                                                                                                                  Similarity
                                                                                                                   AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; T91708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Colon tumour;
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                                                                                                                   Sequence
                                                                                                                                                                   Ouery Match
Best Local 9
                                                                                     agents.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The specification describes a crystal complex comprising at least a Sos contacting region of a Ras protein and at least a Son of sevenless (Sos) protein catalytic region fragment, that effectively diffracts
                                                                                                                                                                                                                                                                       264 apppysavtpppdafsrgvsspiagpagpppwpgpapwsgpafydsseriasrderisvp 323
                                                                                                                                                                                                                                                                                                                                                  324 akrtgilqeakrrsttkpmftfkepkvspnp--elisilqnsegkrgtgaggdsgpeedy 381
                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                   16 APTPAPSTIPGP----REGSGPEIFTFDPLPEPAAAPAGRPS-----ASRGHR---- 59
                                                                                                                                                                                                                                                                                                              -KRS------RRVLYPRVVRRQLPVEEPNPAKRLLFILL-------91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel crystals comprising a Ras-Son of sevenless complex, useful for screening drugs useful in cancer treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amino acid sequence of a Drosophila Son of sevenless (Sos) protein.
insufficient expression of gene 036 protein, and for identifying compounds that modulate 036 protein activity. Such compounds are useful in the diagnosis, prevention and treatment of tumours and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cole P, Kuriyan J;
                                                                                                                                                                                                                                                                                                                                                                                        -----TIVFCQII,MAEECVPAPI,PPEDAPNAASI,AP-TPVSPVLEPFNI,TSEP 138
                                                                                                                                                                                                                                                                                                                                                                                                                              382 lslgaeacnfmqsssakqktpppvapkpavkssssqpvtpvspvwspgvaptqp 435
                                                                                                                                                                                               53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ras; Son of sevenless; Sos; crystal; Ras-Sos complex; cancer; protein coordinate data.
                                                                                                                                                         Length 739;
                                                                                                                                                                                               Indels
                                                                                                                                                           DB 18;
                                                                                                                                                                                             90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bar-Sagi D,
                                                                                                                                                         11.6%; Score 95.5; DF 27.0%; Pred. No. 0.5; ive 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 169-175; 224pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Y68821 standard; protein; 1596 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Horiack-Sjodin A, Margarit SM,
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                                                                                                                                                                           Best Local Similarity 27.0 Matches 47; Conservative
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                                                                                                739 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 SRRV-----LYPR----VVRRQLPVE-----EPNPAKRLLFLLLTIVFCQILMAEEGV 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    106 PAPLPPEDAPNAASLAPT--PVSPVLEPF--NLTSEP----SDYALDLSTFLQQ----H 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transcription factor; probe; reverse transcription; PCR; primer; expression vector; E.coli; COS cell; ras; cancer cell multiplication; polyoma virus; transformation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 SRSCHPTMTILQAPTPAPSTIPGPRRG -- SGPEIFTFDPLPEPAAAPAGRPSASRGHRKR 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ETS transcription factor activated by ras - may be used in the study of cancer cell proliferation and the proliferation of the polyoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The amino acid sequence of the novel ETS transcription factor family
or inhibit the formation of Ras-Sos complex are useful in the treatment of cancer. The present sequence represents a Drosophila % \left( 1\right) =\left\{ 1\right\} =\left\{
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45;
                                                                                                                                                                                                                                                                                                                                                                                                 Length 1596;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein sequence of PEA3-beta -an ETS transcription factor.
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                                                                                                                                                                                                                                                                                                                                                                                     ch 11.6%; Score 95.5; DB 21; Similarity 28.3%; Pred. No. 1.2; 52; Conservative 19; Mismatches 68;
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N-PSDB; 091769.
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Best Local Similarity
                                                                                                                                                                                                                             1596 AA;
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member - PEA3-beta. The gene was isolated from a HepG2 cell line cDNA library. The probe for the screening was prepared by reverse transcription on HepG2 mRNA followed by PCR using primers 091770-1, to produce a probe of 170-200 bp. The screening isolated the full length sequence of the transcription factor. The gene was inserted into protein in E.coli and COS7 cells, respectively. The FTS transcription factor has specificity for and is activated by ras. It is useful as a reagont in studies for the elucidation of the mechanism of cancer cell multiplication or polyoma virus transformation of cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 RRVLYPRVVRRQLPVEFPNPAKRLLFLLLTIVFCQILMAEEGVP-------- 106
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                                                                                                                                                                                                                                                                                                                                 Oucry Match 11.5%; Score 94.5; DB 16; Length 520; Best Local Similarity 22.4%; Pred. No. 0.42; Matches 3%; Conservative 13; Mismatches 62; Indels 57;
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                                                                                                                258
1 GTCCGCCCCCAGCTGCCAGT.....AGCAACACCCGGCCGCCTTC 258
                                                                                                                                                                                                    15983484
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                             7991742 segs, 3503743858 residues
                                                                                                     US-08-799-910-9_COPY_211_468
                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                       OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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gb_est37:
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9b_est2:*;
9b_est4:*;
9b_est5:*;
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9b_est7:*;
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Perfect score:
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                                                             Run on:
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Description

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A1824906 411 bp mRNA EST 16-DEC-1999 WD03206.X1 NOL_CGAP_GC6 HOMO Sapiens CDNA CIONE IMAGE:2304610 3' Similar to SW:IEXI_HUMAN P46695 RADIATION-INDUCIBLE IMMEDIATE-EARLY GENE IEX-1; mRNA sequence.
A1824906 A1824906.1 G1:5445577
                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                                   SUMMARIES
                                                                                                                                                   42 H80073

37 BEB78459

AA143404

35 BE751344

35 BE75116

39 BF040186

39 BF040186

39 BF040186

39 BF040186

39 BF040186

39 BF040186

39 BF0400660
                                                                                                                                                                                                                        143 N57203
135 BE73573
137 AV594384
137 AV594384
139 BF02587
96 AW916683
14 AM367127
139 BE524106
109 BE524106
135 BE784106
135 BE784106
144 AW746658
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2 A
gb_gss25:*
gb_gss26:*
gb_gss27:*
gb_gss28:*
                                                                    Length DB
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Match
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173.6
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163.8
160.8
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em_estrol5:*
em_estrol7:*
em_estrol7:*
em_estrol8:*
em_estrol9:*
gb_ests9:*
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gb_est62:*
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gb_est65:
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em_gss13:
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W77628 me68809.r1
AM762977 mq23c12.r

AI876358 uk74a05.y AA833402 ub58b04.r

us-08-799-910-9_copy_211_468.rst

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/tissue_type="melanotic melanoma"
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/lab.host="Organ: skin, vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; CDNA made by oligo-dT priming. Directionally
ECORI; CDNA made by oligo-dT priming. Directionally
adaptor: GGCAGGG(G). Size-selected >SOUDP for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using 2AP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
225 c 131 g
                                                                                                                                       Homo sapiens

Bukaryota; Mutazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 544)
      601276496F1 NIH_MGC_20 Homo sapiens cDNA clone 1MAGE:3617543 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
                                                                                                                                                                                                                                              National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausbergenih.gov
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The 1.m.A.G.E. Consortium (1.1.NI.)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 258; DB 107; 100.0%; Pred. No. 1.1e-55;
                                                                                                                                                                                                                     NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plate: LLCM284 row: p column: 24
High quality sequence stop: 540.
Location/Qualifiers
1. 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="NIH_MGC_20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref*"taxon:9606"
/clone="IMAGE:3617543"
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                                                                    BE384949.1 GI:9330314
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                             mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                   information can be
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O
                                                                                                                                                                                                                                                                                                                                                                              Sequencing Center
                                                                                                                                                                                                                                                            Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
                                             Euteleostomi;
                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 411)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
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                                                                                                                                                                                                                                                                                                                                                                                                                                        www-bio.lln[.gov/bbrp/image/image.html
Insert Length: 557 Std Error: 0.00
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                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seq primer: -400P from Gibco
High quality sequence stop: 341.
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BE383865 951 bp mRNA EST 21-JUL-2000 601273192F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614255 5'
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                                                                                                                                 212 GTCCGGCGCCAGCTGCCAGTCGAGGAACCGAACCAGCCAAAAGGCTTCTCTTTCTGCTG 271
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Length 544;
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BE275966.1 GI:9150928
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ORIGIN
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TITLE
JOURNAL
COMMENT
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KEYWORDS
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/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; cDNA made by Oligo-dT priming. Directionally
cloned into ECORI(XhoI sites using the following 5;
adaptor: GCACGAG(G). Size-selected >SOUDp for average
insert size 1: 8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
324 c 253 g 164 t.
                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
Tal: (301) 496-1150
Email: Robert Strauspergenih.gov
Tissue Procurement: ArCC/DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin. Laboratory
CDNA Library Preparation: Ling Hong/Rubin. Laboratory
Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Theorye Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, at: image.llnl.gov
High quality sequence stop: 747.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 951)
NHH MGC http://www.ncbi.nlm.nih.gov/MGC/.
National Institutes of Health, Mammalian Gene Colloction (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 100.0%; Score 258; DB 107; Length 951; Best Local Similarity 100.0%; Pred. No. 1.1e-55; Matches 258; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3614255"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="NIH_MGC_20"
                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
             BE383865
BE383865.1 GI:9329230
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                                                                                                                                                                                                   Unpublished (1999)
mRNA sequence
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/lab_host="Dribe (phage resistant)"
/lab_host="Organ: skin; Vector: pOTB7; Site_1: XhOI; Site_2: DcoR1; cDNA made by oligo-d7 priming. Directionally cloned into EcoRI/Xhol sites using the following 5′ adaptor: GGCAGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the labbratory of Gerald M. Rubin (University of California, Berkeley) using 2AP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
Homo sapiens
Eukaryota; Metazoa; Chordala; Craniata; Vertebrala; Euleleoslomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                          Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL.)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM72 row: e column: 07
High quality sequence start: 7
High quality sequence stop: 699.
Location/Qualifiers
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                                                                                     1 (bases 1 to 765)
NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="NIH_MGC_20"
/tissue_type="melanotic melanoma"
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/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                    Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
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/do_xref="taxono'9606"

/do_xref="taxon'9606"

/clone="ImAGE_3895736"

/clone="ImAGE_3895736"

/clone="ImaGE_3895736"

/tlosue_type="epithelioid carcinoma"

/lab_host="PolloB (phage-resistant)"

/note="Organ: pancreas; Vector: pCMV-SPOR76; Site_1: Not1; Site_2: Sal1; Cloned unidrrectionally. Primer: Oligo dT. Avcrage insert size 1.1 kb. library constructed by Life Technologies."
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0
                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                               Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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                                                                                                                  1 (Massa to the Community of MACC).
National Institutes of Health, Mammalian Gene Collection (MCC) (Inpublished (1999)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
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Location/Qualifiers
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                   GI:9892286
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Bost Local Similarity 99.6
Matches 255; Conservative
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BE621346.1
                                                               Homo sapiens
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National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the T.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCMN03 row: f column: 08
High quality Sequence Stop: 659.
Location/Qualifiers
rce
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="leiomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: uterus, Vector: pCMV-SPORT6; Site_1: Not1:
Site_2: Sal1: Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.1 kb.
a 327 c 268 g 134 t
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Subaryotas; Metazoa; Chordata; Craniata; Vertebrata; Eutcleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 603)
NIH-NGC http://www.ncbi.nlm.nlh.gov/NGC/.
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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99.6%; Pred. No. 1.7e-53;
iive 0; Mismatches 1;
                                                              1 (bases 1 to 916)
NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/
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/clone="IMAGE:3906823"
/clone_lib="NIH_MGC_71"
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Best Local Similarity 99.6
Matches 250; Conservative
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Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., Whitc,Y., Wylic,T., Waterston,R. and Wilson,R.
WashU-Merck EST Project 1997
Conpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AW960290 585 bp mRNA EST 01-JUN-2000 EST372361 MAGE resequences, MAGF Homo sapiens CDNA, mRNA sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                            Email: estewatson.wustl.edu
This clone is available royalty-free through LLNI. contact the
This clone is available royalty-free through LLNI.
This consortium (info@imago.llnl.gov) for further information.
Seq primer: -2bml3 rev2 ET from Amersham
High quality sequence stop: 369.
Location/Qualifiers
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                                                                                                                                                                                Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 244.6; DB 7; Length 463; Pred. No. 2.6e-52; 0; Mismatches 4; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                       1. 463
/organism="Homo sapiens"
/db_xref="GDB:5935321"
/db_xref="taxon:9606"
/clone="IMAGE:723904"
/clone_lib="Soares ovary tumor NbHOT"
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196 c 114 q
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Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
                                                                                                                                               Tissue Procurement: DCTD/DTP CONA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Preparation: Ling Hong/Rubin Laboratory Arrayed by: The L.M.A.G.E. Consortium (LLNL.) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov Plate: LLCM186 row: j column: 24 High quality sequence stop: 579.
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Mammalia, Eutherla, Primates, Catarrhini, Hominidae,
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                                                                      Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
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AA410666.1 G1:2069789
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Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleosto
Mammalia: Eutheria: Primates: Catarrhini: Hominidae: Homo.
1 (bases 1 to 810)
NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                              Gaspard, R.,
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                                                Hegde, P., Oi, R., Abernathy, K., Dharap, S., Gaspard, R., I.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. Quackenbush, J.
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Contact: John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 9208
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Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: johnq@tigr.org
Plate: 144
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Matches 248; Conservative
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota, Metazoa; Chordata; Catarrhini; Hominidae; Homo.

(bases 1 to 447), Limeles; Catarrhini; Hominidae; Homo.

Hillier, L., Clark, M., Dubuque, T., Eliston, K., Hawkins, M., Holman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.

The Washu-Marck Est Project
Unpublished (1995)
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/tissue_type="adenocarcinoma" ...
/tab_host="bHIOW (phage-resistant)" ...
/tab_host="bHIOW (phage-resistant)" ...
/tab_host="bHIOW (phage-resistant)" ...
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Clone distribution: MGC clone distribution information found through the I.M.A.G.E. Consortium/LLNL al.: http://mage.llol.gov
Plate: LLCM382 row: k column: 02
High quality sequence stop: 692.
1. cation/Qualifiers
1. c810
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Pred. No. 2.6e-50;
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/db_xref="taxon:9606"
/clone="IMAGE:3688825"
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98.8%;
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/organism="Homo sapiens"
/db xref="Laxon:9606"
/dlone="IMAGE:132240"
/clone="Lib="NoT_CGAE_Kid3"
/clone=lib="NoT_CGAE_Kid3"
/lab_host="DHI0B"
/note="Organ: kidney; Vector: pr7:3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I: Site_2: Eco RI; Ist strand cDNA was primed with a Not I - oligo(dT) primer, double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), diagested with N:1 I and cloned into the Not I and Eco RI sites of the modified pr7:73 vector. mRNA source: 2 pooled kidneys. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo.
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The Washu-Merck EST Project
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97 GAGGGTGTGCCGGCGCCCTGCCTCCAGAGGACGCCCCTAACGCCGCATCCCTGGCGCCC 156
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yv80g11.r1 Soares melanocyte 2NbHM Homo sapiens-cinA clone
IMACE:249092 5' similar to SP:S33363 S33363 GLY96 PROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 513;
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Pred. No. 2.4e-45;
0; Mismatches 3; Indels
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                                                                                                                                                           Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 384.
Location/Qualifiers
  National Cancer Institute, Cancer Genome
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                                                                                                                                              Std Error: 0.00
                                                           Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
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98.6%;
                                                                                                                            unknown library type
Insert Length: 834
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Best Local Similarity 98.6'
Matches 219; Conservative
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                                         Unpublished (1997)
                     Tumor Gene Index
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                                                                                                                                                                                                                                                                  /db_xref="taxon:0506"
/clone="lib"Soares:2806"
/clone="lib"Soares:2806"
/tissue_Ivpe="senescent_fibroblast"
/lab_host="DH10B (ampicillin resistant)"
/note="vector: pf773D (pharmacia) with a modified
polylinker V_TYPE: phagemid; Site_1: Not I; Site_2: Eco RI
: ist strand cDNA was primed with a Not I - oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA743819 513 bp mRNA EST 23-JAN-1998 ob01d04.s1 NC1_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1322407 3' similar to SW:IEX1_HUMAN P46695 RADIATION-INDUCIBLE IMMEDIATE-EARLY
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                           Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 3171 Std Error: 0.00
Seq primer: m0b.REGA+ET
High quality sequence stop: 401.
Location/Qualifiers
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  Louis, MO 63108
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NC1-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
  St.
4444 Forest Park Parkway, Box 8501,
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="GDB:1256850"
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Best Local Si
Matches 245;
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                                                                                                                     This clone is available royalty-free through LLNI,; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: M13RP1
High quality sequence stop: 192.
Location/Qualifiers
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Fukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostou
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1070)
NIH-MCC http://www.ncbi.nlm.nih.gov/MGC/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 205.4; DB 142; Length 212; Pred. No. 2.2e-42; 0; Mismatches 5; Indels 0;
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                      /clone_lib="Soares melanocyte 2NbHM"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              220 GACCTCAGCACTTTCCTCCAGCAACACCCGG 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 GACCTCAGCACTTTCCTCCAGCAACANCCGG 211
                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="GDB:3866798"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                Email: est@watson.wustl.edu
High quality sequence stops: 192
Source: IMAGE Consortium, LLNL
                                                                                                                                                                                                                                                                                     /db_xref="taxon:9606"
/clone="IMAGE:249092"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BE878459.1 GI:10327235
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Best Local Similarity 97.6%;
Matches 206; Conservative
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.1 kb. Library constructed by Life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA143404 504 bp mRNA EST 08-NOV-1997 2066609.rl Stratagene pancreas (#937208) Homo sapiens cDNA clone IMAGE:591880 5' similar to SW:GL96_MOUSE P46694 IMMEDIATE EARLY
Email: Kobert_Strausberg@nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
cDNA Library Preparation: Life Technologies, Inc:
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: .
http://image.llnl.gov
Plate: LLCMGGO row: column: 17
High quality sequence stop: 645.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59 TGC-TCACCATCGTCTTCTGCCAGATCCTGATGGCTGAAGAGGGTGTGCCGGCGCCCCTG 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="large_cell_carcinoma, undifferentiated"
/lab_host="DH10B (phage-resistant)"
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Pred. No. 1e-41;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 78.7%; Score 203; DB Best Local Similarity 98.1%; Pred. No. 1e-4 Matches 258; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                        1. .1070
/organism="Homo saplens"
                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:9606"
/clone="IMAGE:3890248"
/clone_lib="NIH_MGC_69"
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Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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JOURNAL
COMMENT
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AA143404
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us-08-799-910-9_copy_211_468.rst

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                                                                                                                                                                                                                                                                                                                                        /note="Organ: pancreas; Vector: pBluescript SK-; Site_1
ECORI; Site_2: XhOI; Cloned unidirectionally. Primer:
Oligo dT. Pancreatic adenocarcinoma cell line. Average
insert size: 1.0 kb; Oni-ZAP XR Vector; -5' adaptor
sequence: 5' GAATTCGGCACGAG 3' -3' adaptor sequence: 5'
                                                    Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (infe@image.llnl.gov) for further information.
Insert Length: 1695 Std Error: 0.00
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 392.
Location/qualifiers
1..504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 GCTCACCATCGTCTTCTGCCAGATCCTGATGGCTGAAAAGGGTGTGCCGGCGCCCCTGCC 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCCCTTTAATCTGACTTCGGAGCCCTCGG----ACTACGCTCTGGACCTCAGCACTTTCC 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GTCCGGCGCCAGCTGCCAGTCGAGGAACCGAACCC.AGCCAAAAGGCTTCTTTCTGCT 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5;
4444 Forest: Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 504;
                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="GDB:4623266"
/db_xref="taxon:9606"
/clone="IMAGE:591880"
/clone_lib="Stratagene pancreas (#937208)".
/lab_host="SOLR cells (kanamycin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76.7%; Score 197.8; DB 2;
90.7%; Pred. No. 2e-40;
tive 0; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      236 TCCAGCAACACCCGGCC 252
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Search completed: January 30, 2001, 18:47:28 Job time: 28459 sec

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by RNA polymerase II, the RNA polymerase which transcribes messenger RNA. RNA polymerase II transcription proceeds in vitro upon addition of several nuclear fractions designated TFIIA, B, D, E, F, H, I and J to RNA polymerase II holoenzyme. Fraction TFIID, has been shown to contains a TBP and other TAFs. Purification of ItlD and separation of its components reveals T proteins ranging in size from 30.250 kD. Serum raised against the TFIID fraction allowed cloning of the correspecies from lambda-gtil expression libraries.
                                                                                                                                                                                                            GAAGAGGGTGTGCCGGCGCCCTGCCTCCAGAGGACGCCCCTAACGCCGCATCCCTGGCG 153
                                                                                                                                                                                                                                                                     807 GAACCGGATGCCCAGCGATGCTGCCCACGGCCGCCGCATCGCTGCTCCACCTTCTTG 748
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                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids encoding human TATA-binding protein associated factor
                                                                                                                                                                                              34 CCAGCCAAAAGGCTTCTCTTTCTGCTGCTCACCATCGTCTTCTGCCAGATCCTGATGGCT
                                                                                                                                                 Length 1120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TATA-binding protein associated factor; TAF; nuclear protein; RNA polymerase transcription; TATA-binding protein; TBP;
                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TATA-binding protein associated factor, dTAFI140 cDNA.
                                                                                                           Sequence 1120 BP; 307 A; 291 C; 312 G; 210 T; 0 other.
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                                                                                                                                               DB 17;
                                                                                                                                                                      66
                                                                                                                                         0%; Score 33.6; DB 0%; Pred. No. 2.2;
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/*tag= a
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ROJ;
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                                                                                                                                              13.0%;
51.0%;
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93US-0013412.
93US-0087119.
96US-0646715.
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Wang E, Weinzierl
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Best Local Similarity
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30-JUN-1993;
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nucleic acids encoding them, are used to modulate transcription, including transcription initiation. TAFS are nuclear proteins involved in RNA polymerase I, II and III transcription. The peptides act by binding to a different TAF, an activator, or TBP (TATA-binding protein) or competitively inhibiting association of a TAF domain with another compound, typically a protein like TBP or another TAF, an activator,
                                                                                                                                                                                                     (TAF) polypeptide, dTAFI140 (mol. weight 40kD). TAF peptides derived from dTAFI130 alpha, dTAFI130 beta, dTAFI140, dTAFI160, dTAFI180, dTAFI1110, dTAFI1150, and dTAFI1250, their human equivalents and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94 GAAGAGGGTGTGCCGGCGCCCTGCCTCCAGAGGACGCCCCTAACGCCGCATCCCTGGCG 153
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       recombinant peptide(s), used
                                                                                                                                                                            T79601 encodes Drosophila TATA-binding protein associated factor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 33.6; DB
Pred. No. 2.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                        Example 1; Column 61-64; 86pp; English
(TAF) peptide(s) - for production of for modulating transcription of TAFs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              214 GCTCTGGACCTCAGCACTTTCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               687 CCGCCGGAGCTGCCCACCGTTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13.0%;
51.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 104; Conserv
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Caps

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66 DB 15;

Score 33.6; DB Pred. No. 2.2; 0; Mismatches

13.0%; 51.0%;

Lengt.h 1120; Indols

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154 CCCACCCCTGTGTCCCCCGTCGAAACCTTTAATCTGACTTCGGAGCCCTCGGACTAC 213
                                                                                                                                                                                                                                                                                   94 GAAGAGGGTGTGCGGCGCCCCTGCCTCCAGAGGACGCCCCTAACGCCGCATCCCTGGCG 153
                                                                                                                             866 ccAcrccAAccccAGATCCTCCTCCTCCTCCTCCGCTGGCACFFCTGCT-CCC
                                                                                       34 CCAGCCAAAAGGCITCTCTTTTTGCTGCTCACCATCTTTCTGCCACATCCTGATGGCT
                                                                                                                                                                                                                                                                                                                                                  214 GCTCTGGACCTCAGCACTTTCCTC 237
                                                                                                                                                                                                                                                                                                                                                                          687 CCGCCGGAGCTGCCCACCGTTTTC 664
                                          Matches 104; Conservative
                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-JAN-1994;
28-JAN-1993;
30-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-JAN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US5534410-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Screen for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Comai L,
Tjian R,
    Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
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surface molecule 4F2. Antisense DNA or RNA, antibodies, antibody fragments, and peptide and non-peptide antagonists to LA11 are useful as anticancer agents. The present sequence encodes human LAT1, which is specifically claimed in the present invention.
                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The TATA-binding protein associated factor dTAF1140 (including specific antibodies and fusion products) are used in drug screening, diagnostics and therapeutics. They are used in the development of specific biochemical assays for screening compounds that agonise or antagonise selected transcription factors involved in regulating
                                                                                                                                                                                                                                                             8 GCCAGCTGCCAGTCGAGGAACCGAACCCAGCCAAAAGGCTTCTCTTTCTGTGCTCACCA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TATA-binding protein associated factor; dTAFII40; ss; screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleotide sequence and deriv. antibodies, useful
                                                                                                                                                                                                                                                                                                                                               PCCTCTTCTGCCACACCTGATGGCTGAAGAGGCTGTGCCCGGGGGCCCTTGCCTTCCAG
                                                                                                                                                                                                                                                                                                                                                                      CCGLGaactGcLacagcgtgaaggcngcnacncgggtccaggatgccLttgccgccg
                                                                                                                                                                          Length 4539;
                                                                                                         29 other;
                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               therapeutic; gene transcription regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1120 BP; 307 A; 292 C; 311 G; 210 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tanese N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IATA-binding protein-associated factor dTAFII40 cDNA.
                                                                                                                                                                     13.1%; Score 33.8; DB 21; 53.0%; Pred. No. 2.6;
                                                                                                                                                                                                                  53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TATA-binding protein associated protein factors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    expression associated with human pathology.
                                                                                                         Sequence 4539 BP; 765 A; 1450 C; 1297 G; 998 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ruppert S,
                                                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in screening, diagnostics and therapeutics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 89-92; 180pp; English.
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80..913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ), Hoey T, Ru
Weinzierl ROJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q70728 standard; cDNA; 1120 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94WO-US01114.
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93US-0087119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dynlact BD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1994-264019/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wang E,
                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           corresponding
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30-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diagnostic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9417087-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04 - AUG - 1994
                                                                                                                                                                                                                  62;
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Tjian R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila
                                                                                                                                                                          Onery Match
                                                                                                                                                                                              Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            070728;
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                                                                                                                                                                                                                                                                                                                                             89
                                                                                                                                                                                                                                                                                                                                                                                        616
                                                                                                                                                                                                                Matches
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This is the nucleotide sequence encoding the Drosophila TATA-binding protein (TBP) associated factor (TAF) designated TAFI160. The protein is a component of the TFI1D fraction required for reconstituting kNA polymerase II in vitro transcription activity. The encoded protein has an estimated mol. wt. of 60 kD by SDS-PAGE.
The invention relates to purified proteins involved in transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Screen for cpds. that bind human TATA-binding prolein associated factor - by testing ability to bind to polypeptide fragments of the factor, useful as (ant)agonists of transcription factors involved in
                                                                                                                  Drosophila, TATA-binding protein, TBP associated factor, TFIID;
RNA polymerase II; transcription; messenger RNA; huclear fraction;
                                                                                     Drosophila TATA-binding protein associated factor dTAFII60 gene.
                                                                                                                                                                                                                                                                                                                                                                                        ۲
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ruppert S, Tanese N;
                                                                                                                                   RNA polymerase II; transcription; messenger RNA;
holoenzyme; lambda-gtll; expression library; ds.
                                                                                                                                                                                                                                                 /product= Drosophila TAFII60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Examples; Column 61-64; 86pp; English
                                                                                                                                                                                                     Location/Qualifiers
80..916
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dynlacht BD, Hoey T,
Wang E, Weinzierl ROJ;
 ВР
                                                                                                                                                                                                                                                                                                                                                                  94US-0188582.
93US-0013412.
93US-0087119.
T42214 standard; cDNA; 1120
                                                                                                                                                                                                                                                                                                                                        93US-0013412
                                                          (first entry)
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                                                                                                                                                                            Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                             (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                     /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WP1; 1996-333245/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; T42214.
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The present invention describes a cell surface protein which is an L-type amino acid transporter-1 (LAT1), which mediates the transport of neutral amino acids, leucine, isoleucine, phenylalamine, methionine, tyrosine, tryptophan, valine and histidine, into the cell independently of sodium ions. The LAT1 protein conjugates with the cell membrane
                                                                        1201 GTCCAGGGGCACCATTTGAACCAGGAGACCTGGAGGTCCAACTTCACCTTAGCACCAG 1142
                                                                                                                                                                                                                                                                                                                                                                                                          Human L-type amino acid transporter 1 nucleotide sequence SEQ ID NO:1.
                                                                                                               CCAGAGGACGCCCTAACGCCGCATCCCTGGCGCCCACCCCTGTGTCCCCCGGTCCTCGAG 180
                                                                                                                                                                     181 CCCTTTAATCTGACTTCGGAGCCCTCGGACTACGCTCTGCACCTCAGCACTTTCCTCCAG 240
                                                                                                                                                                                     1021 CACCAGGAGCCCGTCTTGGAGCCATGGAGCTGGATTTTCGCCTTGAAGACCAT 962
     GTCCGGCCCCAGCTGCCAGGAACCGAACCCAGCCAAAAGCTTTCTTGCTG 60
                                                          CTCACCATCGTCTTCTGCCAGATCCTGATGGCTGAAGAGGGTGTGCCGGCGCCCCTGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neutral amino acid transporter protein which conjugates with cell membrane protein 4F2 and operates independently of sodium ions is useful for screening potential cancer proliferation inhibitors -
                                                                                                                                                                                                                                                                                                                                                                                                                                                 neutral amino acid transporter; tumour; cancer; proliferation; cell membrane surface 4F2 molecule; anticancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                     L-type amino acid transporter 1; LAT1; 4F2hc; 4F2 heavy chain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 9; Page 125-132; 189pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NISC-) JAPAN SCI & TECHNOLOGY CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "I,AT1"
                                                                                                                                                                                                                                                                                                                         A08372 standard; cDNA; 4539 BP
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/product= "
1590..4474
/*tag= c
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66..1589
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                                                                                                                                                                                                                            241 CAACACC 247
                                                                                                                                                                                                                                                      961 TTTCACC 955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; Y82488
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                               12-JUL-2000
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                                                                                                                                                                                                                                                                                                                                                    A08372;
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5'UTR
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                                                                                                                                                                                              2539 AGGATGCAGCGCCTCTGTCCCTAGGGGACCCCTTTGTGGCCCAGATGCTGACCCCCA 2480
                                                                                                                                                                               98 AGGGTGTGTGCCGCCCCTGCCTCCAGAGGACGCCCCTAACGCCGCATCCCTGGCGCCCA 157
                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1 describes the determination of the presence of a mutation in the pro-alphal(III) gene. Primers used in PCR are given in 030834-48.
attack, neurological disorders, e.g. neuroblastoma, glioblastoma or cancers, or to promote apoptosis in cells, or treat refractory epilepsy. They can also be used for screening test substances for III biological activity. IBI producing cells can be used therapeutically to produce IBI in a subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kit for detecting genetic pre-disposition for vascular uneurysms - contains primer to amplify portions of Type III procollagen DNA and detects mutation in standard procollagen DNA
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                                                                                                                            DB 19; Length 2953;
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                                                                                                                         Score 34.8; DB 19; Length
Pred. No. 1.3;
0; Mismatches 32; Indels
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                                                                                 Sequence 2953 BP; 620 A; 906 C; 840 G; 587 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= a
/label= Type_III_procollagen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13.3%; Score 34.2; DE 46.2%; Pred. No. 1.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  58
                                                                                                                                                                                                                                                                                                                                                                                                                                              Mutation; pro-alphal(III); primer; PCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tromp GC;
                                                                                                                                                                                                                                                    2479 CCCCAGCCCTGCCTTCCCCAGCCCC 2454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 1A-F; 44pp; English.
                                                                                                                                                                                                                                    158 CCCCTGTGTCCCCGGTCCTCGAGCCC 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
103..3690
                                                                                                                                                                                                                                                                                                                                                                                                                    Type III procollagen (prior art).
                                                                                                                                                                                                                                                                                                                         9/c
Q30849 standard; cDNA; 3690 BP
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                                                                                                                         13.5%;
62.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kuivaniemi SH, Prockop DJ,
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                                                                                                            Ouery Match
Best Local Similarity 62.0.
Best Local Similarity 62.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 13.3
Best Local Similarity 46.2
Matches 114; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1992-398878/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P. PSDB; R28916
                                                                                                                                                                                                                                                                                                                                                                                         24-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-MAY-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                              030849;
                                                                                                                                                                                                                                                                                                         RESULT 11
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166 TCCCCCGTCCTCGAGCCCFTTAAFCTGACFTCGGAGCCCTCGGACTACGCTCTGGACCTC 225

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A00010 to A02716 represent polynucleotides isolated from cDNA libraries constructed from human colon cancer cell lines. The present invention also describes a method of detecting differentially expressed genes correlated with a cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample derived from a cell suspected of being cancerous, where detection of the differentially expressed gene product is correlated with a cancerous state of the cell from which the test sample was derived. The polynucleotides sequences can be used in a method for detecting flafferentially expressed genes correlated with a cancerous state of a mammalian cell. The polynucleotides can also be used as probes for detecting and mapping related genes. They can be used in diagnosis and prognosis of diseases and disorders (e.g. identification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Labat 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Polynucleotide library used to determine cancerous states of mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pre-metastatic or metastatic cancerous states, stages of cancer, or responsiveness of cancer to therapy). This is particularly for breast cancer, oestrogen receptor-positive breast cancer, oestrogen receptor-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sudduth-Klinger J;
                                                                                                                                              Human colon cancer cell line polynucleotide sequence SEQ ID NO:2475
                                                                                                                                                                                   Human; colon cancer; tumour; diagnosis; gene expression product; probe detection; cancerous state; metastasis; identification; breast cancer; oestrogen receptor-positive breast cancer; therapy; oestrogen receptor-negative breast cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Escobedo J, Innis MA, Garcia ru, Juran, Ajlese K, Randazzo F, Kennedy GC, Pot D, Kassam A; manac R, Crkvenjakov R, Dickson M, Drmanac S, Lab Kita D, Garcia V, Jones LW, Stache-Crain B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   negative breast cancer, lung cancer, and colon cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1000 BP; 21 A; 53 C; 574 G; 22 T; 330 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 994; 1097pp; English.
                                  A02484 standard; cDNA; 1000 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                           98US-0085537.
98US-0085696.
98US-0105234.
                                                                                                                                                                                                                                                                                                                                                                                       99WO-US10602
                                                                                                                                                                                                                                                                                                                                                                                                                            98US-0085426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-0105877
                                                                                                           19-MAY-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lamson G, Drmanac R,
Leshkowitz D, Kita D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Giese K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CHIR ) CHIRON CORP. (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-126369/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Williams LT,
                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                              W09958675-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                           15-MAY-1998;
15-MAY-1998;
21-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                       13-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                   18-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                          14-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Reinhard C,
                                                                         A02484;
6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cells
                 A02484/C
ID A024
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This cDNA sequence includes an open reading frame encoding rat. islet-brain 1 (IBI, see W80601), a transcriptional activator that is involved in the control of the GLUTZ and insulin genes by interacting with homologous cis-regulatory elements of the GLUTZ and insulin gene promoters. IBI CDNA was isolated from a rat differentiated insulinoma INS-I CDNA was isolated from a rat differentiated insulinoma INS-I CDNA was isolated from a rat care of the GLUTZ promoter. IBI is abundantly expressed in the parcreatic islets in the brain. Human IBI polynucleotide (see W80602) are also claimed. IBI colypeptides, nucleic acids, agonists and antagonists can be used in the Irealment or diagnosis of diabetes, neurodegenerative discoders or cancers, to inhibit cells from undergoing apoptosis, to treat dementia, parkinsonism, Alzheimer's disease, neuronal disabilities
IBI; islet-brain 1; transcription factor; rat; diabetes; dementia; Parkinson's disease; Alzheimer & disease; epilepsy; neuroblastoma; glioblastoma; apoptosis; cancer; autoimmune disease; systemic lupus erythematosus; myocardial infarction; ischaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  such as speech disorders and memory alteration, autoimmune diseases affecting the CNS such as systemic lupus erythematosus, diabetes, heart diseases such as myocardial infarct and ischemia or brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated transcription factor islet-brain 1 - used to develop products for treating e.g. diabetes, neurodegenerative disorders, cancers, autoimmune disease, heart disease or epilepsy
                                                                                                                                                                                                                                                                   Rat transcription factor islet-brain 1 (181) cDNA.
                                          226 ACCACTTTCCTCCAGCAACACCCGGCCGCCTT 257
                                                                           683 CCCCCCNCCCNTCGCCNNCNCCCNCCCNCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 13; Fig 1A; 111pp; English.
                                                                                                                       RESULT 10
V62462/c
ID V62462 standard; cDNA; 2953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98WO-GB00972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97GB-0009920.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97GB-0006731
                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                       diagnosis; therapy; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1998-568278/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KIDDLE S J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bonny C, Waeber G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (NICO/) NICOD P. (WAEB/) WAEBER G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; W80601.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9844106-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-MAY-1997;
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                                                                                                                                                                                                                               15-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-OCT-1998
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                                                                                                                                                                                                 V62462;
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Score 36.2; DB 21; Length 1000; Pred. No. 0.42;): Mismatches 84; Indels 0;

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Conservative

Ouery Match Best Local Similarity Matches 68; Conserv

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14.08;

CCGGCGCCCTGCCTCCAGAGGACGCCCTAACGCCGCATCCCTGGCGCCCACCCCTGTG 165

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Sequences V69704 to V69715 represent introns of the gene encoding an equilibrative nucleoside transport protein (iENTP), which is insensitive to introbency] mercaptopurine riboside (NBMPR). Cells transformed with a construct containing the iENTP nucleic acid can be used to produce the protein recombinantly. iENTP is used to identify specific ligands (preferentially methyiral and antitumnour nucleoside analogues that are preferentially transported into cells) and to raise antibodies. Cells in the iENTP provides all available transport activity are used; contents provides all available transport activity are used; contents protectial drugs). Fragments of the iENTP nucleic acid are used, as probes, primers, antisense molecules, and ribozymes for therapy or diagnosis, and knockout mice in which both alleles encoding iENTP contain an inactivating defect are also useful for drug screening. Cells that have been transduced with iENTP nucleic acid ex vivo are used particularly, for cancer chemotherapy. Vectors in which the iENTP gene
                                                                                                                                             Equilibrative nucleoside transport protein; iENTP; NBMPk; transport; nitrobenzylmercaptopurine riboside; antiviral; antitumour; screening; inhibitor; drug; knockout mice; cancer; chemotherapy; gene therapy; adenosine deaminase; factor VIII; intron; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New equilibrative nucleoside transport protein insensitive to nitrobenzylthio-purine riboside – useful for, e.g. identifying specific therapeutic nucleoside analogues and in gene therapy to protect transduced cells against ablative chemotherapy
                                                                                                          Nucleotide sequence of intron 3 of iENTP gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 is linked to a heterologous gene (e.g. encr
factor VIII) can be used for gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SJUD-) ST JUDE CHILDREN'S RES HOSPITAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 88; 114pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patel DH;
     ВР
                                                                                                                                                                                                                                                                                                                                                              98WO-US07283.
                                                                                                                                                                                                                                                                                                                                                                                                98US-0058389.
97US-0838845.
                                                                            (first entry)
V69706 standard; DNA; 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Belt JA, Crawford CR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1998-594576/50.
                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                               WO9846749-A1
                                                                                                                                                                                                                                                                                                                                                                                                09-APR-1998;
11-APR-1997;
                                                                                                                                                                                                                                                                                                                                                            10-APR-1998;
                                                                      08-FEB-1999
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Sequence 170 BP; 18 A; 77 C; 42 G; 33 T; 0 other;

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                                        101 GTGTGCCGGCGCCCTGCCTCCAGAGGACGCCCTAACGCCGCATCCCTGGCGCCCACCC 160
                          Gaps
                                                       DB 19; Length 170;
                       29;
 Score 37.6; DB Pred. No. 0.12; 0; Mismatches
                                                                                  161 CTGTGTCCCCGGTCCTCGAGCCCT 184
                       ;
0
14.6%;
                       Conservative
Query Match
Best Local Similarity
                      52;
                      Matches
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RESULT 242235/c

111 | 1111 | 1111 | 11111 | ct9c9ccct9ccctccaqccct 84

61

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This invention describes novel polypeptide fragment sequences. (I) and their encoding nucleic acids (II) which are highly expressed in normal bladder tissue and have cytostatic activity. (II) are used for recombinant expression of (I) and to isolate complete genes. (I) are used to identify agents suitable for the treatment of bladder tumours, to directly treat this form of cancer (including expression from gene therapy vectors), or are used in a preparation for cancer trealment. (I) is also used for the generation of specific antibodies. (II) are identified by assembling ESTS (expressed sequence tags) from a particular comparison of expression patterns. This allows a significantly longer fragment of the gene to be revealed, and therefore reduces the number of fallures because of ESTS from different libraries crepresenting different parts of the same unknown gene distorting the estimated frequency of occurrence in a particular itssue. 242122-242248 cepters of in patterns in the contract of includer tissue condary inbrary which encode the protein fragments represented in y60329-y60591.
                                                                                                                                                                                                                                                                                                                                                                                                                Dahl E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 TCACCATCGTCTTCTGCCAGATCCTGATGGCTGAGGGGTGTGCCGGGGGCGCCCTGCCTC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240 TGCTGCTGCAATTGCTGCTGCTGCTGCTGCTGCTGTAACTGCTGGAGCTGCTGCTGCTGC 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122 CAGAGGACGCCCCTAACGCCGCATCCCTGGCGCCCACCCCTGTGTCCCCCGTCCTCGAGC 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 TCCGGCGCCCAGCTGCCAGGCAACCGAACCCAGCCAAAAGGCTTCTCTTTCTGCTGC 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                          treatment; EST; expressed sequence tag; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polypeptides and their nucleic acids, useful for treatment of bladder tumour and identification of therapeutic agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                                                                                                                                                                         Hinzmann B, Schmitt A, Pilarsky C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1526;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1526 BP; 365 A; 523 C; 437 G; 201 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 0.41;
0; Mismatches 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 20;
                                                                                                     Human normal bladder tissue cDNA derived EST 11.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 36.4; DB
                                                                                                                                                                                                                                                                                                                                                                  (META-) METAGEN GES GENOMFORSCHUNG MBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 3; Page 234; 366pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; Y60556, Y60557, Y60558.
       ВР.
242235 standard; cDNA; 1526
                                                                                                                                                                                                                                                                                                   98DE-1018620.
                                                                                                                                                                                                                                                                                                                                   98DE-1018620.
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                                                                     31-JAN-2000 (first entry)
                                                                                                                                                          cancer; gene therapy; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 114; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          Specht T,
                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-602416/52
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                                                                                                                                        bladder;
                                                                                                                                                                                                                          DE19818620-A1
                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                 21-APR-1998;
                                                                                                                                                                                                                                                                                                                                   21-APR-1998;
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/note= "Shares 24% identity to Aquifex pyrophilus esterase 28LC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 9; Page 70-71; 78pp; English.
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                                                                                                                                                                                                                                                    99WO-US20287.
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                                                                                                                                                                 techniques"
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                                               Q
                                                           133..4011
                                                                             /*tag= c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         be used for gene therapy.
                                                                                                                                                                                                                                                                                                            (INCY-) INCYTE PHARM INC.
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Matches 76; Conservative
                                                                                                                        /*tag=
                                                /*tag=
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                                                                                                                                                                                                                                                                                                                                                                   2000-256994/22
                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; Y70474.
                                                                                                                                                                                          A0200014248-A1
                                                                                                                                                                                                                                                   03-SEP-1999;
                                                                                                        misc_binding
                                 sig_peptide
                                                                                                                                                                                                                       16-MAR-2000
                                                              mat_peptide
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V69706
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                                                                                                                                                                                This represents the 5' UTR (untranslated region) of the DNA that

cneedes an equilibrative nucleoside transport protein (iENTP), which
is insensitive to nitrobeacylmercaptopurine riboside (NBMRN). Cells
ctransformed with a construct containing the iENTP nucleic acid can be
cused to produce the protein recombinantly. iENTP is used to identify
cused to produce the protein recombinantly. iENTP is used to identify
considered ic ligands (particularly antiviral and antitumour nucleoside
antibodies. Cells in which iENTP permeants of iENTP and to raise
antibodies. Cells in which iENTP permeants of iENTP and (b) to screen
contibodies. Cells in which iENTP (potential drugs). Fragments of the iENTP
cucleic acid are used, as probes, primers, antisense molecules, and
cribozymes for therapy or diagnosis, and knockout mice in which both
alleles encoding iENTP contain an inactivating defect are also useful for
caruge screening. Cells that have been transduced with iENTP nucleic acid
caruge screening. Cells that have been transduced with iENTP nucleic acid
caruge screening.
caruge the iENTP gene is linked to a heterologous gene (e.g. encoding adenosine
contains and factor VIII) can be used for gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             anti-arterioscierotic; hepatotropic; anti-leukeemic; anti-inflammatory; anti-arterioscierotic; depatotropic; anti-leukeemic; anti-inflammatory; anti-arterior anti-arterior; dematological; neuroprotective, anti-apileptic; cancer; anti-Alzheimer's; anti-Parkinsonian; cerebroprotective; ophthalmological; anti-infertility; anti-allergic; vasotropic; immunosuppressive; hypotensive; gene therapy; prevention; treatment; arteriosclerosis; cell proliferative disorder; autoimmune/inflammatory; diabetes mellitus; neurological; vision; reproductive; smooth muscle; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100 GGTGTGCCGCCCCCTGCCTCCAGAGGACGCCCCTAACGCCGCATCCCTGGCGCCCCACC 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cyclic nucleotide-associated protein-2; CNAP-2; human; cytostatic;
                                                                                   New equilibrative nucleoside transport protein insensitive to nitrobenzylthio-purine riboside - uscill for, e.g. identifying specific therapeutic nucleoside analogues and in gene therapy to protect transduced cells against ablative chemotherapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 6354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human cyclic nucleotide-associated protein-2 (CNAP-2) cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6354 BP; 1322 A; 1797 C; 1873 G; 1355 T; 7 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 38.6; DB; Pred. No. 0.14; 0; Mismatches
(SJUD-) ST JUDE CHILDREN'S RES HOSPITAL
                                                                                                                                                       Example 3; Pages 76-79; 114pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               160 ccrcrccccccrccrccAGcccr 184
                              Patel DH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 251683 standard; cDNA; 4228 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 65.9
nes 56; Conservative
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                           Crawford CR,
                                                        WPI; 1998-594576/50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                           Belt JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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Matches
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The present sequence is the CDNA encoding human cyclic nucleotide associated protein-2 (CNAP-2), identified in Incyte clone 3149674, that is isolated from ADRENOVIO CDNA library. It is expressed in nervous, reproductive, cardiovascular and haematopoietic/immune tissues. CNAP sequences may be used for prevention, treatment and diagnosis of diseases associated with altered CNAP expression such as, cell proliferative disorders (e.g. arteriosclercis; cirrhosis, leukaemia, lymphoma and cancer of the breast, prostate, lung and brain), autoimmune/confined and psoriasis, neurological disorders (e.g. asthma, anaemia, diabetes mellitus, multiple sclerosis and psoriasis), neurological disorders (e.g. applepsy, conjunctivitis, glaucoma, cataracts and retinitis pigmentosa), reproductive disorders (e.g. infertility, uterine fibroids, ectopic pregnancies and impotence) and smooth muscle disorders (e.g. angina).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         135 TAACGCCGCATCCCTGGCGCCCCACCCTGTGTCCCCCGTCCTCGAGCCCTTTAATCTGAC 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patterson C, Tang YT;
                                                                                                          /bound_moiety= "Primer or Probe"
/note= "Useful for amplification or hybridisation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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/product= "Mature CNAP-2 protein"
136..165
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Howells D,

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\ensuremath{\mathsf{New}}. nucleic acid fragment encoding gene products - can be used for genetic analysis and mapping
                                                                                                                                             93WO-GB01467
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                                                                                                                                                                                                                                                                                Starkey M;
                                                                                                                                                                                                                                                                                                                  WPI; 1994-035056/04.
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285 tegecate 292
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                              Homo sapiens.
                                                                                                                                           13-JUL-1993;
                                                                                                                                                                               13-JUL-1992;
                                                                                                                                                                                                                                                        Gross J, Ha
Sibson DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
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                                                                                                        20-JAN-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-APR-1998;
11-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to (A) or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                              lluman; secreted protein; expressed sequence tag; EST; haematopoissis;
tissue growth; activin; inhibin; chemotaxis; chemokinesis; haemostatic;
receptor; ligand; thrombolytic; anti-inflammatory; cadherin; anti-tumour;
gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents a human expressed sequence tag (EST). The polynucleotide, which is a secreted EST, and the encoded protein are predicted to have useful biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, immune stimulating or suppressing activity, haematopolesis regulating activity, tissue growth activity, haematopolesis regulating chamotactic/chemokinetic activity, haemostatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, cadherin/tumour invasion suppressor activity, tumour inhibition activity. The polynucleotide may also be useful for gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          175 CTCGAGCCCTTTAATCTGACTTCGGAGCCCTCGGACTACGCTCTGGACCTCAGCACTTTC 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                193 CTCGAGCCCTTTAATCTGACTTCGGAGCCCTCGGACTACGCTCTGGACCTCAGCACTTTC 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 193;
                                                                                                                                                                                                                                                                                                                                                                                                         Lavallie ER, McCoy JM, Merberg
Treacy M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New polynucleotides encoding human secreted proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 193 BP; 35 A; 39 C; 68 G; 51 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32.6%; Score 84; DB 20; I
100.0%; Pred. No. 4.2e-14;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 164; 618pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       235 CTCCAGCAACACCCGGCCGCCTTC 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               133 CTCCAGCAACACCCGGCCCTTC 110
                                                                                                                                                                                                                                                                                        98WO-US0695
                                                                                                                                                                                                                                                                                                                              97US-0838821
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                   (GEMY ) GENETICS INST INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q77534 standard; DNA; 297
                                                                                                                                                                                                                                                                                                                                                                                                           , Jacobs K,
Spaulding V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human genome fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
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                                      EST clone BY66.
                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                           WO9845436-A2.
                                                                                                                                                                                                                                                                                        10-APR-1998;
                                                                                                                                                                                                                                                                                                                            10-APK-1997;
                                                                                                                                                                                                                                                                                                                                                                                                       Agostino MJ,
                                                                                                                                                                                                                                                  15-0Cr-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                             Racie LA,
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225 tcc99c9ccagttgccagttaa99gaccaaacctcgccagaaggcttctttcgggttga 284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 TCCGGCGCCAGCTGCCAGTCGAGGAACCGAACCCAGAAAGGCTTCTTTTCTGCTGC 61
                                                       Human nucleic acid fragments, isolated from brain, adrenal tissue, the placenta or bone marrow comprise any of: (A) a sequence selected from (Q76401-Q77613), (B) an allelic variation of a
                                                                                                                                                                                                                        Preferred sequences exhibit no more than 90% homology to a human
                                                                                                                                                          sequence as described in (A), or (C) a sequence complementary
                                                                                                                                                                                                                                                                                                                                                                                                                   Length 297;
                                                                                                                                                                                                                                                                                                                                                                                                     DB 15; Length 29'
0.0026;
ches 15; Indels
                                                                                                                                                                                                                                                                                                                Sequence 297 BP; 66 A; 117 C; 61 G; 52 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                         17.1%; Score 44; DB 1:
77.9%; Pred. No. 0.002:
tive 0; Mismatches
Claim 1; Page 575-576; 616pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                V69699 standard; DNA; 6354 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5' UTR sequence of iENTP DNA.
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97US-0838845.
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Matches 53; Conservative
                                                                                                                                                                                                                                                         sequence known per se.
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The patent discloses methods for the treatment and diagnosis of cardiovascular diseases by novel human genes which are differentially expressed in different cardiovascular disease states. Compositions which can modify TGF-beta signalling pathway are identified by screening. These are used therapeutically to treat fibroproliferative and oncogenic disorders, including diabetic retinopathy, artherosclerosis, pancreatic cancer, angiogenesis, inflammation, fibrosis, tumour growth and vascularisation. The present sequence is fichd605 gene which is upergulated in monocytes treated with oxidised LDL (low density lipoprotein) can be used to design cardiovascular disease treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identifying substances for ameliorating symptoms of fibroproliferative diseases or oncogenic related disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTCACCATCGTCTTCTGCCAGATCCTGATGGCTGAAGAGGGTGTGCCCGGCGCCCTGCCT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    271 ctcaccatcgtcttctgccagatcctgatggctgaagagggtgtgccggcgccctgcct 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 CCAGAGGACGCCCCTAACGCCGCATCCCTGGCGCCCACCCCTGTGTCCCCCGTCCTCGAG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             211 glccggcgccagctgccagtcgaggaaccgaacccagccaaaaggcttctttttgctg 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 CCCTTTAATCTGACTTCGGAGCCCTCGGACTACGCTCTGGACCTCAGCACTTTCCTCCAG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GFCCGGCCCAGCTCCAGTCCAGGAACCCACCAAAAGGCTFCTCTTTTTCTGCTG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       strategies. Depending on whether the up-regulation has a pathogenic protective effect treatment methods can be designed to increase or decrease the activity of the protein product of the gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 258; DB 21; Length 1228; 100.0%; Pred. No. 1e-60; Indels 0; tive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1228 BP; 265 A; 361 C; 341 C; 261 T; 0 other;
                                         "fcdh605 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Examples; Fig 5; 214pp; English
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                                                                                                                                                                                                                                                                                                (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                               98US-0126640.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         451 caacacccggccgcctc 468
                                            /product-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          al Similarity 100.
258, Conservative
                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-205414/18
                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; Y45017
                                                                                             WO200006206-A1
                                                                                                                                                                                                30-JUL-1999;
                                                                                                                                                                                                                                               30-JUL-1998;
                                                                                                                                              10-FEB-2000
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..
                                                                                                                                                                                   reated with oxidised low density lipoproteins (LDL). Differential display was used to detect genes that are differentially expressed in monocytes treated so as to simulate the conditions under which comm cells develop during atherogenesis. Both fchd605 and fchd602 (see T94470) are up-regulated under the disease condition of treatment with oxidised LDL. The fchd605 gene product (see W36006) has sequence similarity to mouse gly96. The discovery of the up-regulation of these 2 genes provides a fingerprint profile, e.g. markers for the study of cardiovascular diseases, including and arterial inflammation. Methods are provided for the diagnosis, monitoring in clinical trials, screening for therapeutically effective compounds, and treatment of cardiovascular diseases based on discoveries regarding the expression patterns of novel genes fedels 1 (see T94467), fchd540 (see T94468), fchd545 (see T94469),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diabetic retinopathy; fibroproliferative disorder; artherosclerosis; TGF-beta signalling pathway; TGF, Transforming growth factor; pancreatic cancer; angiogenesis; inflammation; fibrosis; tumour growth; vascularisation; cytostatic; antidiabetic; opthalmological; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  211 gtccggcgccagctgccagtcgaggaaccgaacccagccaaaaggctcttttttgctgctg 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCCTTTPAATCTGACTTCGGAGCCCTCGGACTACGCTCTGGACCTCAGCACTTTCCTCCAG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 CTCACCATCGTCTTCTGCCAGATCCTGATGGCTGAAGAGGGTGTGCCGGCGCCCCTGCCT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCAGAGGACGCCCTAACGCCGCATCCCTGGCGCCCACCCCTGTGTCCCCCGGTCCTCGAG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GTCCGGCCCCAGCTGCCAGTCGAGCAGCCGAACCCAAAAGGCTTCTCTTTTCTGCTG 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 258; DB 18; Length 1228; 100.0%; Pred. No. 1e-60; 0; Mismatches 0; Indels 0;
                                         New genes differentially expressed in cardiovascular disease for diagnosis, drug screening and treatment of cardiovascular disease, e.g. atherosclerosis, restenosis, hypertension, etc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1228 BP; 265 A; 362 C; 340 G; 261 T; 0 other;
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                                                                                                                                              Claim 1; Fig 5; 163pp; English
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BE383865 951 bp mRNA EST 21-JUL-2000 601273192F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614255 5' mRNA sequence.
BE383865
BE383865.1 GI:9329230

RESULT 1 BE383865 LOCUS DEFINITION human

ACCESSION VERSION KEYWORDS SOURCE

ALIGNMENTS

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// organism="Homo sapiens"
// Ab_xref="taxon:966"
// Ab_xref="taxon:966"
// Ab_cos="Impage:1614255"
// Ab_cos="Impage:1614255"
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// Ab_host="bull0 (Apage-resistant)
// A
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National Institutes of Health, Mammalian Gene Collection (MGC)
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert Strausbergenih.gov
Talssue Procurement: ArCC/CCT/DT/DTP
CDNA Library Arrayed by: The 1.MA.G. F. Consortium (LILNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the 1 TM.A.G. F. Consortium/LLNL at: image.llnl.gov
Plate: LLCN276 row: 9 column: 24
High quality sequence stop: 74.
                            Craniata; Vertebrata; Euteleostomi;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 951)
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Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausbergenih.gov
Tasiu 1965-1550
Email: Robert Strausbergenih.gov
Tissue Procurement: ArCC/DCTD/PTP
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone. istribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM72 row: column: 07
High quality sequence start: 7
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11H-MGC http://www.ncbi.nlm.nih.gov/MGC/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Μ
adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using 2AP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
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NIH-MCC http://www.ncbi.nlm.nih.gov/MCC/.
National Institutes of Health, Mammalian Genc Collection (MGC)
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                                                                                                                       3;
                                                                                                  DB 106; Length 765;
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                                                                                                Score 621.4; DB 10
Pred. No. 9.2e-148;
0; Mismatches 1;
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BE621346
BE621346.1 GI:9892286
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11 Similarity 99.4%;
655; Conservative
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="InAGE:389570"
/clone_lib="NH_MGC_70"
/tissue_type="epithelioid carcinoma"
/fab_host="bH108 (phage-resistant)
/note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: NoI1; Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.1 kb. Library constructed by Life Technologies."
1 288 c 193 g 126 t
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                                                                                                 CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LI.NL.) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://mage.lln.gov column: 09
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Pred. No. 2.2e-143;
0; Mismatches 38; Indels
                 Contact: Robert Strausberg, Ph.D
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                    High quality sequence stop: 613.
Location/Qualifiers
1. .762
                                                                                    Tissue Procurement: ATCC
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Local Similarity 93.9%;
nes 705; Conservative
Unpublished (1999)
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/lab.hos="DH10B (phage-resistant)"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.1 kb.
137 c 268 g 134 t
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NIH-MGC http://www.nobi.nlm.nih.gov/MGC/.
                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Tel: (30) 496-1550
Email: Robert_Strausbergenih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://amage.llnl.gov
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                                                                                                                                                                                                       BE882130 916 bp mRNA EST 27-SEP-2000 601505227F2 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3906633 :
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                                                                                                                           715 ATTTCTTATTGCTCCTAATTAATATTATAT 745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High quality sequence stop: 659,
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/clone="IMAGE:3906823"
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                                                                                                                                                                                                                                    mRNA sequence.
HE882130
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DEFINITION
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VERSION
KEYWORDS
SOURCE
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ORIGIN
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone=lib="NIH_MGE:150719]
/clone=lib="NIH_MGC_14"
/tissue_type="renal cell adenocarcinoma"
/labost="DullOB (playe-resistant)"
/note="Organ: kidney; Vector: pOTH7; Site_1: Xho1; Site_2:
ECORI: CDNA made by oligo-dT priming. Directionally
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 603)
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BE273386
BE273386.1 GI:9148012
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Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: DcTD/DrP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at: image.llnl.gov
Plate: LLCM186 row: j column: 24
High quality sequence stop: 579.
                                                                                                                                                                       391 CCCTTTAATCTGACTTCGGAGCCCTCGGACTACGCTCTGGACCTCAGCACTTTCCTCCAG 450
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                  CTCACCATCGTCTTCTGCCAGATCCTGATGGCTGAAGAGGGTGTGCCGGCGCCCCTGCCT
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cloned into EcoRI/XhoI sites using the following 5, adaptor: GCACGGG(G). Size-solected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using 2AP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)." 241 c 154 g 96 t
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1 (bases 1 to 810)
NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
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601'44706F1 NIH_MGG_39 Homo sapiens cDNA clone IMAGE:3688825 :
                                                                                                                                  155 CCAGGGCCTCTGGGGGCACCGAAAGGGCAGGCAGGGTTCTCTACCCTGGAGTGGTCC
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                                                                                                    603;
                                                                                              48.0%; Score 589.4; DB 106; Length 11arity 99.7%; Pred. No. 1.3e-139; Conservative 0; Mismatches 1; Indels
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/tab_nost="DHIOB (phage-resistant)"
/note="Organ: pancreas; vector: pUTB7; Site_1: Xho1;
Site_2: EcoR1; cDNA made by oligo-dT priming.
Directionally cloned into EcoR1/Xho1 sites using the following 5' adaptor: GCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Lite Technologies).
                              Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausbergenih.gov
Tissue Procurement: ATCC
CDNA.Library Preparation: Ling Hong/Rubin Laboratory
CDNA.Library Arrayed by: The J.M.A.G.E. Consortium (LL.NL.)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
Plate: LLCM382 row: k column: 02
Plate: LLCM382 row: k column: 02
High quality sequence stop: 692.
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National Institutes of Health, Mammalian Gene Collection (MCC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  117 CTCCCGGAGCCCGCAGCGGCCCCTGCCGGGCCCCCAGCGCCTCTCGCGGGCAAAG 176
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92.1%; Pred. No. 3e-139;
Live 0; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     145 t
                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon.9606"
/clone="IMAGE:3688825"
/clone_lib="NIH_MGC_39"
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284 c 2
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nes 753; Conservative
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1. .585
/organism="Homo sapiens"
/db_xref=""taxon:9606"
/clone="IMAGE:3903754"
/clone=lib="NIH_MGC_70"
/tissue_type="epithelioid carcinoma"
/tab_host="DHINB (phage=resistant)"
/note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
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Contact: Robert Strausberg Ph.D.

Tel: (301) 496-1550

Email: Robert Strausberg@nih.gov
Tissue Procurement: ATC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM695 row: f column: 11

High quality sequence stop: 585.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 585)
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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540 GCGAGAGGGTATCCCCAACTGG-GACTTCCGAGGCAACTTGAACTCAGAAC-ACTACAGC 597
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                  GGAGACGCCACCC - - GGTGCTTGAGGCGGGACCGAGGCGCA - CAGAGACCGAGG - CGCAT
                                                                                     AGAGACCGAGCACAGCCAGCTGGGGCTAGGCCCGGTGGGAAGGAGAGCGTTAATTT
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119 c
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BE910077
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tumor Gene Index
Unpublished (1997)
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Email: 1000 from Gibco
High quality sequence stop: 471.
                                                                                                                                                                                                                                                                                                                                                                                              TCTGGTGGTGGGTCGTAAGTTTAGGAGGTGACTGCATCCTCCAGCATCTCAACTCCGTCT 1023
                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTCTACTGTGTGAGACTTCGGCGGACCATTAGGAATGAGATCCGTGAGATCCTTCCATCT 1083
                                                                                                                                                                                                                                                                                                                          AAAGTAGGAGAAGAAATGGGGAGGACGACTCGGGTGGGGGAGGTCCCGGCTGGGATGAAG 963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note-"Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) was modified polylinker; Site_1: Not 1; Site_2: Fco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and b-cell
                300
                                                                                                                                                                                                                                                            903
                                                                                                                                                                                                                                                                                            360
                                                                                                                              TGCTCCTAALTAATATTTATATGTATTTATGTACGTCCTCCTAGGIGALGGAGALGTA 783
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                                                                                                                                               TCTCTTGGTATTTATTGAGCTTTGTGGGACTGGTGGAAGCAGGACACCTGGAACTGCGGC
                                                                                                                                                                                                                                                                            604 GCCACCCGGTGCTTGAGGCGGGACCGAGGCGCACAGAGACCGAGGCGCATAGAGACCGAG
                                                                CGTAATATTTATTTTAACTTATGCAAGGGTGTGAGATGTTCCCTCTGCTGTAAATGCAGG
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Mammalia; Eutheria; Primates; Catarrhini; Homi<u>a</u>idae; Homo.
1 (bases 1 to 586)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="IMAGE:2907365"
/clone_lib="Soares_NFL_T_GBC_S1"
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/db_xref="taxon:9606"
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vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M. A.G.E. clones 29480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 598)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
Ncional Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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sapiens cDNA clone IMAGE:2973324 3'
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hi25c07.x1 NCI_CGAP_C014 Homo
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AW662348
AW662348.1 GI:
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                                                        Tissue procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. cDnA Library Preparation: Life Technologies, Inc. cDnA Library Preparation: Life Technologies, Inc. cDnA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution information can be found through the I.M.G.E. Consortium/Lin at: Gound through the I.M.G.E. Consortium/Lin at: Seq primer: -400p from Gibco Seq primer: -400p from Gibco High quality sequence stop: 392.
                                                                                                                                                                                                                             1.:598
//Organism="Homo sapiens"
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/clone="IMAGE:2973324"
/clone="IMAGE:2973324"
/clone="Ib="NCI_CGAP_CO14"
/lissue_type="moderately-differentiated adenocarcinoma"
/lab_host="NOTE"
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Pred. No. 3.9e-137;
0; Mismatches 9;
              Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
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Best Local Similarity 98.5%;
Matches 585; Conservative
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                                         194 ATCCTCCAGCATCTCAACTCCGTCTGTCTGTGTGAGACTTCGGCGGACCTTAGGAA 135
314 AAGCAGGACACCTGGAACTGCGGCAAAGTAGGAGAAAATGGGGAGGATCTCGGGTGGG 255
                                                                                        ATCCTCCAGCATCTCAACTCCGTCTGTCTACTGTGAGACTTCGGCGGACCATTAGGAA
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/Lissue_type="epithelioid carcinoma"
/lissue_type="epithelioid carcinoma"
/labu="Dyga="DH10B (phage-resistant)"
/note="Organ: pancreas; Vector: pCMV-SPOR"6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Perknologies insert size 1:1 kb. Library constructed by Life
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 614)
                                                      BE62160U 614 bp mRNA EST 24-AUG-2000 601493736T1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895736 3'
                                                                                                                                                                                                                                                                                                                 Tissue procurement: ATCC CDNA Library Preparation: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. CONS. Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://mgg-llnl.gov
                                                                                                                                                                                                                         NIH-MGC http://www.mcbi.nlm.nih.gov/MGC/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Pred. No. 5.7e-134;
0; Mismatches 8; Indels
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Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
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High quality sequence stop: 613.
Location/Qualifiers
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/clone="IMAGE:3895736"
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                                                                                                                                                                                                                                                          Unpublished (1999)
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                                                                                     mRNA sequence.
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                                      BE621600/c
                                                                   DEFINITION
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EST368355 MAGE resequences, MAGD Homo sapiens cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                      Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray Unpublished (2000)

Contact: John Quackenbush
FAIT INSTITUTE for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
7el: 301 838 3528
Fax: 301 838 0208
GGGTTGGGGGGTTGGTGGCCTGTCACGGAGCGACTCTCTCGAGATCGCCTAGTATGTTCTGTG 1178
                                                                                                                                                                                                                                                                                                                                                                                                                             , Gay,C., I
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, I.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. a
Quackenbush, J.
                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 588)
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98.3%; Pred. No. 1.5e-132;
Live 0; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="MAGE resequences,
/note="Vector: pBluescriptSKm"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                              AW956285
AW956285.1 GI:8145968
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(bases, 1 to 617)

Mu,T., Oian,H., Huang,O., Huang,C., Kang,B., Gao,X., Xu,Z., Xiao,H., Xu,X., Li,N., Peng,Y., Liu,F., Qu,J., Song,H., Cheng,Z., Zeng,L., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G., Yang Homo, sapiens cDNA GK - clones

Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
Shaujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Site_2:
                                                                                                                                                                                                                                      TCGTAAGTTTAGGAGGTGACTGCATCCTCCAGCATCTCAACTCCGTCTGTGTACTGTGTG 1035
                                                                                                                                                                                                                                                                                                                                                                                                                                            AV690660 617 bp mRNA EST 25-SEP-2000
AV690660 GKC Homo sapiens cDNA clone GKCBAAU4 5', mRNA sequence
                                                                                                                                                                                                                                                                                          856 TATTGAGCTTTGTGGGACTGGTGGAAGCAGGACACCTGGAACTGCGGCAAAGTAGGAGAA 915
                                                                                                                                               sk(-); Site_1: EcoR1;
                                                                                                                                                                                                                                                                                                                                               others
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/dev_stage="Adult"
/lab_host="SOLR"
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Xho1"
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/db_xref="taxon:9606"
/clone="GKCBAA04"
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Length 617;

DB 38;

557;

Score

45.48;

Query Match

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"Instance of the control of the cont
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                                                                277 ATCGTCTTCTGCCAGATCCTGATGGCTGAGGGTGTGCCGGCGCGCCCCTGCCTCCAGAG 336
                                                                                                                                                                                  TTGAACTCAGAACACTACAGCGGAGACGCCACCCGGTGCTTGAGGCCGGGACCGAGGCGCA 636
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                                                                                                                                                        337 GACGCCCTAAACGCCGCATCCCTGGCGCCCACCCCTGTGTCCCCCGTCCTCGAGCCCTTT 396
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                                                                                                                                                                                                                                                                                                                                        AW263252 548 bp mRNA EST 28-DE xn79g02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2700722 3', mRNA sequence.
                            Indels
    2.3e-131;
ches 21;
                          Mismatches
    Pred. No.
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AW263252.1 G1:6640068
95.58;
                     Conservative
Best Local Similarity
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                     Matches 596;
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/clone=lib="NIH_MGC_69"
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Site_2: Sall; Cloned undirectionally. Primer: Oligo dr.
Average insert size 1.1 kb. Library constructed by Life
Technologies.
1 332 g 168 t
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National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CGCCCCAGGGCTCTCGCGGGCACCGAAAGCGCAGCCGTCAGGGTTCTCTACCCTCGATG 60
                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: DCTD/JNTP/Gazdar
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MCC clone distribution information can if cound through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM660 row: c_column: 17
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                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, E
Mammalia, Eutheria, Primates, Catarrhini, Hominidae,
1 (bases 1 to 1070)
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llarity 95.6%; Pred. No. 3.3e-127,
Conservative 0; Mismatches 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                            High quality sequence stop: 645.
Location/Qualifiers
  G1:10327235
                                                                                                                                                                                  Unpublished (1999)
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                                                                 Homo sapiens
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Matches 675; Conserv
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                                                                                                                                        AUTHORS
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                                                                                                                   /note="Organ: pooled; Vector: py773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Ecc RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI_CGAP_GCBI) were mixed, and so circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.-A.E. "clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo.
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                                                          /clone="IMAGE:2700722"
/clone_lib="Soares_NFL_T_GBC_S1"
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                     /organism="Homo sapiens"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutoleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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NCI-CGAP http://www.ncbl.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@lange.llnl.gov) for further information.
Insert Length: 662 Std Error: 0.00
Seq prime: -40UP from Glbco
High quality sequence stop: 456.
                         540
                                                                                                                                                                                                                                                         A1800828 521 bp mRNA EST 19-DEC-1999 wg13f12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2365007 3', mRNA sequence.
                                                                                                                      624 GGACCGAGGCGCACAGAGACCGAGGCGCATAGAGAGCCGAGGCACAGCCCAGCTGGGGGCTA
                                                   743 TAYGTATTTATGTACGTCCTCCTAGG - - - - TGATGGAGATGTGCTACGTAATATTTTT
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/db_xref="taxon:9606"
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
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Sequence 2393, P
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Sequence 9454, P
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1778, A
10469,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 88514,
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/cgn2_6/ptodata/2/pna/US6019_COMB.seq:*
/cgn2_6/ptodata/2/pna/US6010_COMB.seq:*
/cgn2_6/ptodata/2/pna/US6012_COMB.seq:*
/cgn2_6/ptodata/2/pna/US6022_COMB.seq:*
/cgn2_6/ptodata/2/pna/US6023_COMB.seq:*
/cgn2_6/ptodata/2/pna/US6025_COMB.seq:*
/cgn2_6/ptodata/2/pna/US6025_COMB.seq:*
/cgn2_6/ptodata/1/pna/US0025_COMB.seq:*
/cgn2_6/ptodata/1/pna/US06_NIN_COMB.seq:*
/cgn2_6/ptodata/1/pna/US06_NIN_COMB.seq:*
/cgn2_6/ptodata/1/pna/US08_NIN_COMB.seq:*
/cgn2_6/ptodata/1/pna/US08_NIN_COMB.seq:*
/cgn2_6/ptodata/1/pna/US08_NIN_COMB.seq:*
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US-09-699-998-1025

US-09-699-998-1025

US-09-699-998-1025

US-09-716-473-2500

US-09-716-772-260

US-09-726-712-288-772

US-09-699-998-1046

US-09-726-109-10087

US-09-652-109-10087

US-09-652-109-10087

US-09-652-109-10087

US-09-652-109-10087

US-09-652-109-10087

US-09-726-102-986-103

US-09-652-109-103

US-09-726-103-103

US-09-726-103-103

US-09-726-103-103

US-09-726-103-103

US-09-726-103-103

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US-09-726-103-103

US-08-726-103-103

US-09-726-103-103

US-09-726-103-103

US-09-726-103-103

US-09-726-103-103

US-09-652-108-103

US-09-652-108-103-103

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US-09-726-711-2410

US-09-726-711-2410

US-09-726-711-703-1
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CTCACCATCGTCTTCTGCCAGATCCTGATGGCTGAAGAGGGTGTGCCGGGCCCCCTGCCT 120
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                                                           Length 506;
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GENERAL INFORMATION:
APPLICANT: Shyjan, Andrew W.
APPLICANT: Shyjan, Andrew W.
APPLICANT: MocCarthy, Sean A.
APPLICANT: Monchan, John
APPLICANT: Richardson, Jannifer
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREFOR
FILE REFRENCE: 1600.1182.001
CURRENT APPLICATION NUMBER: US/09/644,869
CURRENT FILING DATE: 2000.08-28
PRIOR FILING DATE: 1999-08-27
NUMBER OF SEQ ID NOS: 9708
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 356
LENGTH: 521
                                                                                         Indels
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                                                      Score 258; DB 24;
Pred. No. 7.5e-52;
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                                                                                      0; Mismatches
                                                    100.0%;
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                                                                Best Local Similarity 100.
Matches 258; Conservative
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US-09-644-869-356
US-09-726-805-429
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                                                  Ouery Match
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APPLICANT: Holtzman, Douglas A.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THERENOR RELICATION THERENOR FILE REPERENCE: 1600.2017-001
CURRENT APPLICATION NUMBER: US/09/726,805
CURRENT FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: 60/168,140
NUMBER OF SEQ ID NOS: 2158
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 429
LENGTH: 506
                                                              APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Dickson, Mark
APPLICANT: Jones, Lee W.
TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
TITLE OF INVENTION: From Various Libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 100.0%; Score 258; DB 19; Best Local Similarity 100.0%; Pred. No. 7.4e-52; Matches 258; Conservative 0; Mismatches 0;
                                                                                                                                                        FILE REFERENCE: 774
CURRENT APPLICATION NUMBER: US/09/528,409
CURRENT FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: 60/125,453
PRIOR FILING DATE: 1999-03-19
NUMBER OF SEQ ID NOS: 116231
SOFTWARE: HY-Patent.pl Version 3.1
                  ; Sequence 88514, Application US/09528409; GENERAL, [NFORMATION:
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COTHER INFORMATION: n = A,T,C OF US-09-528-409-88514
                                                  Drmanac, Radoje T.
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ORGANISM: Homo sapiens
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US-09-726-805-429
                                                                                                                                                                                                                                                                                                             TYPE: DNA
                                                 APPLICANT
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APPLICANT: BUSIGLA, SAMENTHA J.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A TITLE OF INVENTION: HUMAN ESOPHAGUS LIBRARY FILE REFERENCE: MLN98-48pm
CURRENT APPLICATION NUMBER: US/09/396,885
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/106,444
PRIOR FILING DATE: 1998-10-30
PRIOR FILING DATE: 1998-10-30
PRIOR FILING DATE: 1999-03-30
NUMBER OF SEQ ID NOS: 5360
SOFTWARE: FERSEEQ for Windows Version 3.0
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100.0%; Pred. No. 7.6e-52;
Live 0; Mismatches 0;
    Pred. No. 7.5c-52;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                    Sequence 430, Application US/09396885 GENERAL INFORMATION:
APPLICANT: Gearing, David P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COCATION: (1)...(617)
COTHER INFORMATION: n = A,T,C or G
US-09-396-885-430
100.08;
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Best Local Similarity 100.
Matches 258; Conservative
         Best Local Similarity 100.
Matches 258; Conservative
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ORGANISM: Homo sapiens
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                                                                                                             Sequence 2355, Application US/60196718
GENERAL INFORMATION:
APPLICANT: Bonazzi, Vivien
TITLE OF INVENTION: USOLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CL000456
CURRENT APPLICATION NUMBER: US/60/196,718
CURRENT FILING DATE: 2000-04-13
NUMBER OF SEQ ID NOS: 7494
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 CCAGAGGACGCCCCTAACGCCGCATCCCTGGCGCCCACCCCTGTGTCCCCCGTCCTCGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GTCCGGCGCCAGCTGCCAGTCGAGGAACCGAACCCAGAAAAGGCTTCTCTTTTCTGCTG
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                                                                                                                                                                                                                                                                                                                                                                                   Length 521;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4785, Application US/09699998

GENERAL INFORMATION:
APPLICANT: Holtzman, Douglas A.
APPLICANT: Gearing, David P.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREFOR
FILE REPERENCE: 1600.2008-001
                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23;
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Pred. No. 7.5e-52;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 1600.2008-001
CURRENT APPLICATION NUMBER: 05/09/699,998
CURRENT FILING DATE: 2000-10-30
PRIOR APPLICATION NUMBER: 60/162,362
PRIOR FILING DATE: 1999-10-29
                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 2355
                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
Best Local Similarity 100.0%; P. Matches 258; Conservative 0;
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                     NUMBER OF SEQ ID NOS:
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US-09-699-998-4785
                                                                                                  RESULT 4
US-60-196-718-2355/c
                                                                                                                                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: HUMAN
US-60-196-718-2355
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US-09-699-998-4785
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LENGTH: 529
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Belt, Judith A.
APPLICANT: Belt, Judith A.
APPLICANT: Patel, Divyen
TITLE OF INVENTION: (NAMPR) INSENSITIVE, EQUILIBRATIVE, NUCLEOSIDE TRANSPORT
TITLE OF INVENTION: (NAMPR) INSENSITIVE, EQUILIBRATIVE, NUCLEOSIDE TRANSPORT
TITLE OF INVENTION: USE
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSE: David A. Jackson, Esq.
STREET: #11 Hackensack Ave, Continental Plaza, 4th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 3.1%; Score 38.6; DB 3; Length 6354; Best Local Similarity 65.9%; Pred. No. 1; Matches 56; Conservative 0; Mismatches 29; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 07601

ZIP: 07601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/058,389A

FILING DATE: April 9, 1998
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY AGENT INCOME.
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-013N
TELECHONE: 201-487-5800
TELEPHONE: 201-343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ 1D NO: S: SEQUENCE CHARACTERISTICS: LENGTH: 6354 base pairs TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                   CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
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Search completed: January 30, 2001, 21:28:30 Job time: 19992 sec

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TCCAGCAACACCCGGCCGCCTTCTAACTGTGACTCCCCGCACTCCCCAAAAGAATCCGA 505
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        159 CGCCTCTCGCGGGCACCGAAAGCGCCACCGCAGGGTTCTCTACCCTCGAGTGGTCCGGC 217
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                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Florkiewicz, Robert 2.
APPLICANT: Baird, Andrew
TITLE OF INVENTION: INHIBITORS OF LEADERLESS PROTEIN EXPORT
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1120;
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6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Version #1.30
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REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 760100.418C1
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, vCURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/030,613 FILING DATE: 25-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51,4%; PICL
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                                                                                                                                                                                                                                                       Sequence 1, Application US/09030613
Patent No. 6083706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPALIBLE OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleic acid
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STATE: Washington
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Matches 92; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
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US-09-058-389A-5
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51.1%; Pred. No. 0.3;
iive 0; Mismatches 90; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "HUMDAFC1 (Promotor and 5
end of Exon 1, genomic sequence)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                     1100 Peachtree Street, Suite 2800
                                                                                                                                                                                                                                                                            APPLICANT: Bell, Leonard*

PPLICANT: Squinto, Stephen
TITLE OF INVENTION: Universal Donor Cells
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/US92/05920
FILING DATE: 19920714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GenBank HUMDAF; HUMDAFC1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                           Sequence 2, Application PC/TUS9205920 GENERAL INFORMATION:
                                                                                                                                                              Sims, Peter J.
Bothwell, Alfred L.M.
Elliott, Elleen A.
Flavell, Richard A.
Madri, Joseph
Rollins, Scott
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/CDCKET NUMBER: OMRF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-815-6500
                                                                                                                                                                                                                                                                                                                                                                      Kilpatrick & Cody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAR 404-615-6555
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2847 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature;
LOCATION: 1.819
OTHER INFORMATION: /not;
PCT-US92-05920-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 51.19
Matches 94; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 19
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Georgia COUNTRY: U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: CI
                                                                                                                                                                                                                                                                                                                                                                                                          Atlanta
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 506 AAAA 509
                                    685 CCAA 688
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APPLICANT:
APPLICANT:
                                                                                                          PCT-US92-05920-2
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APPLICANT: Sims et al. TITLE OF INVENTION: Universal Donor Cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.3%; Score 40; DB 1; Length 2847;
51.1%; Pred. No. 0.3;
tive 0; Mismatches 90; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: 1.819
COTHER INFORMATION: /note= "HUMDAFCI (Promotor and 5'
CTHER INFORMATION: end of Exon 1, genomic sequence)"
US-08-087-007-2
                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNBER: US/08/087,007
FILING DATE: 19930701
                                                       ADDRESSEE: Kilpatrick & Cody
STREET: 1100 Peachtree Street, Suite 2800
TITLE OF INVENTION: Universal Donor Cells
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFRENCE/DOCKET NUMBER: OMRP135
TELEPHONE: 404-815-6500
TELEPAX: 404-815-6555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GenBank HUMDAF; HUMDAFC1
                                                                                                                                                    Z1P: 30309-4530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-483-433-2
; Sequence 2, Application US/08483433
; Patent No. 6100443
; GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 2847 base pairs
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IMMEDIATE SOURCE:
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Matches 94; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                     Georgia
: U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY CD MOLECULE TYPE: CD
                                                                                                                                                                                                                                                                                                                   FILING DATE: 19
CLASSIFICATION:
                                                                                                CITY: Atlanta
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HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGINAL SOURCE:
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                                                                                                                                      COUNTRY:
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326 IGCCICCAGAGGACGCCCCIAACGCCGCAICCCIGGCGCCCCACCCCIGIGICCCCCCGCC 385
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LOCATION: 1..819
COTHER INFORMATION: /note= "HUMDAFC1 (Promotor and 5'
COTHER INFORMATION: end of Exon 1, genomic sequence)"
US-08-483-433-2
                                                                                              CITY: Allanta STATE: Georgia COUNTR: Georgia COUNTR: U.S. 2.1P: 30309-3450
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE COMPUTER: IBM PC COMPATIBLE COMPUTER: IBM PC COMPATIBLE STATEM: PC-DOS/MS-DOS SOFWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION NUMBER: US/08/483,433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OMRF135c1p2 div
                                    ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
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                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/087,007
FILING DATE: July 1, 1993
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
FILING DATE: June 29, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: PADST, PATERA L.
REGISTRATION NUMBER: 31, 284
REFERENCE/DOCKET NUMBER: OMRF
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              404-873-8794
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Best Local Similarity 51.1'
Matches 94; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIBRARY: Genbank HUMD!
CLONE: Human DAF CDNA
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acid
EDNESS: single
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 800
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                                                      APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 04404/052001
CURRENT APPLICATION NUMBER: US/09/128,155
CURRENT PILING DATE: 1998-08-07-02
EARLIER PILING DATE: 1998-07-02
EARLIER PILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FASTSEQ for Windows Version 3.0
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3.3%; Score 40.6; DB 3;
Best Local Similarity 44.3%; Pred. No. 1.2;
Matches 166; Conservative 0; Mismatches 209;
Sequence 16, Application US/09128155
                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LCCATION: (1)...(153331)
CTHER INFORMATION: n = A,T,C or G
US-09-128-155-16
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Bothwell, Alfred L.M.
Elliott, Elleen A.
Flavell, Richard A.
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Patent No. 5705732
Patent No. 5705732 5684223
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Rollins, Scott
Bell, Leonard
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LENGTH: 152331
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APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3.4%; Score 41.2; DB 3; Length 4524; 53.8%; Pred. No. 0.18; 1tive 0; Mismatches 73; Indels 0.
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     155 CCAGCGCCTCTCGCGGGCACCGAAAGCGCAGCCGCAGG 192
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                                                                                                              APPLICANT: Van Baren, Nicolas
APPLICANT: Coulie, Pierre G.
APPLICANT: De Smet, Charles
APPLICANT: Lucas, Sophie
APPLICANT: Lucas, Sophie
TITLE OF INVENTION: LEUKEMIA ASSOCIATED GENES
NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                       ADDRESSEE: Wolf, Greenfield & Sacks, P.C. STREET: 600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       L0461/7008
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APPLICATION NUMBER: 08/845,998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Van Amsterdam, John R.
REGISTRATION NUMBER: 40,212
REFERENCE/DOCKET NUMBER: L0461,
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)720-3500
TELEPAX: (617)720-3441
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                            Sequence 7, Application US/09206537
Patent No. 6130052
                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
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STRANDEDNESS: double
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hes 85; Conserva
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                                                                                                        GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                     Boston
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                                         US-09-206-537-7/c
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US-09-206-537-7
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US-09-128-155-16
                                                                                                                                                                                                                                                                                                                                                        STATE: MA
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Best Local Si
Matches 85;
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155 CCAGCGCCTCTCGCGGGCACCGAAAGCGCAGCCGCAGG 192
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Best Local Similarity
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                                                                                                                               US-08-845-998-7/c
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US-08-845~998-7
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                                                                                  : 74 CCGAAAGCGCAGCCGCAGGGTTCTCTACCCTCGAGTGGTCCGGCGCCAGCTGCCAGTCGA 233
                                                                                                                                                  234 GGAACCGAACCCAGCCAAAAGGCTTCTCTTTCTGCTCGTCACCATCGTCTTCTGCCAGAT 293
                 115 -GACCCTCTCCCGGAGCCCGCAGCGCCCCTGCCGGGCGCCCCCAGCGCCTCTCGCGGGGCA 173
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Pred. No. 0.069;
0; Mismatches 73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Weissman, Sherman
APPLICANT: Weissman, Namadev
TITLE OF INVENTION: AMPLIFICATION OF NUCLEIC ACIDS
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 701 Fifth Avenue, 6300 Columbia Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/758,662
FILING DATE: 29-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: No. 6114150tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 390036.402C1
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/08758662
Patent No. 6114150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                6155 CCCCGGCGCCACCAGCACAG 6136
                                                                                                                                                                                                                                                                                 354 ATCCCTGGCGCCCACCCTG 373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 53.89
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TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Washington
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95 GTCCTGAGATCTTCACCTTCGACCCTCTCCCGGAGCCCGCAGCGGGCCCCTGCCGGGCGCC 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SISIEM: To Losying DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURREWA APPLICATION DATA:
APPLICATION NUMBER: US/08/845,998
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Van Amsterdam, John R.
REGISTRATION NUMBER: 40,212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 41.2; DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  155 CCAGCGCCTCTCGCGGGCACCGAAAGCGCAGCCGCAGG 192
318 CCCGCGCCCCGCGCCGCCATGAGCGCGACGG 281
                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: LEUKEMIA ASSOCIATED GENES NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.18;
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                  Sequence 7, Application US/08845998
Patent NO. 5879892
GENERAL INFORMATION:
APPLICANT: Van Baren, Nicolas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: LO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)720-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.4%;
                                                                                                                                                                                                 APPLICANT: Coulie, Pierre G.
APPLICANT: De Smet, Charles
APPLICANT: Lucas, Sophie
APPLICANT: Boon, Thierry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4524 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (617)720-2441
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                     Pseudorabies Virus Deletion Mutants
Involving The EPO and LLT Genes
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Pred. No. 0.15;
0; Mismatches 165; Indel's
                                                                                                                                                                                                                                                                                                                                                                              SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                 ADDRESSEE: Curtis P. Ribando
STREET: 1815 No. 5352596th University Street
CITY: Peoria
                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/945, 283
                                                                                Sequence 1, Application US/07945283
Patent No. 5352596
GENERAL INFORMATION:
APPLICANT: Cheung, Andrew K.
APPLICANT: Wesley, Ronald D.
TITLE OF INVENTION: Pseudorables V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Ribando, Curtis P
REGISTRATION NUMBER: 27976
TELECOMMUNICATION INFORMATION:
TELEPHONE: 309-685-4011 ext.513
TELEFAX: 309-685-4128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Pseudorabies virus
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IBM PC compatible
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replace(7010, "g")
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MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis P.
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Matches 153; Conservative
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MEDIUM TYPE: Floppy
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622..6495
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                              USA
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ORIGINAL SOURCE
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                                                                JS-07-945-283-1/c
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LOCATION:
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LOCATION:
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US-07-945-283-1
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                                                                                                                                                                                                                                                                 CITY:
STATE:
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Conservative 214; Mismatches 156; Indels
                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 43.8; DB Pred. No. 0.046;
                                                                                                                                                                                                                                                                                                                                                                                                                                 30472/114 IMMU
                                               ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                                               EP 91 114 300.
                                                                                                                                                                                                  PC-DOS/MS-DOS
                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
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TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                              29,768
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TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
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ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (703)836-9300
(703)683-4109
                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                              CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PT2gpt-F1s
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Best Local Similarity
Matches 9; Conserve
                                                                                                                COUNTRY: USA
Z.IP: 22313-0299
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US-08-232-463-14
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                      CCCGCACTCCCCAAAAAGAATCCGAAAAACCACAAAAAACACACAGGCGTACCTGGTGCG
                                GACGCCACCCGGTGCTTGAGGCGGGACCGAGGCGCACAGAGACCGAGGCGCATAGAGACC
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                                                                CGAGAGCGTATCCCCAACTGGGACTTCCCAGGCAACTTGAACTCAGAACACCTACAGGGGA
                                                                          TATTGCTCCTAATTAATATTTATATGTATTTATGTACGTCCTCCTAGGTGATGGAGGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL PROMATION:
APPLICANT: SCHEIFLINGER, F. APPLICANT: SCHEIFLINGER, F. APPLICANT: FALKNER, F. G. TUTE OF INVENTION: RECOMBINANT FOWLPOX VIRUS NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGTCAAAAAAAAAAAAAAAACTCGAG 1228
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ADDRESSEE: FOLEY & L
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COMPUTER READABLE FORM:
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97 CCTGAGATCTTCACCTTCGACCCTCTCCGGAGCCCGCAGCGGCCCCCTGCCGGGCGCCCC 156
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MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC COMPATIDIO
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACEDIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION 135
PRIOR APPLICATION DATA:
FILING DATE:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          h 4.1%; Score 49.8; DB 1; Similarity 1.6%; Pred. No. 0.0012; 6; Conservative 220; Mismatches 147;
                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 30472/114 IMMU TELECOMMUNICATION INFORMATION: TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                  EP 91 114 300.
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                                                                                                                                                                                                                                                                                                                  29,768
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Best Local Similarity 1.68;
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                                                                                                                                                                                                                                APPLICATION NUMBER: EP 9:
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 899149
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                     (703)683-4109
                                                                                                                                                                                                                                                                                               NAME: BENT, Stephen A. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleic acid
EDNESS: single
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US-08-232-463-14
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TOPOLOGY: lin
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APPLICANT:
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
TITLE OF INVENTION: 1953-126
CURRENT FILING DATE: 1996-07-30
EARLIER APPLICATION NUMBER: 08/79,410
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-02-13
EARLIER FILING DATE: 1996-02-16
NUMBER OF SEQ ID NOS: 44

SOUTWARE: FastSEO for Windows Version 4.0
61 CCCTCCACCATCCCGGGACCCCGGGGGGTCCTGAGATCTTCACCTTCGACCT 120
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                                                                                                           1201 TGTCAAAAAAAAAAAAACTCGAG 1228
                                                                                           1201 TGTCAAAAAAAAAAAAAAAAACTCGAG
                                                                                                                                                                               ; Sequence 5, Application US/09126640A; Patent No. 6099823
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Best Local Similarity 100.
Matches 1228, Conservative
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: TYPE: DNA

: ORGANISM: Homo sapiens

US-09-126-640-5
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                                                                                                                                                                                                                                                                                                                           APPLICANT: Falb, Dean
TITLE OF INVENTION: COMPOSITIONS AND METHOUS FOR
TITLE OF INVENTION: THE TREATMENT AND DIAGNOSIS OF
NUMBER OF INVENTION: CARDIOVASCULAR DISEASE
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                              TGTCAAAAAAAAAAAAAAACTCGAG 1228
                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,495
                                                                                                                                                                                                            08/799,910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YSTEM: DOS
FastSEQ Version 2.0
                                                                                                                                                                                                                                                                         US-08-944-495-9 .
; Sequence 9, Application US/08944495
; Patent No. 6087477
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)7909090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/79
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 1228 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFA: (212)869741
TELEX: 66141 PENNIE
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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OTHER INFORMATION:
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LOCATION: 1...468
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Best Local Similarity
Matches 1228; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: N
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                                            Length 1228;
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                                          DB 3;
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                                       Score 1228;
Pred. No. 0;
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                                       100.0%;
llarity 100.0%;
Conservative 0;
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                                       Query Match
Best Local Simi
Matches 1228;
US-08-826-246-9
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Patent No. 6048709
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: FAID.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: THE TREATMENT AND DIAGNOSIS OF
TITLE OF INVENTION: CARDIOVASCULAR DISEASE
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
US-09-135-021-1
US-08-135-021-5
US-08-458-568A-11
US-08-410-468-6
US-08-510-6468-6
US-08-510-6468-6
US-08-926-926-6
US-09-926-926-6
US-09-933-682-6
US-08-726-213
US-08-726-214-1
US-08-726-214-1
US-08-10-729A-2
US-08-916-745-2
                                                                                                                                                                                                                                       ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Coruzzi, Laura A
RECISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-078-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)7909090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDUM TYPE: Diskerte
COMPUTER: Diskerte
COMPUTER: Diskerte
COMPUTER: Diskerte
COMPUTER: SeatEGD Version 2.0
SOFTWARE: FastEGD Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/826,246
FILING DATE: 28-MAR-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/799,910
FILING DATE: 13-FEB-1997
FILING DATE: 13-FEB-1997
FILING DATE: 13-FEB-1997
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION
NAME: COLUZZI, LAURA A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (212)8699741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ 1D NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1228 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
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LOCATION: 1...468
OTHER INFORMATION:
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4: /cgn2_6/ptodata/2/ina/pcfu/s_COMB.seq:*
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           GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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January 30, 2001, 16:08:34 ; Search time 77.57 Seconds (without alignments) 5947.064 Million cell updates/sec
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                           The patent discloses methods for the treatment and diagnosis of cardlovascular diseases by novel human genes which are differentially expressed in different cardiovascular disease states. Compositions which can modify TGF-beta signaling pathway are identified by screening discretes, especially TGF (Transforming growth factor) beta related disorders, especially TGF (Transforming growth factor) beta related disorders, including diabetic retinopathy, artherosclerosis, pancreatic cancer, angiogenesis, inflammation, fibrosis, tumour growth and regularisation. The present sequence is Chid605 gene which is upregulated in monocytes treated with oxidised LDL (low density lipoprotein) can be used to design cardiovascular disease treatment strategies. Depending on whether the up-regulation has a pathogenic or protective effect treatment methods can be designed to increase or decrease the activity of the protein product of the gene.
                            substances for ameliorating symptoms of libroprollierative oncogenic related disorders
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Fond605 is a novel human gene that is up-regulated in monocytes treated with oxidised low density lipoproteins (LDL). Differential display was used to derect genes that are differentially expressed in monocytes treated so as to simulate the conditions under which (see T94470) are up-regulated under the disease condition of teatment with oxidised LDL. The Echd605 gene product (see W3606) has sequence similarity to mouse gly96. The discovery of the up-regulation of these 2 genes provides a fingerprint profile.

The study of cardiovascular diseases, including and arterial inflammation. Methods are provided for the diagnosis, and arterial inflammation. Methods are provided for the diagnosis, monitoring in clinical trials, screening for therapeutically effective compounds, and treatment of cardiovascular diseases based of diseases regarding the expression patterns of novel genes (chd602 and fchd605), fchd340 (see T94468), fchd345 (see T94469), New genes differentially expressed in cardiovascular disease -for diagnosis, drug screening and treatment of cardiovascular disease, e.g. atherosclerosis, restenosis, hypertension, etc Claim 1; Fig 5; 163pp; English. WPI; 1997-424966/39. P-PSDB; W36006 Falb DA;

Sequence 1228 BP; 265 A; 362 C; 340 G; 261 T; 0 other;

ö CCCICCACCATCCCGGGACCCCGGGGGGGCTCCTGAGATCTTCACCTTCGACCT 120 CTCCCGGAGCCCCCAGCGGCCCCTGCCGGGCGCCCCAGCGCCTCTCGCGGGCACCGAAAG 180 240 AACCCAGCCAAAAAGGCTTCTCTTTTCTGCTCACCATCGTCTTCTGCCAGATCCTGATG 300 420 480 Gaps CGCAGCCGCAGGGTTCTCTACCCTCGAGTGGTCCGGCGCCCAGCTGCCAGTCGAGGAACCG GCGCCCACCCTGTGTCCCCCGTCCTCGAGCCCTTTAATCTGACTTCGGAGCCCTCGGAC TACGCTCTGGACCTCAGCACTTTCCTCCAGCAACACCCGGCCGCCTTCTAACTGTGACTC CCCGCACTCCCCAAAAAAATCCGAAAAACCACAAAAAACACCAGGCGTACCTGGTGCG DB 18; Length 1228 . 0 1; Indels 99.9%; Score 1226.4; 99.9%; Pred. No. 0; ive 0; Mismatches Query Match
Best Local Similarity 99.9°
Matches 1227; Conservative 61 61 121 121 181 241 181 301 361 361 121 301 121 481 481 ò g õ g ò a ò qq ô g ô a ò QQ ò g ò

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                                                                                                                              GTACGTAATATTTTAACTTATGCAAGGGTGTGAGATGTTCCCTCTGCTGTAAATGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; gene expression product; diagnosis; tumour; colon cancer colorectal adenocarcinoma; cell line SW480; cell proliferation; cytostatic; sarcoma; breast cancer; neoplasia; dysplasia;
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                                                                                                                                                              human colorectal adenocarcinoma (colon cancer) cell line SW480. The CDNA clones can be used to generate antisense oligonucleotides which can be used for identifying and/or classifying cancerous cells present in a human tumour, particularly in solid tumours, e.g. carcinomas and sarcomas, e.g. breast or colon cancers. The CDNA clones can be used for developing agents for the diagnosis and treatment of disorders
                                                                                                                                                      to 280766 represent double stranded cDNA clones isolated from the
                                                                                                                                                                                                                                         Involving unwanted cell proliferation, such as neoplasia, dysplasia or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTGGTGGTGGGTCGTAAGTTTAGGAGGTGAC'TGCATCCTCCAGCATCTCAACTCCGTCTG 1024
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                                                                                        Novel nucleic acids, used to develop products for the diagnosis and treatment of disorders involving unwanted cell proliferation, particularly cancers, especially colon cancer
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Monahan JE;
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                            Steinmann KE, Astle JH, Burgess CC, Rushnell
Catino TJ, Derti A, Ford DM, Lewis ME, Monah
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                                                                                                                                                                                                                                                                        Sequence 427 BP; 115 A; 138 C; 78 G; 96 T; 0 other;
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Pred. No. 6.4e-102;
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                                                                                                                                  Claim 15; Page 356; 469pp; English.
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422; Conservative
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Matches 422;
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                                                        Expressed sequence tag; secreted protein; haematopoicsis regulator; tissue growth; activin; inhibin; tumour invasion suppressor; EST; human; chemotaxis; chemokinesis; haemostaxis; gene therapy; thrombolysis; receptor; ligand; anti-inflammatory; tumour inhibitor; ds.
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Pred, No. 6.3e-89;
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Treacy M;
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98.5%;
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Spaulding N
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clone 0417
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Racie LA, Sp
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                                                                                                                                                                                                                       Human; secreted protein; expressed sequence tag; EST; haematopoiesis;
tissue growth; activin; inhibin; chemotaxis; chemokinesis; haemostatic;
receptor; ligand; thrombolytic; anti-inflammatory; cadherin; anti-tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents a human expressed sequence tag (EST). The polynucleotide, which is a secreted EST, and the encoded protein are predicted to have useful biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, immune stimulating or suppressing activity, hematopoiesis regulating activity, tissue growth activity, hemostatic and thrombolytic chemotactic/chemokinetic activity, hemostatic and thrombolytic activity, receptor/ligand activity, hemostatic and thrombolytic activity, receptor/ligand activity, tumour inhibition activity, the polynucleotide may also be useful for gene therapy.
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Pred. No. 4.5e-35;
0; Mismatches 3;
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                                                                   375 aggacacetggaactgcgccaaagtaggcga 405
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                                             884 AGGACACCTGGAACTGCGGCAAAGTAGGAGA
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Treacy M;
                                                        Claim 1; Page 164; 618pp; English
                                                                                                                             V89271 standard; cDNA; 193 BP
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Best Local Similarity 98.3%;
Matches 169; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                          97US-0838821.
                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                (GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                                        Agostino MJ, Jacobs K,
Racie LA, Spaulding V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-070077/06.
                                                                                                                                                                                                                                                           gene therapy; ss
                                                                                                                                                                                                 EST clone BY66.
                                                                                                                                                                                                                                                                                Homo sapiens
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                                                                                                                                                                           15-FEB-1999
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                                                                                                                                                    V89271;
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                                                                                                                  V89271/c
                                                                                                       RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 CCCTCCACCATCCCGGGACCCCGGGGGGCTCCGGTCCTGAGATCTTCACCTTCGACCT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76 octeaegttategtecagecacaaata-getgeegeeetgagatetecaeetteagaeeet 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human nucleic acid fragments, isolated from brain, adrenal tissue, the placenta or bone marrow comprise any of: (A) a sequence selected from (Q76401-Q77613), (B) an allelic variation of a sequence as described in (A), or (C) a sequence complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ATGTGTCACTCCCGCACCTGCCGACCATGACCATCCTGCAGGCCCCGGACCCCGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTCCCGGAGCCCGCAGCGGCCCCTGCCGGGCGCCCCAGCGCCTCTCGCGGGCACCGAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 CGCAGCCGCAGGGTTCTCTACCCTCGAGTGGTCCGGCGCCAGCTGCCAGTCGAGGAACCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to a human
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                                                                                                                                                                                                                                                                                      Brain; placenta; bone marrow; genetic analysis; gene mapping;
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                     65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequences exhibit no more than 90% homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 G; 52 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 151; DB 15;
Pred. No. 1e-30;
                                                                                                                                                                                                                                                                                                      detection; homology; human; adrenal tissue; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kelly M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 575-576; 616pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Howells D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 297 BP; 66 A; 117 C;
                                                                                                                                  ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92GB-0014857.
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                                                                                                                                                                                                          (first entry)
                                                                                                                                Q77534 standard; DNA; 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 76.0
Matches 212; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hadfield KM,
Starkey M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence known per se.
                                                                                                                                                                                                                                               Human genome fragment.
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Preferred sequ
                                                                                                                                                                                                          23-SEP-1994
                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                            409401548-A.
                                                                                                                                                                                                                                                                                                                                                                                                                   20-JAN-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gross J, Ha
Sibson DR,
                                                                                                                                                                     077534;
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                                     73
                                                                                             RESULT
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.. ? A02484/c ID A02484 standard; cDNA; 1000 BP.

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tgacgccaccaacagctgcagcccctgagatcttcaccttagaccctccccgaagccc 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74 CGGGACCCCGGCGGGCTCCGGTCCTGAGATCTTCACCTTCGACCCTCTCCCGGAGCCCG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        134 CAGGGGCCCCTGCCGGGCGCCCCAGGGCCTCTCGCGGGCACCGAAAGCGCAGCCGCAGGG 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33 getgeaaceaceceglggeecectaceageeceaatelecaaacecegeacgtegatea 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 GCTGCCACCGGCCATGACCATCCTGCAGGCCCCGA---CCCCGGGCCCCCTCCACCATCC 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human nucleic acid fragments, isolated from brain, adrenal tissue, the placenta or bone marrow comprise any of: (A) a sequence selected from (Q76401-077613), (B) an allelic variation of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to (A) or (B). Preferred sequences exhibit no more than 90% homology to a human {\tt Preferred}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              194 ITCTCTACCCTCGAGTGGTCGGCGCGCGAGCTGCCAGTCGAGGAACCGAACCCAGC 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.7%; Score 70.4; DB 15; Length 267; 64.7%; Pred. No. 1.9e-09; Live 0; Mismatches 77; Indels 6;
                                                                                                                                                                                                      Brain; placenta; bone marrow; genetic analysis; gene mapping; detection; homology; human; adrenal tissue; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence as described in (A), or (C) a sequence complementary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 267 BP; 58 A; 117 C; 49 G; 42 T; 1 other;
             241 AACCCAGCCAAAAGGCTTCTTCTGCTGCTCACCATC 279
                                                                                                                                                                                                                                                                                                                                                                                                                          Kelly M,
                                                                                                                                                                                                                                                                                                                                                                                                                         Howells D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 586; 616pp; English
                                                                                                ВР
                                                                                                                                                                                                                                                                                                                                      93WO-GB01467.
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                                                                                                                                                   (first entry)
                                                                                             Q77554 standard; DNA; 267
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Best Local Similarity 64.7'
Matches 152; Conservative
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Sibson DR, Starkey M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence known per se.
                                                                                                                                                                                fragment.
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A00010 to A02716 represent polynucleotides isolated from cDNA libraries constructed from human colon cancer cell lines. The present invention also describes a method of detecting differentially expressed genes correlated with a cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample derived from a cell suspected of being cancerous, where detection of the differentially expressed gene product is correfated with a cancerous state of the cell from which the test sample was derived. The polynucleotides sequences can be used in a method for detecting differentially expressed genes correlated with a cancerous state of a mammalian cell. The polynucleotides can also be used as probes for detecting and mapping related genes. They can be used in diagnosis and prognosis of diseases and disorders (e.g. identification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 n A; .
Labat I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Polynucleotide library used to determine cancerous states of mammalian cells -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pre-metastatic or metastatic cancerous states, stages of cancer, or responsiveness of cancer to therapy). This is particularly for breast cancer, oestrogen receptor-positive breast cancer, oestrogen receptor-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47 CCCCGACCCCGGCCCCTCCACCATCCCGGGACCCCGGGGGGTCCGGTCCTGAGATCT 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                      Human colon cancer cell line polynucleutide sequence SEQ ID NO:2475.
                                                                                                                        Human; colon cancer; tumour; diagnosis; gene expression product; probs; detection; cancerous state; metastasis; identification; breast cancer; oestrogen receptor-positive breast cancer; therapy; oestrogen receptor-negative breast cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Escobedo J, lunis MA, García PD, Sudduth-Klinge
Lase K, Randazzo F, Kennedy GC, Pot D, Kassam
anac R, Crkvenjakov K, Dickson M, Drmanac S, L
Kita D, García V, Jones LW, Stache-Crain B;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1000 BP; 21 A; 53 C; 574 G; 22 T; 330 other;
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Pred. No. 9.6e-06;
0; Mismatches 286;
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98US-0085696.
98US-0105234.
98US-0105877.
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                                                  19-MAY-2000 (first entry)
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Matches 160; Conservative
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Reinhard C, Giese K,
Lamson G, Drmanac R,
Leshkowitz D, Kita D,
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(HYSE-) HYSEQ INC.
                                                                                                                                                                                                                     Homo sapiens.
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21-OCT-1998;
27-OCT-1998;
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                A02484;
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qq
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A00010 to A02716 represent polynuclectides isolated from cDNA libraries
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GCCAGATCCTGATGGCTGAAGAGGGTGTGCCGGGGCCCCTGCCTCCAGAGGACGCCCCTA 346
                                                                                                                                                                         347 ACGCCGCATCCCTGGCGCCCACCCCTGTGTCCCCCGTCCTCGAGCCCTTTAATCTGACTT 406
                                                                                                                                                                                                                                                                        512 CCCCNCGCCNCCCNCCCNNCCCCCNGCGNCCTNNCNCCCNNCGNCCCCCCNCGCCTCCNCNC 453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human colon cancer cell line polynucleotide sequence SEQ ID NO:2479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; colon cancer; tumour; diagnosis; gene expression product;
probe; detection; cancerous state; metastasis; identification;
breast cancer; oestrogen receptor-positive breast cancer; therapy;
oestrogen receptor-negative breast cancer; lung cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J, Innis MA, Garcia PD, Sudduth-Klinger,
Randazzo F, Kennedy GC, Pot D, Kassam A;
Crkvenjakov R, Dickson M, Drmanac S, Lab
Garcia V, Jones LW, Stache-Crain B;
                                                                                           227 CAGTCGAGGAACCGAACCCAAAAGGCTTCTCTTTCTGCTGCTCACCATCGTCTTCT
                                       167 GCGGGCACCGAAAGCGCAGCGCAGGGTTCTCTACCCTCGAGTGGTCCGGCGCCGCAGCTGC
                                                                407 CGGAGCCCTCGGACTACGCTCTGGACCTCAGCACTTTCCTCCAGCAACACCCGGCCGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Polynucleotide library used to determine cancerous states of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 995-996; 1097pp; English.
                                                                                                                                                                                                                                                                                                                            392 CCCNNCNNCCCCCNCCNCCCCCC 367
                                                                                                                                                                                                                                                                                                           467 TCTAACTGTGACTCCCGCACTCCCC 492
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98US-0085537.
98US-0085696.
98US-0105234.
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Lamson G, Drmanac R,
Leshkowitz D, Kita D,
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Reinhard C, (
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constructed from human colon cancer cell lines. The present invention also describes a method of detecting differentially expressed genes correlated with a cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample derived from a cell suspected of being cancerous, where detection of the differentially expressed gene product is correlated with a cancerous state of the cell from which the test sample was derived. The polynucleotides sequences can be used in a method for detecting differentially expressed genes correlated with a cancerous state of a mammalian cell. The polynucleotides can also be used as probes for detecting and mapping related genes. They can be used a diagnosis and prognosis of diseases and disorders (e.g. identification of
                                                                                                                                                                                                                                                      pre-metastatic or metastatic cancerous states, stages of cancer, or responsiveness of cancer to therapy). This is particularly for breast cancer, oestrogen receptor-positive breast cancer, cancer, and colon cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCCCNNNTCNCCNCCNCCCNCCNNCCNNCCNNCCCCCNCNNCCCCCNGNNNCCNNNN 641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               105 CTTCACCTTCGACCCTCTCCCGGAGCCCGCAGCGGCCCCTGCCGGGCGCCCCCAGCGCCTC 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             165 TCGCGGGCACCGAAAGCGCAGCCGCAGGGTTCTCTAACCCTCGAGTGGTCCGGCGCCCAGCT 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45 GCCCCCGACCCCGCCCCCCTCCACCATCCCGGGACCCCGGGGGGGTCCGGGTCCTGAGAT 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human, gene, gene expression product; diagnosis; therapy; probe; detection; mapping; tissue typing; profiling: forensic; cancer; genetic analysis; colorectal cancer; breast cancer; lung cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        580 CCCCNCCNNCCNNNCNCNNNNNCNCNNCCCCCNNNANCNNCGNNGNNCCCCCCCNNNNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              225 GCCAGTCGAGGAACCGAACCCAGCCAAAAGGCTTCTTCTTGTTGCTGCTCACCATCGTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               285 CTGCCAGATCCTGATGGCTGAAGAGGTGTGCCGGCGCCCCTGCCTCCAGAGGACGCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         105 TTCGGAGCCCTCGGACTACGCTCTGGACCTCAGCACTTTCCTCCAGCAACACCCGGCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               345 TAACGCCGCATCCCTGGCGCCCACCCTGTGTCCCCCGGTCCTCGAGCCCTTTAATCTGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           465 CTTCTAACTGTGACTCCCGCACTCCCCAAAAAGAATCCGAAAAACCAC 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human gene expression product cDNA sequence SEQ ID NO:4735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                            Sequence 1218 BP; 9 A; 31 C; 494 G; 37 T; 647 other;
                                                                                                                                                                                                                                                                                                                                                                                                                         Score 55.2; DB 21;
Pred. No. 4e-05;
0; Mismatches 343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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Similarity 26.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 126;
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local 3
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247 GCCAAAAGGCTTCTCTTTTTGCTGCTCACCATCGTCTTTCTGCCAGATCCTGATGCCTGAA 306

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WO9938972-A2

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The present invention describes a library of human polynuclectides comprising the sequences given in 21233 to 21779. Also described is a method of detecting differentially expressed genes correlated with the cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample from a cell suspected of being cancerous, where the gene product is encoded by one of the 5248 polynucleotide sequences given in 212332 to 217779. The polynucleotides can be used as a source of primers and probes, which can be used for a variety of purpose, or detection of expression levels, mapping, tissue typing or profiling, forensics, genetic analysis and detection of polynuclotikans. Polypeptides encoded by the polynuclocides can be used for raising antibodies for experimental, diagnostic and therapeutic purposes. The polynuclocitides may also be used to construct arranged in a properties of detection of inflamostics (which may be used to determine function of an analysis for diagnostics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      encoded protein); and to detect differences in expression levels between two cells (e.g. to identify abnormal or diseased tissue in a human, to identify a genetic predisposition or susceptibility to a disease such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Titly a genetic predisposition or susceptibility to a disease such as per). The polynucleotides of the invention are especially used in the posits, prognosis and management of colorectal cancer, breast cancer, lung cancer. The polynucleotides can also be used to screen for
                                                                                                                                                                                                                                                                                                              Crkvenjakov R, Dickson M, Drmanac R, Drmanac S;
Escobedo J, Garcia PD, Garcia V, Giese K, Innis MA;
Jones ML, Kassam A, Kennedy GC, Kita D, Labat I;
Lamson G, Leslkowitz D, Pot D, Randazzo F, Reinhard C;
Stache-Crain B, Sudduth-Klinger J, Williams LT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel human genes and their expression products which are differentially expressed in different cell types
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1337 BP; 42 A; 577 C; 27 G; 22 T; 669 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 2250-2251; 2479pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      peptide analogues and antagonists,
                                                                                                                                                98US-0072910.
98US-0075954.
98US-0080114.
98US-0080515.
                                                                                     99WO-US01619
                                                                                                                           9990800-sn86
                                                                                                                                                                                                                                                                                                  Crkvenjakov R, Dicksu...
7 Garcia PD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-494092/41.
                                                                                                                                                                                                                                                            CORP.
                                                                                                                                                                                                                                                       (CHIR ) CHIRON COR (HYSE-) HYSEQ INC.
                                                                                 28-JAN-1999;
                                                                                                                                                                                                               03-APR-1998
                                        05-AUG-1999
                                                                                                                              03-APR-1998
                                                                                                                                                  28-JAN-1998
                                                                                                                                                                      24-FEB-1998
                                                                                                                                                                                             31-MAR-1998
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67 ACCATICCCGGGACCCCGGCGGGGGTCCTGAGATCTTCACCTTCGACCCTCTCCCG 126
                                                                                                                                                               7 CACTUTGGCAGCTGCCACCGACCATGACCATCCTGCAGGCCCCGACCCGGGCCCCTCC 66
                                                                                                                                                                                                                                                             CGCAGGGTTCTCTACCCTCGAGTGGTCCGGCGCCAGCTGCCAGTCGAGGAACCGAACCCA
                                                                                                                                                                                                                                                                                              127 GAGCCCGCAGCGCCCCTGCCGGGCCCCCAGCGCCTCTCGCGGGCCACCGAAAGCGCAGC
                                                                                                                                                                                                                              Length 1337;
                                     393; Indels
   Score 52.2; DB 20;
Pred. No. 0.00026;
                                  0; Mismatches
4.3%;
                                Matches 114; Conservative
                  Best Local Similarity
 Ouery Match
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A00010 to A02716 represent polynucleotides isolated from cDNA libraries constructed from human colon cancer cell lines. The present invention also describes a method of detecting differentially expressed genes correlated with a cancerous state of a mammalian cell, comprising detecting at less one differentially expressed gene product in a test sample derived from a cell suspected of being cancerous, where detection of the differentially expressed gene product is correlated with a cancerous state of the cell from which the test sample was derived.
                          ACCCCTGTGTCCCCCGTCCTCGAGCCCTTTAATCTGACTTCGGAGCCCTCGGACTACGCT 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Polynucleotide library used to determine cancerous states of mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J, Innis MA, Garcia PD, Sudduth-Klinger J;
Randaszo F, Kennedy GC, Pot D, Kassam A;
Crevenjakov R. Dickson M, Drmanac S, Labat
Garcia V, Jones LW, Stache-Crain B;
                                                                                                                                                                                                                                                                                                                                                             Human colon cancer cell line polynucleotide sequence SEQ 1D NO:2529.
                                                                                                                                                                                                                                                                                                                                                                                                     probe; detection; cancerous state; metastasis; identification; breast cancer; oestrogen receptor-positive breast cancer; therapy; oestrogen receptor-negative breast cancer; s
307 GAGGGTGTGCCGGCGCCCCTGCCTCCAGAGGACGCCCCTAACGCCGCATCCCTGGCGCC
                                                                                   CTGGACCTCAGCACTTTCCTCCAGCAACACCCGGCCGCCTTCTAACTGTGACTCCCCGCA
                                                                                                                                                                                                                                                                                                                                                                                        Human; colon cancer; tumour; diagnosis; gene expression
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                                                                                                                                                                       487 CTCCCCAAAAGAATCCGAAAAACCAC 513
                                                                                                                                                                                                                                                                             BP.
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98US-0085537.
98US-0085696.
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ID A02538 standard; cDNA; 1126
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98US-0105877
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Drmanac R,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Williams LT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14 - MAY - 1998;
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15-MAY-1998;
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The polynucleotides sequences can be used in a method for detecting differentially expressed genes correlated with a cancerous state of a mammalian cell. The polynucleotides can also be used as probes for detecting and mapping related genes. They can be used in diagnosis and prognosis of diseases and disorders (e.g. identification of
                                                                                                   pre-metastatic or metastatic cancerous states, stages of cancer, or responsiveness of cancer to therapy). This is particularly for breast cancer, oestrogen receptor-positive breast cancer, oestrogen receptor negative breast cancer, and colon cancer.
                                                                                                                                                                                                                                                                                                                                                                                       508 CCCGNNCGCTCCNNCAACNNCGGCCTCCCCAGNNCGCCATTCCCNCNCCGCCCNNTCAAG 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                         133 GCAGCGGCCCCTGCCGGGCGCCCCCAGCGCCTCTCGCGGGCACCGGAAAGCGCCAGCCGCAGG 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             433 CTCAGCACTTTCCTCCAGCAACACCCGGCCGCCTTCTAACTGTGACTCCCCGCACTCCCC 492
                                                                                                                                                                                                                                                                                                                                                 13 CGCAGCTGCCACCCGACCATGACCATCCTGCAGGCCCCGGACCCCGGGCCCCCTCCACCATC 72
                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                313 GTGCCCCCCCCCCCTGCCTCCAGAGGACGCCCCTAACGCCCCCATCCCTGGCGCCCACCCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        372 GGCCTCCNCCTCTCNCCCNCGGCTACNCCCNCCCACCGCNCCCNCCCTNCGCNTCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              373 GTGTCCCCCCGTCCTCGAGCCCTTTAATCTGACTTCGGAGCCCTCGGACTACGCTCTGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     253 AGGCTTCTCTTTCTGCTGCTCACCATCGTCTTCTGCCAGATCCTGATGGCTGAAGAGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              493 AAAAAGAATCCGAAAAACCACAAAAAAAACACCAGGCGTACCTGGTGCGCGAGAGCGTATC
                                                                                                                                                                                                                                                                                                               4 ;
                                                                                                                                                                                                                                                                  Query Match 4.0%; Score 49.6; DB 21; Length 1126; Best Local Similarity 33.2%; Pred. No. 0.0012; Matches 192; Conservative 0; Mismatches 383; Indels 4;
                                                                                                                                                                                                         Sequence 1126 BP; 101 A; 102 C; 575 G; 57 T; 291 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72 NNTNCCNNNCNNCCCCTNNNCNNNNCNNNCNNCNC
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double-stranded DNA (or its complementary strand or the corresp.

double-stranded DNA) which comprises one of the 7837 "GS" sequences
given in T19001-T26837 and which is able to hybridise to part of
given in T19001-T26837 and which is able to hybridise to part of
human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)
sequences were obtained from 3'-directed cDNA libraries prepared
from various human tissues; syntheais of cDNA was initiated from the
GY and mRNA by using poly(T) as the sole primer. Since the 3'-
untranslated sequence is unique to a particular mRNA species, almost
all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library
is constructed so as to reflect accurately the relative abundance of
different mRNAs in the particular tissue from which it was derived.
The appearance frequency of a given GS in a cDNA library can be
determined (sep. using primers and probes derived from the GS
sequences) as a means of diagnosing abnormal cell function or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cyclic nucleotide-associated protein-2; CNAP-2; human; cytostatic; anti-arteriosclerotic; hepatotropic; anti-leukaemic; anti-inflammatory; immunomodulatory; anti-asthmatic; anti-anemic; anti-dibatic; diagnosis; anti-sclerotic; dermatological; neuroprotective; anti-epileptic; cancer; anti-infertility; anti-allergic; vasotropic; immunosuppressive; anti-infertility; anti-allergic; vasotropic; immunosuppressive; hypotensive; gene therapy; prevention; treatment; arteriosclerosis; cell proliferative disorder; autoimmune/inflammatory; diabetes mellitus; neurological; vision; reproductive; smooth muscle; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                           e.9.
                                                                                                                                                                                                                                                                                                     Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1158 GATCGCCTAGTATGTTCTGTGAACACAAAATAAAATTGATTTACTGTCAAAAA 1210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human cyclic nucleotide-associated protein-2 (CNAP-2) cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 48.2; DB 16
Pred. No. 0.00069;
); Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 53 BP; 18 A; 9 C; 9 G; 17 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 723; 2245pp; Japanese.
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94.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   251683 standard; cDNA; 4228
                                                                                                                              12-NOV-1993; " 93JP-0355504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-JUL-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 3.99
Best Local Similarity 94.37
Matches 50; Conservative
                                                                                                                                                                                                                              χ.
                                                                                                                                                                                                                                                               WPI; 1995-206931/27.
                                                                                                                                                                    (MATS/) MATSUBARA K.
                                                                                                                                                                                                                              Okubo
                                                                                                                                                                                        OKUB/) OKUBO K.
                                                                                           11-NOV-1994;
                                                                                                                                                                                                                            Matsubara K,
               W09514772-A1
                                                     01-JUN-1995.
                                                                                                                                                                                                                                                                                                                                                               tissues
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Homo sapiens

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The present sequence is the cDNA encoding human cyclic nucleotide associated protein-2 (CNAP-2), identified in Incyte clone 3149674, that is isolated from ADREMONG CDNA library. It is expressed in nervous, reproductive, cardiovascular and haematopoietic/immune tissues. CNAP sequences may be used for prevention, treatment and diagnosis of diseases associated with altered CNAP expression such as, cell proliferative disorders (e.g. arteriosclerosis, cirrhosis, leukaemia, lymphoma and cancer of the breast, prostate, lung and brain), autoimmune/ inflammatory disorders (e.g. asthma, anaemia, diabetes mellitus, multiple sclerosis and psoriasis), neurological disorders (e.g. epilepsy, conjunctivitis, glaucoma, cataracts and strokes), vision disorders (e.g. reproductive disorders (e.g. infertility, uterine fibroids, ectopic pregnancies and impotence) and smooth muscle disorders (e.g. angina, musch fellos chock, Kearns-Sayre syndrome and hypertension). It can also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ς;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  967 accagccctgtgcggggctccaagaatggtcagcacctcagctacagacgagccagg 1026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73 CCGGGACCCCGGCGGGCTCCTGAGATCTTCACCTTCGACCTCTCCCG----- 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolated cyclic nucleotide associated proteins useful for preventing, diagnosing and treating cell proliferative, autoimmune/inflammatory, neurological, vision, reproductive and smooth muscle disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13 CGCAGCTGCCACCCGACCATGACCATCCTGCAGGCCCGGACCCCGGGCCCCTCCACCATC 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tang YT;
                                      /product= "Human CNAP-2 protein"
/note= "Shares 24% identity to Aquifex pyrophilus
esterase 28LC"
                                                                                                                                                                                                                  /bound_moiety= "Primer or Probe"
/note= "Useful for amplification or hybridisation
techniques"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.9%; Score 47.8; DB 21; Length 4228;
48.2%; Pred. No. 0.0063;
Live 0; Mismatches 207; Indels 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patterson C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4228 BP; 793 A; 1365 C; 1324 G; 746 T; 0 other;
                                                                                                                                                     '*tag= c
'product= "Mature CNAP-2 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Corley NC,
 Location/Qualifiers
31..4014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 9; Page 70-71; 78pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Guegler KJ,
                                                                                                                                                                                                                                                                                                                                                   99WO-US20287.
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                                                                                                                    Ω
                                                                                                                                133. 4011
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  be used for gene therapy.
                                                                                                                                                                                   136..165
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                                                                                                                                                   /*tag=
                                                                                                                                                                                                    /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yue H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 202; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WP1; 2000-256994/22.
                                                                                                                                                                                                                                                                                  WO200014248-A1.
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                                                                                                                                                                                 misc_binding
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                                                                                                                                                                                                                                                                                                                                                                                    04-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hillman JL,
                                                                                                                                                                                                                                                                                                                  16-MAR-2000.
                                                                                                 sig_peptide
                                                                                                                                  mat_peptide
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127 --GAGCCCGCAGCGGCCCCTGCCGGGCGCCCCTCTCGCGGGCACCGAAAGCGCA 184

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The specification describes antisense oligonuclectides (x52869-x55271) directed against at least 2 mRNas selected from target genes, coding and non-coding regions of RNAs corresponding to target genes, gene initiation codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'-end and the juxta-section between coding and non-coding regions and all segments of RNAs encoding proteins associated with one or more diseases, conditions or mixtures. The antisense oligonucleotides of specifically x55180-271 can be used for the antisense treatment of diseases and conditions. Typical diseases and conditions are those associated with impaired respiration and inflammation, including lung diseases, pulmonary vasoconstriction, inflammation,
                                                               1087 cctgtgaagcccacatccctggaaacccctcggcccctctgctgagccgctgcgtctcc 1146
                                                                                                                                                                                          1147 atgccaggggacatctcaggct--tgcagggtggccccgctccgacttcgacatggcct 1204
                                                                                                                                                                                                                                                                                                                     1205 atgagogtggcoggatotocgtgtccotgcaggaagaggcotocgggggggtccotggcag 1264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Implacement of the control of the co
185 GCCGCAGGGTTCTCTACCCTCGAGTGGTCCGGCCCCAGCTGCCAGTCGAGGAACCGAACC 244
                                                                                                                                                                                                                                                      305 AAGAGGGTGTGCCGGCGCCCTGCCTCCAGAGGACGCCCTAACGCCGCATCCCTGGCGC 364
                                                                                                                                                                                                                                                                                                                                                                                                                   365 CCACCCTGTGTCCCCCGTCCTCGAGCCCTTTAATCTGACTTCGGAGCCCTCGGACTAC 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New antisense oligonucleotides used in treatment of, e.g. pulmonary
                                                                                                                              CAGCCAAAAGGCTTCTCTTTTGTGCTGCTCACCATCGTCTTCTGCCAGATCCTGATGGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antisense oligonucleotide; multiple target; antisense treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human adenosine Al receptor antisense oligonucleotide fragment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-229400/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            prostate cancer; ss
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X53491/c
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allergic rhiuilis, acute asthma, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g. colon cancer, breast cancer, lung cancer, pancreatic cancer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as well as all types of cancers which may metastasize or have metastasized to the lungs, including breast and prostate cancer.
                                                                                                                                                                                                                                                                                           108469 CCCCCCCCCCNNHNNNSCCAGCCAGCCAGCCCCCCCCCCCCCCCCCANHNNNSCCAGCCA 108410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73 CCGGGACCCCGGGGGGTCCGGTCCTGAGATCTTCACCTTCGACCCTCTCCGGAGCCC 132
                                                                                                                                                                                                                                                                                                                                                                                            GCAGCGGCCCCTGCCGGGCGCC; CAGCGCCTCTCGCGGGCACCGAAAGCG -- CAGCCGCA 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGGT"TCTCTACCCTCGAGTGGTCCGGCGCCAGCTGCCAGTCGAGGAACCGAACCCAGCCA 250
                                                                                                                                                                                                                                                            13 CGCAGCTGCCACCCGACCATGACCATCCTGCAGGCCCCGACCCCGGGCCCCTCCACCATC 72
                                                                                                                                           Sequence 114955 HP; 6071 A; 29417 C; 36712 G; 21328 T; 21427 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human colon cancer cell line polynucleotide sequence SEQ ID NO:2495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probe; detection; cancerous state; metastasis; identification; breast cancer; oestrogen receptor-positive breast cancer; therapy; oestrogen receptor-negative breast cancer; ss.
                                                                                                                                                                                                                                                                                                                                                         108649 NNNSGCCGCCCCCCCCCCCCCCCNHNNNSAGGCGCCCCCCCCCCCCCCNHNNNSCAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             251 AAAGGCTTCTCTTTTCTGCTGCTCACCATCGTCTTCTGCCAGATCCTGATGGCTGAAGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTGTGCCGGCGCCCCTGCCAGAGGACGCCCCTAACGCCGCATCCCTGGCGCCCACCC
                                                                                                                                                                                                    Length 114955;
                                                                                                                                                                                                3.8%; Score 47.2; DB 20; Length
38.9%; Pred. No. 0.041;
ive 21; Mismatches 210; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; colon cancer; tumour; diagnosis; gene expression
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98US-008537.
98US-0085696.
98US-0105234.
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A02504 standard; cDNA; 1593
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Matches 149; Conservative
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15-MAY-1998;
21-OCT-1998;
27-OCT-1998;
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                                                                                                                                                                                               Query Match
Best Local 9
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A02504/
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                                                                                                                                                                                                                                                                                             A00010 to A02716 represent polynucleotides isolated from cDNA libraries constructed from human colon cancer cell lines. The present invention also describes a method of detecting differentially expressed genes correlated with a cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample derived from a cell suspected of being cancerous, where detection of the differentially expressed gene product is correlated with a cancerous state of the cell from which the test sample was derived. The polynucleotides sequences can be used in a method for detecting differentially expressed genes correlated with a cancerous state of ammanian cell. The polynucleotides can also be used as probes for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            detecting and mapping related genes. They can be used in diagnosis and prognosis of diseases and disorders (e.g. identification of prognosis of diseases and disorders (e.g. identification of permetastatic cancerous states, stages of cancer, or responsiveness of cancer to therapy). This is particularly for breast cancer, oestrogen receptor-positive breast cancer, oestrogen receptor-
                                                                                                                                                                                                                   mammalian
                                                                         J, Innis MA, Garcia PD, Sudduth-Klinger J;
Randazzo F, Kennedy GC, Pot D, Kassam A;
Crvenjakov R, Dickson M, Drmanac S, Labat
Garcia V, Jones LW, Stache-Crain B;
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32.9%; Pred. No. 0.025;
ive 0; Mismatches 314;
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Best Local Similarity 32.99
Matches 155; Conservative
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Drmanac R,
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                 (CHIR ) CHIRON CORP. (HYSE-) HYSEO INC.
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Search completed: January 30, 2001, 21:29:29 Job time: 19255 sec

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442
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SCO O O O O O O O O O O O O O O O O O O	2000		08, 08, 10,	: Chordata; Primates;	ibmed=9703 ad K.V.S. s inhibit	(1998). 2558.1; - 2344.1; - 21028 MW;	. 0.	LLFLLLTIV LFLLLTIV	STFLQQHPA 	ARY;
SCO O O O O O O O O O O O O O O O O O O				s (Human) Metazoa; utheria; 9606;	OM N.A. 69175; Pu Z., Pras apoptosi	:998-1001 067; AAC3 596; AAC7 193 AA;	ilarity Conserva	VEEPNPAKR VEEPNPAKR	SPSDYALDL SPSDYALDL	PRELIMIN
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C STRAIN=BRISTOL N.S.

A MEDLINE—94150718; Pubmed=7906398;

Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,

A Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,

A Craxton M., Dear S., Du Z., Durbin R., Faulton L.,

A Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,

Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,

Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,

Parsons J., Percy C., Riken L., Roopra A., Saunders D., Shownkeen R.,

Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,

A Thierry-Mieg J., Thomas K., Vaudin M., Vaudin M., Vaudin M., Wachlaman P.;

T. 2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                               Nagase T., Ishikawa K., Suyama M., Kikuno R., Miyajima N., Tanaka A., Kotani H., Nomura N., Obara O.;

Frediction of the coding sequences of unidentified human genes. XI. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";

Fig. 1 ange proteins in vitro.";

Fig. 1 ange 
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Rhabditidae; Peloderinae; Caenorhabditis.
NCBL_TaxID=6239;
                                                                                                      Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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SEQUENCE 637 AA; 70516 MW; DEBFB005BA9B9CDD CRC64;
01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence.update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
KIAAQ781 PROTEIN (FRAGMENT).
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MEDLINE-99087487; PubMed-9872452;
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                                                                                                                                                                                                               SEQUENCE FROM N.A.
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28; Indels 11; Gaps
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MEDLINE=97206572; PubMed=9172827;
MEDLINE=97206572; PubMed=9172827;
MEDLING 2., Ghosh S., Jacobs M.E., Klobutcher L.A.;
"Conjugation-specific genes in the ciliate Euplotes crassus: gene expression from the old macronucleus.";
J. Eukaryot. Microbiol. 44:1-11(1997).
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Jacobs M.E., Ling 2., Klobutcher L.A.;
"condA8 encodes a novel and abundant protein targeted to the developing macronucleus in Euplotes crassus.";
Submitted (DEC.1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF116196; AAD29625.1;
                                                                                                                                                                                                                                                                                                                            18.4%; Score 81.5; DB 5; Length 102; 24.7%; Pred. No. 0.13; ive 19; Mismatches 28; Indels 1
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18.4%; Score 81.5; DB 5; Length 452;
Best Local Similarity 34.5%; Pred. No. 0.61;
Matches 30; Conservative 10; Mismatches 30; Indels 17
Nelson J., Gattung S.;
"The sequence of C. elegans cosmid R160.";
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                   Waterston R.;
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF099001; AAC68734.1; -.
SEQUENCE 102 AA: 11426 MW; AFD366C3932EB26C CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DEVELOPMENTAL-SPECIFIC PROTEIN CONZAB (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 24.7%,
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66 QVVIKIDPTESDVDMTS 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 --- LTSEPSDYALDLST 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                  SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID-5936;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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            RROLPVEEPNPAKRLLFLLLTIVFCOILMAEGVPAPLP-----PEDAPNAA-SLAPT
                                                                                                                                                        01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05, 01-OCT-2000 (TrEMBLrel. 15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                              Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4352 PLVELPTEP 4360
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Best Local Similarity
Matches 21; Conserv
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                Canaani E.;
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                                                                                                                                               014687;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          54
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                                                                                      Eukaryota; Alveolata; Ciliophora; hypotrichs; Euplotida; Euplotidae;
                                                                                                                                         STRAIN-G1;
MDDINE-2056572; PubMed-9172827;
Ling 2. Ghosh S. Jacobs M. E., Klobutcher L.A.;
Conjugation-specific genes in the ciliate Euplotes crassus: gene expression from the old macronucleus ";
J. Eukaryot. Microbiol. 44:1-11(1997)
                                                                                                                                                                                                                                                    Klobutcher L.A., Gygax S.E., Podoloff J.D., Vermeesch J.R., Price C.M., Tebeau C.M., Jahn C.L.; Conserved DNA sequences adjacent to chromosome fragmentation and tellomere addition sites in Euplotes crassus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 ROLPVEEP----NPAKRLLFLLLTIVFCQILMAEEGVPAPLPPEDAPNAASLAPT----P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Aviadenovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                   17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 302;
                                                                                                                                                                                                                                                                                                                                                                                                             18.4%; Score 81.5; DB 5; Length 468; larity 34.5%; Pred. No. 0.63; Conservative 10; Mismatches 30; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                        Ling Z., Klobutcher L.A.;
Ling Z., Klobutcher L.A.;
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF061334; AAD31724.1; -.
SEQUENCE 468 AA; 51457 MW; 70996125317C592A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ojkic D., Nagy E.;
"The DNA sequence of fowl adenovirus B.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF083975; AAD50348.1; -
SEQUENCE 302 AA; 34763 MM; BF34DF42FF026CCC CRC64;
                    Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
Last sequence update)
Last annotation update)
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 468 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SAPSLEPSSTLASEPRDIIPDPSAALK 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55 VSPVLEPFN-LTSEPSDYALDLSTFLQ 80
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                           MEDLINE-98391748; PubMed-9722644;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel. 13, C
(TrEMBLrel. 13, I
(TrEMBLrel. 13, I
                   (TrEMBLrel. 12, TremBLrel. 12, TremBLrel. 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
 PRELIMINARY;
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Matches 24; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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01-MAY-2000 (TEEMBI
33 KDA PROTEIN.
fowl adenovirus 8.
                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                SEQUENCE FROM N.A.
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                                                                            Euplotes crassus
                                                                                                          NCBI_TaxID=5936;
                                                    CONZAS PROTEIN.
                   01-NOV-1999
01-NOV-1999
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                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                Euplotes
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Structure and expression pattern of human ALR, a novel gene with strong homology to ALL-1 involved in acute leukemia and to Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 VRROLPVEEPNPAKRLLFILLTIVFCOILMAEEGVPAPLPPEDAPNAASLAPTPVSPVLE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-97388474; PubMed-9247308;
Prasad R., Zhadanov A.B., Sedkov Y., Bullrich F., Druck T.,
Rallapalli R., Yano T., Alder H., Croce C.M., Huebner K., Mazo A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Euteleostomi;
Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Wakaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PRO1217; PRICHEXTENSN, PROSITE; PS00398; RECOMBINASES_2; UNKNOWN_1. SEQUENCE 4957 AA; 531848 MW; 1026562E1419CEBD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, R
Mammalia, Eutheria, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
                                                                                                                                                                                                                 4957 AA
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                                         ||||| : :| :| : :: :|::::|:
PVSPAVS--DLKAEILNLLVEIESFVRKNPS 258
54 PVSPVLEPFNLTSEPSDYALDLSTFLQQHPA 84
                                                                                                                                                                                                                                                                          Created)
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EMBL; AF010401; AC51735.1; -.
INTERPRO; IPR001214; -.
INTERPRO; IPR001822; -.
INTERPO; IPR001965; -.
PFAM; PF00628; PFAM; PF00628; PFAM; PF00656; SET; 1.
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Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,
Phan H., Velasco N., Do L., Regala W., Terry A., Garnes J.,
Danganan L., Erler A., Christensen M., Georgescu A., Avila J., Liu S.,
Attix C., Andreise T., Trankheim M., Amico-Keller G., Coefield J.,
Duarte S., Lucas S., Bruce R., Thomas P., Ouan G., Kronmiller B.,
Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,
Olsen A.S., Carrano A.V.;
"Sequence analysis of a 3.5 Mb region in 19p13.1 between OLFR and
                                                                                                 in acute leukemia and to Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 VRRQLPVEEPNPAKRLLFLLLTIVFCQILMAEEGVPAPL,PPEDAPNAASLAPTPVSPVLE 60
                  Prasad R., Zhadanov A.B., Sedkov Y., Bullrich F., Druck T.,
Rallapalli R., Yano T., Alder H., Croce C.M., Huebner K., Mazo A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 783-1568 FROM N.A.

Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,

Burkhart-Schultz K., Gordon L., Dias J., Brower A., Ramirez M.,

Stilwagen S., Phan H., Velasco N., Do L., Regala W., Terry A.,

Garnes J., Danganan L., Erler A., Christensen M., Georgescu A.,

Avia J., Liu S., Attix C., Andreise T., Trankheim M.,

Anico-Keller G., Coeffeld J., Duarte S., Lucas S., Bruce R.,

Thomas P., Quan G., Kromiller B., Arellano A., Sanders C., Ow D.,

"Sequence analysis of an -1.5 Mb contig in 19p13.1 between OLFR and
                                                                                 of human ALR, a novel gene with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            095785 PRELIMINARY; PRT; 1568 AA.
01-MAY-1999 (TEMBLEE). 10, Created)
01-MAY-1999 (TEMBLEE). 10, Last sequence update)
01-JUN-2000 (TEMBLEE). 14, Last annotation update)
HUMAN HOMOLOG OF MUS MUSCULUS WIZL PROTEIN (HUMAN HOMOLOG OF MUS MUSCULUS WIZL PROTEIN (HUMAN HOMOLOG OF MUS
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                           17.6%; Score 78; DB 4; Length 5262; 30.4%; Pred. No. 18;
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Live 12; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                 PRAMI: FECUSO, J., PRICHEXTENSN.
PROSITE; PS00398; RECOMBINASES_2; UNKNOWN_1.
SEQUENCE 5262 AA; 564181 MW; 26B7C74CAD417E44 CRC64;
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                                                                           "Structure and expression pattern
strong homology to ALL-1 involved
MEDI.INE-97388474; Pubmed-9247308;
                                                                                                                                Oncogene 15:549-560(1997).
EMBL: AF010403: AAC51734.1; -
INTERPRO: IPPR001214; -
INTERPRO: IPR001822; -
INTERPRO: IPR001841; -
INTERPRO: IPR001865; -
INTERPRO: IPR002665; -
PFAM: PF00628; PHD: 5-
PFAM: PF00656; SET: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                               21; Conservative
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Best Local Similarity
Matches 21; Conserve
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4657 PLVELPTEP 4665
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RA MEDLINE-2019(6006): Pubbed-10731132;

RA MEDLINE-2019(6006): Pubbed-10731132;

RA Adams N.D. Celniker S.E., Holt R.W., Hoskins R.A., Galle R.F.,

George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

Ballew R.W., Boyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Abril J.F., Agbayani A., An H.-J. Andrews-Pérnnkoh C., Baldwin D.,

Rabillaw R.W., Basu A., Baxendale J., Bayraktaroglu L. Beasley E.M.,

Ballew R.W., Basu A., Buxendale J., Bayraktaroglu L. Beasley E.M.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Borkova D., Botcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Gebris B., Cong E., Gorrell J. H., Calieu E., Center A., Chandra I.,

RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,

Glodek A., Gong F., Gorrell J. H., Gu Z., Kennison J.A., Houck J.

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.

RA Liu X., Mattei B., Warlnosh T.C., Morris J., Mosheri M. S.,

Liu X., Mattei B., Warlnosh T.C., Morris J., Wosheri M. S.,

RA Balan M. Wallshina N.V., Mobarry C., Morris J., Mosheri M. S.,

RA Bloor D.R., Mulshina N.V., Mobarry C., Morris J., Warl M., Marphy B., Murphy B., Murphy B., Murphy B., Sunder R., Randon K., Sanith T.,

RA Shue B.C., Siden Klanos J., Simpson M., Skupski M.P., Smith T.,

RA Shre B.C., Siden Klanos J., Simpson M., Skupski M.P., Smith T.,

RA Bangzolo M., Woodage T., Wolley C., Wang S., Pollado D. N.,

Wallams S.M., Woodage T., Wolley C., Wang S., Pollado D. N.,

Wallams S.M., Woodage T., Woolly C., Wallan S., Pollado D. N
                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster (Fruit fly).
Eukaryota: Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota: Neoptera: Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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8
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SEQUENCE 1568 AA; 170077 MW; 74F0D34D45F565D0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                    908 LALAGSPTFKNPEDKSPQLSLSPRPASPKAQWPQSEDEGPLNLTSGP 954
                                                                                                                                                                                                                                                                                                                                   30 MAEEGVPAPLPPEDAPNAASLAPTPVSPVLE-----PFNLTSEP 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, Created)
U-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
CG2174 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2424 AA
                                                                                PFAM; PF00096; z1-C2H2; 10.
PROSITE; PS00028; ZINC_FINGER_C2H2; 8.
Zinc_finger; Metal-binding; DNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-BERKELEY;
MEDLINE-20196006; Pubmed-10731132;
EMBL; AC007059; AAD19818.1; --
EMBL; AC006128; AAC97985.1; --
EMBL; AC07059; AAD19817.1; --
INTERPRO; IPRO00822; --
                                                                                                                                                                                                                                            Ouery Match 17.49
Best Local Similarity 40.49
Matches 19; Conservative
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Q9VZ48;
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Q9VZ48
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MEDLINE-2017575; PubMed-10710307;
Tottelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E., Elsen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodgson R.J., Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A., Mason M.C., Letchor M.D., Utterback T.R., Khouri H., Oln H., Vamathevan J., Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.; "Complete genome sequence of Neisscria meningitidis serogroup B strain
                                                                                                                                                                                                                              Neisseria meningitidis (serogroup B).
Bacteria: Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
NCBI_TaxID=491;
                                                                                                                                                                                                                 28 ILMAEEGVPAPLPPEDAPNAASLAPTPVSPVLEPFNLTSEPS-DYALDLSTFLQQHPAAF 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                          Score 77; DB 5; Length 2424;
Pred. No. 10;
7; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17.2%; Score 76; DB 2; Length 148; 40.5%; Pred. No. 0.75; 1ve 5; Mismatches 17; Indels
                                                                                            PFAM; PF00063; myosi_head; 1.
PFAM; PF00612; 10; 3.
PFAM; PF00784; MyTH4; 1.
PRINTS; PF00193; MYOSINHEAVY.
SEQUENCE 2424 AA; 267616 MW; BAD62AA33F9AA5D0 CRC64;
                                                                                                                                                                                                29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       148 AA; 16332 MW; 28E9B40D502D80B4 CRC64;
                                                                                                                                                                                                                                                                                                      09JZR7;
01-CCT-2000 (TrEMBLrel. 15, Created)
01-CCT-2000 (TrEMBLrel. 15, Last sequence update)
01-CCT-2000 (TrEMBLrel. 15, Last annotation update)
ACYL COA THIOESTER HYDROLASE FAMILY PROTEIN.
Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
EMBL; AR603484; AAF47980.1; -.
HSSP: P08799; IMND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18 FLLLTIVFCQILMAEEGVPAPLPPEDAPNAASLAPTP 54
                                                                                                                                                                                                                                                                                                  148 AA
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                                                    FLYBASE; FBgn0030252; CG2174.
INTERPRO; IPR000048; -.
                                                                                                                                                                        17.4%;
ilarity 36.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Science 287:1809-1815(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15; Conservative
                                                                                                                                                                                                                                                                                               PRELIMINARY;
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                                                                                    :NTERPRO; IPR001609; -.
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                                                                           NTERPRO; IPR000857
                                                                                                                                                                                    Similarity
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Best Local Simi
Matches 22; (
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RY SELOENCE FROM N.A.

RATAIN-BERKELES,

RA Addams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

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RA Addams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Addams M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Button G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,

RA Ballew R.M. Basu A., Ravandale J., Bayarktaroglu L., Beasley E.M.,

RA Ballew R.M., Basu A., Ravandale J., Bayarktaroglu L., Beasley E.M.,

RA Ballew R.M., Benos P.V., Berman B.P., Bhandari D., Bollahakov S.,

RA Burtis K.C., Buckhan M.R., Bouw J., Bornandale J., Bayarktaroglu L., Bollahakov S.,

RA Burtis K.C., Buckhan M.R., Bouw J., Bornandari D., Bollahakov S.,

RA Burtis K.C., Buckhan M.R., Bouw J., Bornandari D., Bollahakov S.,

RA Durbin K.J., Evangelista C.C., Ferrac C., Ferrica C., Ferlas C.M.

RA Durbin K.J., Evangelista C.C., Ferrac C., Ferrica S., Plakschman W.,

RA Durbin K.J., Boungelista C.C., Ferrac C., Ferrac C., Ferrac C.,

RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,

RA Jalali M., Kalush F., Karpen G. H., Ke Z., Kennison J.A., Ketchum K.A.,

Luu X., Mattei B., McInton T.C., Morite M., Index J.M., Narlos D.,

RA Balazzolo M., Pittman G.S., Pan S., Wolley M., Nelson D.L.,

RA Balazzolo M., Pittman G.S., Pan S., Pollard J., Worlier S., Shon H.

Spier E., Spradling A.C., Stapleton M., Stupski M.P., Shur H.

Spier E., Spradling A.C., Stapleton M., Stupski M.P., Shur H.

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Spier E., Spradling A.C., Stapleton M., Stupski M.P., Shur H.

Spier E., Spradling A.C., Stapleton M., Stupski M.P., Shur H.

Spier E., Spradling G.W., Weissenbach J., Wassernbach J., Wassernbach J., Wassern D. C., Stapleton G. C., Wassernbach J., Wassernbach J., Wassern
                                                                                 Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26 CQILMAEEGVPAPLPPEDA--PNAASLAPTPVS-----PVLEPFNLTSEPSDYALDL 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SH3; 1.
; 89233 MW; AOF5C824663DC391 CRC64;
01-OCT-2000 (TrEMBLrel. 15, Last annotation update) CG2258 PROTEIN.
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Best Local Similarity
Matches 21; Conserv
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Search completed: January 30, 2001, 23:11:30 Job time: 3995 sec
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                RESULT 15
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"Sequence and transcriptional analysis of terminal regions of the fowl adenovirus type B genome.";
J. Gen. Virol. 79:2507-2556(1998).

EMBL; AF021254; AAC71673.1;
SEQUENCE 114 AA; 13266 MW; 866DEEC6636EABA6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                Leishmania tropica.
Eukaryota, Euglenozoa, Kinetoplastida; Trypanosomatidae; Leishmania.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32 EEGVPAPLP-----PEDAPNAA-SLAPTPVSPVLEPFNLTSEPSDYALDLSTFLQQHP 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37 APLP-----PEDAPNAASLAPTPVSPVLEPFN------LTSEPSDYALDLST 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Aviadenovirus.
NCBL_TaxID=66295;
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                                                                                                                                                                                                                                                                                                                                                    Length 1677;
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                                                                                                                                                                                                                                                                                                                                                                            15; Indels
                                                                                                                                                                                                                                                                          PROSITE; PS00030; RNP 1; UNKNOWN 1.
PROSITE; PS00211; ABC_TRANSPORTER; UNKNOWN_1.
PROSITE; PS00962; RIBOSOMAL_S2_1; UNKNOWN_1.
SEQUENCE 1677 AA; 183006 MW; C49208921B71563A CRC64;
                                                                                                                                                       Lafuente E., Castanys S., Gamarro F.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
EMBL: U55381; AAB51191.1;
HSSP: P13569; INBD.
                                   01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
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Last annotation update)
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Pred. No. 9;
6; Mismatches
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             PRT;
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MEDLINE=98451338; Pubmed=9780058;
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PFAM; PF00664; ABC_membrane; 2.
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Best Local Similarity 33.9%;
Matches 20; Conservative
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01-MAY-1999 (TrEMBLrel. 10,
01-MAY-1999 (TrEMBLrel. 10,
01-MAY-2000 (TrEMBLrel. 13,
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Matches 19; Conservative
            PRELIMINARY;
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                                                                      P-GLYCOPROTEIN E
                                                                                                         NCBI_TaxID=5666;
                                                                                                                                           STRAIN-LRC-L39;
                                                                                                                                                                                                                                         NTERPRO;
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Gaps
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                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .;
                                                                                                                                                                                                                                                                                                                                                             TISSUE-BRAIN;
Matsumoto K., Ishii N., Yoshida S., Shiosaka S., Wanaka A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 955;
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PRINTS; PR00048; ZINCFINGER.
PROSITE; PS00028; ZINC_FINGER_CZH2; S.
Zinc-finger; Metal-binding; DNA-binding;
SEQUENCE 955 AA; 102777 MW; D4DD03A02BECCAAC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34 GVPAPLPPEDAPNAASLAPTPVSPVLE-----PFNLTSEP
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16.7%; Score 74; DB 11;
Best Local Similarity 41.9%; Pred. No. 8.3;
Matches 18; Conservative 2; Mismatches 15
  955 AA
PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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Sequence 10, Appl. Sequence 11386, A Sequence 1102, Appl. Sequence 167, Appl. Sequence 167, Appl. Sequence 169, Appl. Sequence 169, Appl. Sequence 170, Appl. Sequence 170, Appl. Sequence 170, Appl. Sequence 2750, Appl. Sequence 2750, Appl. Sequence 2811, Appl. Sequence 21250, Appl. Sequence 21250, Appl. Sequence 21296, A Sequence 21050, A Sequence 22007, A Sequence 2007, A

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TITLE OF INVENTION:

PAPLICANT:

TITLE OF INVENTION:

TARDOVASCULAR DISEASE

NUMBER OF SEQUENCES:

ADDRESSE:

ADDRESS
7 US-09-372-044-10
2 US-60-197-371-17386
2 US-60-196-181-6102
PCT-USO0-15136-166
PCT-USO0-15136-167
PCT-USO0-15136-167
PCT-USO0-15136-167
PCT-USO0-15136-167
PCT-USO0-15136-169
PCT-USO0-15136-169
PCT-USO0-15136-169
US-60-196-718-339
US-60-196-718-339
US-60-196-718-329
US-60-191-637-28141
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Sequence 10, Application US/08799910

GENERAL INFORMATION:

APPLICANT: Falb, Dean
      1114.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Description
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| cgn2_6/ptodata/2/paa/US06_COMB.pep:*
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| cgn2_6/ptodata/2/paa/US08_COMB.pep:*
| cgn2_6/ptodata/2/paa/US09_COMB.pep:*
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| cgn2_6/ptodata/1/paa/US09_COMB.pep:*
| cgn2_6/ptodata/1/paa/US09_USW_COMB.pep:*
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Compugen Ltd
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US-08-825-486-10
US-08-826-248-10
US-08-870-434-11
US-08-925-588-10
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                                 GenCore version
Copyright (c) 1993 - 2000
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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length: 2000000000
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Match Length DB
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Score

823 823 823 823 823

Minimum DB seq Maximum DB seq

Database

Perfect score:

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OM protein

Run on:

Scoring table:

Searched:

Sequence 30133, A Sequence 4244, Ap Sequence 49, Appl Sequence 37506, A

Gaps

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61 RSRRVLYPRVVRRQLPVEEPNPAKRLLFLLTIVFCQILMAEEGVPAPLPPEDAPNAASL 120
                                                                                                                                                                                                                                                                                                                                                                    1 MCHSRSCHPTMT1LQAPTPAPST1PGPRRGSGPEIFTFDPLPEPAAAPAGRPSASRGHRK 60
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                                                                                                                                                                                                      Length 156;
                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: THE TREATMENT AND DIAGNOSIS OF VITLE OF INVENTION: CARDIOVASCULAR DISEASE OF NUMBER OF SEQUENCES: 44

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                              Query Match 100.0%; Score 823; DB 12; Best Local Similarity 100.0%; Pred. No. 3.2e-60; Matches 156; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                         121 APTPVSPVLEPFNLTSEPSDYALDISTFLOOHPAAF 156
                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FASTSEQ VERSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/826,248
FILING DATE: 28-MAR-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/799,910
FILING DATE: 13-FEB-1997
PRIOR APPLICATION NUMBER: 60/011,787
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 10, Application US/08826248 GENERAL INFORMATION:
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TELECOMMUNICATION INFORMATION:
       SEQUENCE CHARACTERISTICS:
LENGTH: 156 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IBM Compatible
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REGISTRATION NUMBER: 3(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (212)8699741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Falb, Dean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM COM
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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                                                                                                                                           US-08-825-486-10
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STATE:
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                                                                                                                                                                                                                                                                                                                                                                 Length 156;
                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 10, Application US/08825486
GENERAL INFORMATION:
APPLICANT: Falb, Dean
TITLE OF INVENTION: COMPOSITIONS AND METHODS FUR
TITLE OF INVENTION: THE TREATMENT AND DIAGNOSIS OF
TITLE OF INVENTION: CARDIOVASCULAR DISEASE
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 823; DB 11;
100.0%; Pred. No. 3.2e-60;
11ve 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 APTPVSPVLEPFNLTSEPSDYALDLSTFLQQHPAAF 156
             NAME: COruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-067-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)7909090
TELEFRAX: (212)869941
TELER: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Diskette
COMPUTER: IDM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FASISEO VERSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/825,486
FILING DATE: 28 MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 1155 Avenue of the Americas
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PENNIE & EDMONDS LLP
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APPLICATION NUMBER: 08/799,910
FILING DATE: 13-FEB-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
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TELEPHONE: (212)7909090
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                  LENGTH: 156 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                         TOPOLOGY: unknown
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-799-910-10
                                                                                                                                                                                                                                                                                                                                                       Query Match 100.
Best Local Similarity 100.
Matches 156; Conservative
                                                                                                                                                                                                                             unknown
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2IP: 10036-2711
COMPUTER READABLE FORM:
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FRAGMENT TYPE: internal SEQUENCE DESCRIPTION: SEQ ID NO: 10:
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APPLICATION NUMBER: 08/799,910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FRASEQ Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                  Sequence 10, Application US/08925588 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5: (212)7909090
(212)8699741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 156 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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MEDIUM TYPE: Diskette
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: protein TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                          CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
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Best Local Similarity
Matches 156; Conserv
                                                                                                                                                                                                                                                                                                                                                                                            STATE: NY
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                                                                                                                                                                    RESULT
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GENERAL INFORMATION:
APPLICANT: Falb, Dean
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennle & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 RSRRVLYPRVVRRQLPVEEPNPAKRLLFLLLTIVFCQILMAEEGVPAPLPPEDAPNAASL 120
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100.0%; Pred. No. 3.2e-60;
ive 0; Mismatches 0;
                                                                Score 823; DB 12;
Pred. No. 3.2e-60;
; Mismatches 0;
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SOFTWARE: FASTEM: VENTON 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/870,434
FILING DATE: 06-JUN-1997
CLASSIFICATION: 800
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REFERENCE/DOCKET NUMBER: 7853-084
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/799,910
FILING DATE: 13-FEB-1997
ATTORNEY/AGENT INFORMATION:
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100.0%; Pr
tive 0;
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COMPUTER: IBM Compatible
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 156 aming acids
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COMPUTER READABLE FORM:
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nes 156; Conserv
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Best Local Similarity
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CITY: New York
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; FRAGMENT TYPE:
US-08-826-248-10
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Best Local Si
Matches 156;
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61 RSRRVLYPRVVRRQLPVEEPNPAKRLLFLLLTIVFCQILMAEEGVPAPLPPEDAPNAASL 120
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ATTORNEY/AGENT INFORMATION:
NAME: COIUZEI, LAURA
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-067-999
TELECOMMUNICATION INFORMATION:
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                   121 APTPVSPVLEPFNLTSEPSDYALDLSTFLQQHPAAF 156
                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
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TITLE OF INVENTION:
TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: USES THEREOF
CURRENT APPLICATION UNABER: US/60/196,718
CURRENT FILING DATE: 2000-04-13
SOFTWARE: FASTER
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Pred. No. 8.2e~28;
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TITLE OF INVENTION: 50 Human Secreted Proteins
FILE REPERENCE: PS551PCT
CURRENT APPLICATION NUMBER: PCT/US00/15136
CURRENT FILING DATE: 2000-06-01
EARLIER APPLICATION NUMBER: 60/138,629
EARLIER FILING DATE: 1999-06-11
NUMBER OF SEQ ID NOS: 198
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 168
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100.0%; Pred. No. u.
... 0; Mismatches
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121 APTPVSPVLEPFNLTSEPSDYALDLSTFLQ0 151
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PCT-US00-15136-96
; Sequence 96, Application PC/TUS0015136
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Best Local Similarity 93.5
Matches 86; Conservative
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ORGANISM: HOMO
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LENGTH: 123
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                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 10, Application US/09372044A
GENERAL INFORMATION:
APPLICANT: Dean FALB et al.
TITLE OF INVENTION: Treatment and Diagnosis of Cardiovascular Disease
TITLE OF INVENTION: Treatment and Diagnosis of Cardiovascular Disease
TITLE REFERENCE: 7853-152
CURRENT APPLICATION UNMBER: US/09/372,044A
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PASSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MCHSRSCHPTWTILQAPTPAPSTIPGPRRGSGPEIFTFDPLPEPAAAPAGRPSASRGHRK 60
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APPLICANT: Tanaka, Hiroaki
APPLICANT: Dumas Milne Edwards, Jean Baptiste
APPLICANT: Jobert, Severin
APPLICANT: Jobert, Severin
APPLICANT: Glordano, Jean-Yves
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: 81.0S1.PRO
CURRENT APPLICATION NUMBER: US/60/197,873
CURRENT FILING DATE: 2000-04-18
NUMBER OF SEQ ID NOS: 52153
                                                                                                                                                                                                                                                                                                                               100.0%; Score 823; DB 17;
100.0%; Pred. No. 3.2e-60;
ilve 0; Mismatches 0;
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100.0%; Pred. No. 7.5e-58;
iive 0; Mismatches 0;
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Best Local Similarity 100.(
Matches 156; Conservative
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Best Local Similarity 100.C
Matches 151; Conservative
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US-60-197-873-17386
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                           US-09-372-044-10
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LENGTH: 151
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NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROPEINS,
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Best Local Similarity 97.1
Matches 66; Conservative
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                                                                                                                                                                                                                                                                               Conservative
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Best Local Similarity
------ 70; Conserve
TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                     SOFTWARE: Fas
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LOCATION: (83)
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PCT-USO0-15136-96
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                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
                                                                                                                                                                                                                                                                                                                                                               51.4%; Score 423; DB 1;
100.0%; Pred. No. 1.2e-27;
ive 0; Mismatches 0;
         APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: 50 Human Secreted Proteins
FILE REFERENCE: PS551PCT
CURRENT APPLICATION NUMBER: PCT/USO0/15136
CURRENT FILING DATE: 2000-06-01
EARLIER APPLICATION NUMBER: 60/138,629
EARLIER FILING DATE: 1999-06-11
NUMBER OF SEQ ID NOS: 198
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 96
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TITLE OF INVENTION: 50 Human Secreted Proteins
FILE REFERENCE: PS551PCT
CURRENT APPLICATION NUMBER: PCT/USO0/15136
CURRENT FILING DATE: 2000-06-01
EARLIER APPLICATION NUMBER: 60/138,629
EARLIER APPLICATION NUMBER: 60/138,629
EARLIER FILING DATE: 1999-06-11
NUMBER OF SED ID NOS: 198
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 167, Application PC/TUS0015136 GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 82; Conservative
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                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CT-USO0-15136-167
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Best Local Similarity
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US-60-196-718-4945
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TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: UNCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: USES THEREOF
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                                                                                                                                                                                                                                                                                             Score 381; DB 22;
Pred. No. 3.7e-24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 169, Application PC/TUS0015136
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: 50 Human Secreted Proteins;
FILE REFERENCE: PS551PCT
CURRENT APPLICATION NUMBER: PCT/US00/15136
CURRENT FILING DATE: 2000-06-01
EARLIER APPLICATION NUMBER: 60/138,629
HUMBER OF SEQ ID NOS: 198
SOFTWARE: Patentin Ver 2:0
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                                                                                                     FastSEQ for Windows Version 4.0
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FILE REFERENCE: CLOO0456
CURRENT APPLICATION NUMBER: US/60/196,718
CURRENT FILING DATE: 2000-04-13
NUMBER OF SEQ ID NOS: 7494
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CURRENY PAPLICATION NUMBER: US/60/196,718
CURRENT FILING DATE: 2000-04-13
NUMBER OF SEO ID NOS: 7494
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GENERAL INFORMATION:
APPLICANT: Bonazzi, Vivien
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100.0%; Pre
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; SEQ ID NO 5439 ; LENGTH: 92 ; TYPE: PRT ; ORGANISM: HUNAN US-60-196-718-5439

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                                                                                           1 MCHSRSCHPTWTilgaptpapstipgprrgsgpeiftfdplpepaaapagrpsasrghrk 60
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Best Local Similarity 100.0%; Pred. No. 6.8e-21;
Matches 62; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                          TTLE OF INVENTION: 50 Human Screeces, Inc.
TTLE OF INVENTION: 50 Human Secreted Proteins
FILE REFERENCE: PS51PCT:
CURRENT APPLICATION NUMBER: PCT/US00/15136
CURRENT FILING DATE: 2000-06-01
EARLIER FILING DATE: 1999-06-11
NUMBER OF SEQ ID NOS: 198
SOFTWARE: Patentin Ver. 2.0
LENGTH: 72
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Job time: 6037 sec
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PCT-US00-15136-170
: Sequence 170, Application PC/TUS0015136
: GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
PCT-US00-15136-170
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RS 62
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US-08-231-193A-50 US-08-480-474-50 US-08-940-086A-50 US-08-21-193A-48 US-08-480-474-48 US-08-480-474-48 US-08-480-474-48 US-08-980-086A-48 US-08-980-474-6 US-08-480-474-6 US-08-480-474-52 US-08-480-474-52 US-08-480-474-52 US-08-480-474-52 US-08-480-474-52 US-08-940-086A-6 US-08-480-474-52 US-08-480-474-52 US-08-480-474-52

Sequence

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APPLICANT: Falb, Dean
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: THE TREATMENT AND DIAGNOSIS OF
TITLE OF INVENTION: CARDIOVASCULAR DISEASE
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                         E: PENNIE & EDMONDS LLP
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/826,246
FILING DATE: 28-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 28-MAR-1997
CLASSIFICATION: 800
PRIOR APPLICATION BAR-1997
APPLICATION UNBER: 08/799,910
FILING DATE: 13-FEB-1997
PRIOR APPLICATION DATA: 800/11,787
FILING DATE: 16-FEB-1996
ATORNEY/AGENT INFORMATION: NAME: COLUZZI, LAULA A RECISTRATION NUMBER: 30,742
                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 10036-2711
COMPUTER READABLE, FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fast SEQ Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                         Sequence 10, Application US/08826246 Patent No. 6048709 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (212)7909090
TELEFAX: (212)8699741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 156 amino acids
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TOPOLOGY: unknown
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USA
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COUNTRY:
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STREET:
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 January 30, 2001, 19:24:41; Search time 36.91 Seconds (without alignments) 75.895 Million cell updates/sec
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1 MCHISRSCHPTMTILOAPTPA......EPSDYALDLSTFLQQHPAAF 156
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Sequence 11,
Sequence 24,
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Sequence 9,
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Sequence 7
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Sequence 2
Sequence 2
Sequence 6
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2: /cgn2_6/ptcdata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptcdata/2/iaa/6_COMB.pep:*
4: /cgn2_6/ptcdata/2/iaa/pcyrUS_COMB.pep:*
5: /cyn2_6/ptcdata/2/iaa/pcyrUS_COMB.pep:*
      GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-09-126-640-11

US-09-135-648-24

US-09-135-648-24

US-08-574-959A-7

US-08-574-959A-7

US-08-10-255-7

US-08-10-255-7

US-08-10-255-7

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US-08-10-255-7

US-08-10-255-1

US-08-10-255-1

US-08-10-265-1

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                                                OM protein - protein search, using sw model
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seq length: 200000000
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7853-078-999

Length 156;

Query Match

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Shyjan, Andrew W.
APPLICANT: Shyjan, Andrew W.
TITLE OF INVENTION: COMPOSITIONS AND METHONS FOR THE
TITLE OF INVENTION: GROWTH AND PROLIFERATION
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                  APPLICANT: FALB, Dean A.

APPLICANT: FALB, Dean A.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
FILE REFERENCE: 7853-126

CURRENT FILING DATE: 1998-07-30

EARLIER APPLICATION NUMBER: 08/79,344

EARLIER FILING DATE: 1997-06-06

EARLIER FILING DATE: 1997-06-13

EARLIER FILING DATE: 1996-02-13

EARLIER FILING DATE: 1996-02-16

SOFTWARE: Fatish DATE: 1996-02-16
                             RSRRVLYPRVVRRQLPVEEPNPAKRLLFLLLTIVFCQII.MAEEGVPAPLPPEDAPNAASI, 120
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Pred. No. 4e-75;
; Mismatches 0;
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                                                                                                          121 APTPVSPVLEPFNLTSEPSDYALDLSTFLQQHPAAF 156
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: Patent No. 6099823
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ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Homo sapiens
US-09-126-640-11
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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STATE: MA
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                                              Gaps
                                                                                                   1 MCHSKSCHPTMT1LQAPTPAPSTIPGPRRGSGPEIFTFDPLPEPAAAPAGRPSASRGHRK 60
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                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Falb, Dean.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: THE TREATMENT AND DIAGNOSIS OF NUMBER OF SEQUENCES: 44

CORRESPONDENCE ADDRESS:
                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 823; DB 3; 100.0%; Pred. No. 4e-75;
Score 823; DB 3
Pred. No. 4e-75;
                                                                                                                                                                                                                                            121 APTPVSPVLEPFNLTSEPSDYALDLSTFLQQHPAAF 156
                                                                                                                                                                                                                                                                 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-067-999
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US/08/944,495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/799,910
FILLING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                  Sequence 10, Application US/08944495
Patent No. 6087477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: DOS
SOFTWARE: FastESEO Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,
  100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (212)7909090
TELEFAX: (212)8699741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 156 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
                     Best Local Similarity 100.
Matches 156; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: unknown
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Y: USA
10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-944-495-10
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Best Local Si
Matches 156;
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Gaps

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1354 TESCADMAQKRQAP-DAP-TLP-PRDGELSPP-----PIPPRLNHSTGISYLRQSHGKS 1404
                                                                                                                               1405 KEFVGNSSLLLPNTSSIMIRRNSAIEKRAAATSQPNQAAAGPLSTTLVTVSQAVATDEPL 1464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | | | | : | : | : | : | | : | | ETFGGRVPRPAFVHYDKEEASDVEISLESDSDOSVVIVPEGLP-PLPP---PPPSGATPP 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          460 AGPVPSEPWTSTTANLLGLLSRPSVCPPRLLPGPENHRAGSNEDPILAPSGTPPPTIPPD 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----RVVRRQLPVEEPNPAKRLLFLLTIVFCQILMAEEGVPAPLPPEDAPNASLAPT 123
                                                                                                                                                                           106 PAPLPPEDAPNAASLAPT--PVSPVLEPF--NLTSEP----SDYALDLSTFLQQ----H 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 HPTMTILQ-----APTPAPSTIPGPRRGSGPE-----IFTFDPLPEPAAAPAGRPSAS 55
SRSCHPTMT1LQAPTPAPST1PGPRRG - - SGPETFTFDPLPEPAAAPAGRPSASKGHRKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 905;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RELATED POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Jackyoon Shin, Insil Joung, Racha K. Vadlamudi
APPLICANT: and Jackyoon Strominger
TITLE OF INVENTION: p62 POLYPEPTIDES, RELATED POLYPEPTIDES
TITLE OF INVENTION: AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----VLYP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/574,959A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 93.5; DB 2;
; Pred. No. 0.18;
17; Mismatches 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11.4%; Score 93.5; 23.1%; Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: DFN-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: MASSEL: LAHIVE & COCKFIELD STREET: 60 State Street, Suite STATE: Massell
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 9, Application US/08574959A Patent No. 5962224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Mandragouras, Amy E. REGISTRATION NUMBER: 36,207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 19-DEC-95
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 905 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Rest Local Similarity 23.1.
As 45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 2: CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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1520 PAIY 1523
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Borrack Sjodin, Ann
APPLICANT: Borrack Sjodin, Ann
APPLICANT: Borrack Si, Dafna
APPLICANT: Cole, Philip
APPLICANT: Cole, Philip
APPLICANT: Cole, Philip
TITLE OF INVENTION: A CRYSTAL OF A RAS-SOS COMPLEX AND METHODS OF USE
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 600-1-228N
CURRENT FOLICATION NUMBER: US/09/356,952
CURRENT FILING DATE: 1999-07-19
EARLIER FILING DATE: 1998-07-21
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       264 APPPYSAVTPPPDAFSRGVSSPIAGPAQPPPWPQPAPWSQPAFYDSSERIASRDERISVP 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16 APTPAPSTIPGP----RRGSGPEIFTFDPLPEPAAAPAGRPS-----ASRGHR---- 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 -KRS-----RRVLYPRVVRRQLPVEEPNPAKRLLFLLL-------RRVLYPRVVRRQLPVEEPNPAKRLLFLLL-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          324 AKRTGILQEAKRRSTTKPMFTFKEPKVSPNP--ELLSLLQNSEGKRGTGAGGDSGPEEDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92 -----TIVFCQILMAEEGVPAPLPPEDAPNAASLAP-TPVSPVLEPFNLTSEP 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11.6%; Score 95.5; DB 3; 27.0%; Pred. No. 0.089; tive 14; Mismatches 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 3;
SOFTWARE: FastSEO for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/035,648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.6%; Score 95.5; D 28.3%; Pred. No. 0.22
Live 19; Mismatches
                                                                                                                                                                                              NAME: Meiklejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE-DOCKET NUMBER: 07334/003001
TELEPHONE: 617-542-5070
TELEPHONE: 617-542-8906
TELEFAX: 200154
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
                                                                                                            PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/818,829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/09356952
Patent No. 6117663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT; ORGANISM: Drosophila melanogaster
US-09-356-952-3
                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                     : 739 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 28.3%
Matches 52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity 27.09
Matches 47; Conservative
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FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                        CLASSIFICATION:
                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPULOGY:
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63 RRVLYPRVV------RRQLPVEEPNPAKRLLFLLLTIVFCQILMAEEGVPAPLPP 111
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US-08-465-713-7

Sequence 7, Application US/08465713

Sequence 7, Application US/08465713

Patent No. 6121419

GENERAL INFORMATION:
APPLICANT: ROWIEY, Janet D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: DETECTING GENE REARRANGEMENTS AND
TITLE OF INVENTION: DETECTING GENE REARRANGEMENTS AND
TITLE OF INVENTION: TRANSLOCATIONS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White 6 Durkee
STREET: P. O. Box 4433
CITY: HOUSTON
STATE: Texas
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 1400;
APPLICANT: Diaz, Manuel O.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: DETECTING GENE REARRANGEMENTS AND
TITLE OF INVENTION: TRANSLOCATIONS
                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.2%; Score 92; DB 1; 22.1%; Pred. No. 0.42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PERKEY, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: ARCD:072/PAR
TELECOMMUNICATION INFORMATION:
                                                                                                       ANDRESSEE: Arnold, White & Durkee STREET: P. O. Box 4433
CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/080,255
FILING DATE: 19930617
                                                                                                                                                                                                                                                                                                                         PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                    STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (512) 320-7200
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1400 amino acids TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 11.2%
Best Local Similarity 22.1%
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single
TOPOLOGY: linear
                                                                                 NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, W
                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 19 CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           690 AGPVPSEPWTSTTANLLGLLSRPSVCPPRLLPGPENHRAGSNEDPILAPSGTPPPTIPPD 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 HPTMTILQ-----APTPAPSTIPGPRRGSGPE-----IFTFDPLPEPAAAPAGRPSAS 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 1135;
                                                                                                                               Sequence 7, Application US/08574959A
Patent No. 596224
GENERAL INFORMATION:
APPLICANT: Jackyoon Shin, Insil Joung, Ratna K. Vadlamudi
APPLICANT: and Jack L. Strominger
TITLE OF INVENTION: p62 POLYPEPTIDES, RELATED POLYPEPTIDES
TITLE OF INVENTION: AND USES THEREFOR
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---HRKRSRR--VLYP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 19-DEC-95
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 11.4%; Score 93.5; DB Best Local Similarity 23.1%; Pred. No. 0.23; Matches 45; Conservative 17; Mismatches
                                                                                                                                                                                                                                                                                                                      ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 36,207
REGISTRATION NUMBER: 36,207
REFRENCE/POCKET NUMBER: DFN-008
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7, Application US/08080255
Patent No. 5487970
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                        |::| | |:|
576 PIAPTGPP---TASP 587
  124 PVSPVLEPFNLTSEP 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124 PVSPVLEPFNLTSEP 138
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                                                                                                                                                                                                                                                                                                                                                                                                      Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                    STATE: Ma
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                                                                                                                       US-08-574-959A-7
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112 EDAPNAA --- SLAPTPVSPV 128
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                                                                                                                   TELEPHONE: (512) 320-7200
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 7:
      FILING DATE: 17/06/92
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                          LENGTH: 1400 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       608-251-9166
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                                                                                                                                                                                                                                                                            linear
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ZIP: 53701-2113
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                                                                                                                                                                                                                                                                        ; TOPOLOGY: Li
; MOLECULE TYPE:
PCT-US93-05857-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -08-217-327-4
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STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15 QAPTPAPSTIPGPRRGSGPEIFTFDPLPE------PAAAPAGRPSASRGHRKRS 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 3; Length 1400;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/05857
                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: US/08/465,713
FILING DATE: 06-JUN-1995
CLASSIFCCATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Board of Regents
APPLICANT: The University of Texas System
APPLICANT: The University of Texas System
TITLE OF INVENTION: GENE REARRANGEMENTS AND TITLE OF INVENTION: GENE REARRANGEMENTS AND TOWNERS OF SEQUENCES:
ADDRESSEE: Arrold, white & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             519 KOVSOPALVIPPOPPTTGPPRKEVPKTTPSEPKK-
                                                                                                                                                                                                                                                                        NAME: Parker, David L.
REGISTRATION UNDRER: 32,165
REFERENCE/DOCKET NUMBER: ARCD:072/PAR
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.2%; Score 92; 22.1%; Pred. No. (
                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/080,255
FILING DATE: 17 JUNE 1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPEKATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7, Application PC/rUS9305857 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic) US-08-465-713-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     112 EDAPNAA---SLAPTPVSPV 128
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TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1400 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               single
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
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MTORNEY/ACREE INCOME.

MTORNEY/ACREE INCOME.

MESSIGNATION NUMBER: 2.165

REEDERSENCE/DOCKT NUMBER: 2.165

REEDERSENCE/DOCKT NUMBER: 2.165

REEDERSENCE/DOCKT NUMBER: 2.165

TELECOMMUNICATION NUMBER: 2.165

TELECOMMUNICATION NUMBER: 2.165

TELECOMMUNICATION NUMBER: 2.165

TELECOMMUNICATION NUMBER: 2.165

TOWNLOAD: 1.100 min on acids
TYPE: Min on acids
TY
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receptor linked to admylyl cyclase activation and expression of the receptor protein in plasmid-transfect
                                                                                                                    1 :1: 1 :1: 372 PDFRKAFQGLLCCARRAARRRHATHGDRPRASGCLARPGP-PP--SPGAASDDDDUVVG 428
                                                        312 KALKTLGIIMGVFTLCWLPFFLANVVKAFHRELVPDRLFVFFNWLGYANSAFNPIIYCRS 371
                                                                                                ---PAPLPPEDAPNAAS-----1,A 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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620 Newport Center Drive, Sixteenth Floor
                      MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
SOGTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              CDNA encoding the rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Altman, Daniel E. REGISTRATION VUNBER: 34,115
REFERENCE/DOCKET NUMBER: N1H065.001FW]
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/444,734A FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/029,917
FILING DATE: 03-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/548,714
FILING DATE: 06-JUL-1990
                                                                                                                                                                                                122 PTPVSPVLEPF----NLTSEPSDYALD 144
                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/08444734A
Patent No. 5610282
                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Sibley, David R. APPLICANT: Monsma, Frederick J. APPLICANT: Mahan, Lawrence C. APPLICANT: McVittie, Loris D.
                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: CDNA encodi
TITLE OF INVENTION: exceptor 11
TITLE OF INVENTION: expression
TITLE OF INVENTION: cell lines
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24.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 477 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 10.7%
Best Local Similarity 24.2%
Matches 50; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                Patent No. 5610282
GENERAL INFORMATION:
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US-08-444-734A-4
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                                                                                                                                                                                                                                                                                        US-08-444-734A-4
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                                                                                                                                                                                                                                                                                63 RRVLYPRVVRRQLPVEEPNPAKRLLFLLTIVFCQILMAEEGVPAPLPPEDAPNAASLAP 122
                                                                                                                                                                                                                                                                                                                            -----TPPPATPPPAPLASPPAT 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                264 PSPSPSPVPAPAPPPPGP------PRPAAAATAPLANGRAGKRRPSRLV----ALRED 313
                                                                                                                                                                                                                                      94; Gaps
                                                                                                                                                                                                            9 PTMTILQAPTPAPSTIPGPRRGSGPEIFTFDP-----L.PEPAAAPAGRPSASRCHRKRS 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17 PTPAPSTIPGPRRGSGPEIFTFDPLPEPAAAPAGRPSAS--RGHRKRSRRVLYPRVVRRQ 74
                                                                                                                                                                          33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Sealfon, Stuart C.
TITLE OF INVENTION: Cloning and Expression of
TITLE OF INVENTION: Gonadotropin-Releasing Hormone Receptor
                                                                                                                                    Length 214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 468,
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FILLING DATE: US/08/390,000A
FILLING DATE: 17-FEB-1995
                                                                                                                                Score 90.5; DB 1; I
Pred. No. 0.066;
8; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10.7%; Score 88; 24.2%; Pred. No. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Pennie & Edmonds LLP
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7, Application US/08390000A Patent No. 5985583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: FLORDY disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MC-NOFTWARE: PATOLING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 69,
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 212 869-8864/9741
TELEF. 6614 PENNIE
INFORMATION FOR SEQ ID NO. 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                            114 PPASPPPATP---PPATPPPA---
                                                                                                                                  11.0%; 27.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 17-FEB-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                  123 TP-VSPVLEPFNLTSEPS 139
                                                                                                                                                                                                                                                                                                                                                                                      468 amino acids
amino acid
: 214 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 10.7%
Rest Local Similarity 24.2%
Matches 50; Conservative
                                                                                                                                                      Best Local Similarity 27.5
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein US-08-390-000A-7
                            TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-217-327-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & 3
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 12
US-08-390-000A-7
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  LENGTH:
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----PAPLPPEDAPNAAS-----LA 121
                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: NUCLEIC ACID, ENCODING TRANSCRIPTION TITLE OF INVENTION: FACTOR P300 AND USES OF P300 NUMBER OF SEQUENCES: 13 CORRESPONDENCE ADDRESS: ADDRESS: ADDRESS: ADDRESSEE: Weingarten, Schurgin, Gagnebin & Hayes
                                                                                                                                                                                                                                                                                                                                                                                            Weingarten, Schurgin, Gagnebin & Hayes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Version #1.25
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; Pred. No. 2.5;
23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 APTPVSPVLEPF----NLTSEPSDYALDLST 147
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                                                                                                 122 PTPVSPVLEPF----NLTSEPSDYALD 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/227,536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY AGENT INFORMATION:
NAME: Williams Ph.D., Kathleen A.
REGISTRATION NUMBER: 34,380
RECERENCAPOCKET NUMBER: DFCI-308:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-2290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                               Ten Post Office Square
                                                                                                                                                                                                       Sequence 2, Application US/08227536
Patent No. 5658784
                                                                                                                                                                                                                                          ENERAL INFORMATION:
APPLICANT: Excher, Richard
APPLICANT: Exen, Mark
APPLICANT: Livingston, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity 22.4%;
Matches 34; Conservative 2:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: protein US-08-227-536-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
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APPLICANT: Emorine, Jean L.
APPLICANT: Strosberg, Donny A.
TITLE OF INVENTION: Nucleitale Sequences Encoding the Murine
TITLE OF INVENTION: Beta3-Adrenergic Receptor and Their Applications
                       | :|:
| DPFRKAFQGLLCCARRAARRHATHGDRPRASGCLARPGP-PP--SPGAASUDDDDDVVG 437
                                                                                                        321 KALKTLGIIMGVFTLCWLPFFLANVVKAFHRELVPDRLFVFFNWLGYANSAFNPIIYCRS 380
                                                                                                                                               ------LA 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 273 PSPSPSPVPAPAPPPGP----PRPAAAATAPLANGRAGKRRPSRLV----ALREQ 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                         ---1VFCQ- 97
17 PYPAPSTIPGPRESGPEIFTFDPLPEPAAAPAGRPSAS--RGHRKRSKRVLYPRVVRRQ 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17 PTPAPSTIPGPRRGSGPEIFTFDPLPEPAAAPAGRPSAS--RGHRKRSRRVLYPRVVRRQ 74
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                                                                         -- LPVEEPNPAKRL------LFLL1,"--
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STREET: Post Office Drawer 34009
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/087,772A
                                                                                                                                                                                                                                              438 ATPPARLLEPWAGCNGGAAADSDSSLD 464
                                                                                                                                                                                                                     122 PTPVSPVLEPF----NLTSEPSDYALD 144
                                                                                                                                                                                                                                                                                                                                                 Sequence 16, Application US/08087772A Patent No. 5691155 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Charlotte
No. 5691155th Carolina
XY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 26,419
REFFRENCE/ODCKET NUMBER: 333
TELECOMMUNICATION:
TELEPHONE: 919-8140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 24.2%;
Matches 50; Conservative 1
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NAME: Linker, Raymond O.
REGISTRATION NUMBER: 26,4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 919-881-3175
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: peptide US-08-087-772A-16
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                                                                                                                                               --ILMAEEGV-----
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
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US-08-087-772A-16
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831 SPSPVPSRTPTPHHTPPSIGAQOPPATTIPAPVPTPPAMPPGPQSQALHPPPRQTPTPPT 890
                                                                                                                                                                                          65 VLYPRVVRRQLP----VEEPNPAKRLLFLLLTIVFCQILMAEEGVPAPLPPEDAPNAASL 120
                                                                                                                                                                                                                           Gaps
                                                                                          16 APTPAPSTIPGPRR-----GSGPEIFTFD-PLPEPAAAPAGRPSASRGHRKRSR----R 64
                                           38;
DB 1; Length 2414;
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January 30, 2001, 18:47:31; Search Lime 54.97 Seconds (without alignments) 97.039 Million cell updates/sec
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823
1 MCHSRSCHPTMTILQAPTPA......EPSDYALDLSTFLQQUPAAF 156
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1: /cgn2_2/gcgdata/geneseq/geneseqp/AA1980.DAT:*
2: /cgn2_2/gcgdata/geneseq/geneseqp/AA1981.DAT:*
3: /cgn2_2/gcgdata/geneseq/geneseqp/AA1982.DAT:*
4: /cgn2_2/gcgdata/geneseq/geneseqp/AA1983.DAT:*
5: /cgn2_2/gcgdata/geneseq/geneseqp/AA1984.DAT:*
6: /cgn2_2/gcgdata/geneseq/geneseqp/AA1986.DAT:*
7: /cgn2_2/gcgdata/geneseq/geneseqp/AA1986.DAT:*
8: /cgn2_2/gcgdata/geneseq/geneseqp/AA1988.DAT:*
9: /cgn2_2/gcgdata/geneseq/geneseqp/AA1988.DAT:*
7: /cgn2_2/gcgdata/geneseq/geneseqp/AA1988.DAT:*
9: /cgn2_2/gcgdata/geneseq/geneseqp/AA1988.DAT:*
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/cgn2_2/gcgdata/geneseq/geneseqp/AA1991.DAT:*
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      268485 seqs, 34193795 residues
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

S		Description		Profesio encoded by	Human PohdAn	DID 00000 1 100000	naud snacococona inc	Streptococcus pneu	mond amproportionals	State Coccus pilet	pricebrococcus buen	Streptococcus pnen	TRACK CALLED STOM	Monage mental mena-	wonse neural Mena+	Mouse neural Mena+	Cardinate Colon	ייייי איליייייי	Amino acid sequenc
SUMMARIES		ID	0.00	14501/	M36006	W14574		W145/3	W14569	W1 A 5.6 V	7001	W14570	W37151	W37152	701101	W37153	Y68732		Y68731
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Identifying substances for ameliorating symptoms of fibroproliferative diseases or oncogenic related disorders $\dot{\cdot}$

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47	26		166	18	W14568	
25	92	ή.	167	18	W14575	Streptococcus pneu
56	92	ä	1400	15	R44514	ಌ
27	92	į.	1400	17	R92705	
28	92	Ξ.	3910	14	R38470	protein
29	92	Ξ.	3910	16	R66462	2 ۔
30	σ	Ξ.	1012	20	Y17406	Human atroobin-1 r
31	90.5	÷.	214	17	R86913	Cotton fiber-speci
32	06	o.	171	20	Y29034	T good!! imminooo
33	90	Ö.	171	20	Y29074	1000
34	90	10.9	254	20	729061	T gondii immunoge
35	6	Ċ.	999	19	W72911	tonog .
36	89.5	Ċ	999	20	Y21928	Amino acid concor
37	æ	0	788	21	Y54466	Amino acid sequenc
38	8	0	807	21	Y54467	Amini and compan
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7 .	. 0	٠,	/81	8	W14579	Streptococcus pneu
ν. 1 .	p q	٠.	188	18	W14580	
9 1	3. S		688	21	Y57898	Human transmembran
45	ω	<u>.</u>	711	19	W80602	Human transcriptio
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					ALIGNMENTS	
RESULT	,					
Y45017	•					
ID Y45	45017 star	standard; 1	Protein;	156	AA.	
××						
	4 10 11					

RESULT Y45017	LT 1
o x	Y45017 standard; Protein; 156 AA.
AC	Y45017;
. E. S	31-MAY-2000 (first entry)
DE	Protein encoded by fchd605 gene.
X X	fchd605 gene; human; cardlovascular disease; oncogenic disorder;
X X	diabetic retinopathy; fibroproliferative disorder; ameherosclerosis;
X	pancreatic cancer; andiogenesis; inflammation; fibrosis; tumour orows
3 ×	vascularisation; cytostatic; antidiabetic; opthalmological.
SO	Homo sapiens.
ZZ X	WO200006206-A1.
PD	10-FEB-2000.
XX	30-JUL-1999; 99WO-US17394.
P.K	30-JUL-1998; 98US-0126640.
A A	(MILL-) MILLENNIUM PHARM INC.
XX	Falb DA;
Z Z Z Z	WP1; 2000-205414/18. N-PSDB; 250711.
PT TT	Identifying substances for ameliorating symptoms of fibroproliferative diseases or oncodenic related disorders

r growth;

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Streptococcus pneumoniae surface protein PspC and truncated PspA .
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Swiatlo E, Tart
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                                                                                                                                                                                                                                                             99.1%;
ilarity 99.4%;
Conservative 0
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                             6; F19 5; 163pp;
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                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                            AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference 50
                                                                                                                                                                                                                          156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         McDaniel LS,
                                                                                                                                                                                                                                                             Query Match
Best Local Simi
Matches 155;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           meningitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-SEP-1995;
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                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
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                                        Cardiovascular diseases by novel human genes which are differentially expressed in different cardiovascular disease states. Compositions which can modify Tor-beta signaling pathway are identified by screening. These are used therapeutically to treat fibroproliferative and oncogenic disorders, especially ToF (Transforming growth factor)-beta related cancer, anglogenesis, including diabetic retinopathy, artheroscierosis, pancreatic cancer, anglogenesis, inflammation, fibrosis, tumour growth and growth and growth is up-regulated in monocytes treated with oxidised LDI. (low density lipoprotein) can be used to design cardiovascular disease (treatment strategies. Depending on whether the up-regulation has a pathogenic or protective effect treatment methods can be designed to increase or decrease the activity of the protein product of the gene.
                              palent discloses methods for the treatment and diagnosis of ilovascular diseases by novel human genes which are differentially
                                                                                                                                                                                                                                                                                                                                                      RSRRVLYPRVVRRQI.PVEEPNPAKRLLF1.L1.T1VFCQILMAEEGVPAPI.PPEDAPNAASI, 120
                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                      1 MCHSRSCHPTMT1LQAPTPAPST1PGPRRGSGPETFTFD9LPEPAAAPAGRPSASRGHRK 60
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fchd605 gene; differential expression; monocyte; human; foam cell; cardiovascular disease; atherosclerosis; ischeemia; reperfusion; hypertension; restenosis; arterial inflammation; therapy; diagnosis; drug screening; marker.
                                                                                                                                                                                                                                                            Length 156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New genes differentially expressed in cardiovascular disease for diagnosis, drug screening and treatment of cardiovascular
                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                          Score 823; DB 21;
Pred. No. 7.4e-69;
                                                                                                                                                                                                                                                                                                                                                                                                    121 APTPVSPVLEPFNLTSEPSDYALDLSTFLQQHPAAF 156
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 823; D Best Local Similarity 100.0%; Pred. No. 7.4 Matches 156; Conservative 0; Mismatches
        Example; Fig 5; 214pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W36006 standard; Protein; 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97US-0799910.
96US-0011787.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human Fchd605 gene product.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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N-PSDB; T94471.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9730065-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-FEB-1997;
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16-FEB-1996;
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                                                                                                                                                                                                                     Sequence
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W36006
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This protein is encoded by the novel human fichd605 gene (swift) that is up-regulated in monocytes treated with oxidised low density lipoproteins that simulate the conditions under which foam cells develop during atherogenesis. The protein has sequence similarity to the mouse gly96 gene and to EST T49532. Novel fichd531, fichd540, fichd540, fichd602 and fichd605 genes (see T94467-71) provide a fingerprint for the study of cardiovascular diseases, including atherosclerosis, ischaemia/reportusion, hypertension, restenosis and arterial inflammation. Methods are provided for the diagnosis, monitoring in clinical trials, screening for therapeutically effective compounds, and treatment of cardiovascular diseases based on discoveries regarding the expression patterns of these novel genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RSRRVI.YPRVVRRQI.PVEEPNPAKRI.LFLLI.T.IVFCQILMAEKGVPAPLPPEDAPNAASL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MCHSRSCHPTWTILQAPTPAPSTIPGPRGSGPEIFTFDPLPEPAAAPAGKPSASKGHRK 60
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disease, e.g. atherosclerosis, restenosis, hypertension, etc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pneumococcal surface protein; vaccine; otitis media; itis; bacteraemia; pneumonia.
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R, Yother J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 816; DB 18;
Pred. No. 3.3e-68;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 APTPVSPVLEPFNLTSEPSDYALDLSTFLQQHPAAF 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus pneumoniae PspA central region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus pneumoniae strain Db15.
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                                                                  English.
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This sequence shows the central portion, including the C-terminus of the alpha-helix region and some of the proline-rich region, of premococcal surface protein A (PspA) of Stroptococcus pneumoniae strain E6796. Comparison of the N-terminal and central regions (W14533-57 and W14562-91) of PspA polypeptides from different pneumococcal strains can be used to divide the strains into several families based on sequence homologies. PspA polypeptides, or ragaments of them, can be used in vaccines to protect animals against S. pneumoniae infection and hence for the prevention of diseases such as otitis media, meningitis, bacteraemia and pneumonia. The sequence of the 3' half of the PspA alpha-helical region and the immediate S' tip of the coding sequence are likely to be the critical sequences for predicting PspA cross-reactions and vaccine
                6; Fig 13; 296pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference 97
                                                                                                                                                                                                                                                                               129 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference
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                                                                                                                                                                                                                                               composition.
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                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                              diseases such as otitis media, meningitis, bacteraemia and pneumonia. The sequence of the 3' half of the PspA alpha helical region and the immediate 5' tip of the coding sequence are likely to be the critical sequences for predicting PspA cross-reactions and vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                  100 tpapapapapapapapapapapapapkpapapkpapapk-----papapkpapa 147
                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                     18 TPAPSTIPGPRRGSGPEIFTFDPLPEPAAAPAGRPSASRGHRKRSRRVLYPKVVRRQLPV 77
                                                                                                     pneumococcal surface protein A (PspA) of Streptococcus preumoniae strain Db15. Comparison of the N-terminal and central regions (W14533-57 and W14562-91) of PspA polypeptides from different pneumococcal strains can be used to divide the strains into several families based on sequence homologies. PspA polypeptides, or fragments of them, can be used in vaccines to protect animals against S. pneumoniae infection and hence for the prevention of
                                                                         This sequence shows the central portion, including the C-terminus
                                                                                         of the alpha-helix region and some of the proline-rich region, of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus pneumoniae surface protein PspC and truncated PspA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78 EEPNPAKRIJFLIJTIVFCQIIMAEEGVPAPLP-PEDAPNAASLAPTPVSPVLEP 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               148 pkpapapk-----papapapapapapapapap-apapapkpekpaekp 187
                                                                                                                                                                                                                                                                                                                                                                                         28;
used in vaccines for protecting animals against S.pneumoniae Infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            used in vaccines for protecting animals against S.pneumoniae
                                                                                                                                                                                                                                                                                                                                                        13.0%; Score 107; DB 18; Length 206; 29.6%; Pred. No. 0.01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pneumococcal surface protein; vaccine; otitis media;
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J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus pneumoniae PspA central region.
                                                                                                                                                                                                                                                                                                                                                                                       8; Mismatches
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Tart R, Yother
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus pneumoniae strain Ef6796.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   meningitis; bacteraemia; pneumonia.
                                            Example 6; Fig 13; 296pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W14573 standard; Protein; 129 AA.
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McDaniel 1,5, Swiatlo E, T
                                                                                                                                                                                                                                                                                                                                                                                       34; Conservative
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                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                          206 AA;
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                                                                                                                                                                                                                                                                             composition.
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                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                          Query Match
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96
                                            Gaps
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                                                                                                50;
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                                                                                                                                                                          Length 129;
                                                                                                                                                                                                                                                                                                                                                                                                                              pneumococcal surface protein; vaccine; otitis media;
                                        Indels
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J;
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   Score 104; DB 18;
Pred. No. 0.012;
8; Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "unidentified amino acid"
186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid"
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                                                                                                                                                                                                                                                                                                                                                                                            Streptochecus pneumoniae PspA central region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note= "unidentified amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tart R, Yother
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Crain MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus pneumoniae strain Bg8743.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                   meningitis; bacteraemia; pneumonia.
                                                                                                                                                                                                                                                                                W14569 standard; Protein; 190 AA.
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Query Match 12.6%;
Best Local Similarity 26.5%;
Matches 30; Conservative 8
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W09709994-A1
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W14570
\overset{\mathsf{A}}{\times} \overset{\mathsf{A}}{\times} \overset{\mathsf{A}}{\times} \overset{\mathsf{A}}{\circ} \overset{\mathsf
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                                                                                                                                                                                                                                                                                                                                                                                               This sequence shows the central portion, including the C-terminus of the alpha-helix region and some of the proline-rich region, of pneumococcal surface protein A (PspA) of Streptococcus pneumoniae strain B99163. Comparison of the N-terminal and central regions (W14533-57 and W14562-91) of PspA polypeptides from different pneumococcal strains can be used to divide the strains into several families based on sequence homologies. PspA polypeptides, or Iragments of them, can be used in vaccines to protect animals against S. pneumoniae infection and hence for the prevention of diseases such as otitis media, meningitis, bacteraemia and pneumonia. The sequence of the 3' half of the PspA alpha-helical region and the immediate S' tip of the coding sequence are likely to be the critical population.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16 APTPAPSTIPGPRRGSGPEIFTFDPLPEPAAAPAGRPSASKGHRKRSRRVLYPRVVRRQL, 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PVEEPNPAKRILFLLLTTVFCQILMAEEGVPAPLP-PEDAPNAASLAPTPVSPVLEP 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus pneumoniae surface protein PspC and truncated PspA used in vaccines for protecting animals against S pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus pneumoniae surface protein PspC and truncated PspA used in Vaccines for protecting animals against S.pncumoniae infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pneumococcal surface protein; vaccine; otitis media;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hollingshead
J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus pneumoniae PspA central region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Crain MJ,
R, Yother
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              meningitis; bacteraemia; pneumonia.
                                                                                                                                                                                                                                                                                                                 Example 6; Fig 13; 296pp; English,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W14562 standard; Protein; 180 AA.
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Swiatlo E, Tart
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Best Local Similarity 27.49
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    McDaniel LS, Swiatlo E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UABR-) UAB RES FOUND.
               WP1; 1997-202002/18
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                                                                                                                                                                                                                    infection
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This sequence shows the central portion, including the C-terminus of the alpha-helix region and some of the proline-rich region, of pneumococcal surface protein A (PspA) of Streptococcus pneumoniae strain 092134c. Comparison of the N-terminal and central regions (W14533-57 and W14562-91) of PspA polypeptides from different pneumococcal strains can be used to divide the strains into several families based on sequence homologies. PspA polypeptides, or fragments of them, can be used in vaccines to protect animals against S. pneumoniae infection and hence for the prevention of the sequence of the 3' half of the PspA alpha-helical region and the immediate 5' tip of the coding sequence are likely to be the critical and manners for predicting PspA cross-reactions and vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98 etpapapapapapek-----paekpapapapekpapapek-----paekpae 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15 QAPTPAPST1PGPRGSGPEIFTFDPLPEPAAPAGRPSASRGHRKRSRRVLYPRVVRRQ 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence shows the central portion, including the C-terminus of the alpha-helix region and some of the proline-rich region, of pneumococcal surface protein A (PspA) of Streptococcus pneumoniae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75 LPVEEPNPAKRLLFLLLTIVFCQ1LMAEEGVPAPLPPEDAPNAASLAPTPVSP 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12.3%; Score 101; DB 18; Length 180; 27.4%; Pred. No. 0.032; 1ive 8; Mismatches 34; Indels 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pneumococcal surface protein; vaccine; otitis media;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus pneumoniae strain Bg9739.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   meningitis; bacteraemia; pneumonia.
Example 6; Fig 13; 296pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W14570 standard; Protein; 183 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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Best Local Similarity 27.4
Matches 31; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UABR-) UAB RES FOUND.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180 AA;
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strain Bg9739. Comparison of the N-terminal and central regions (W14533-57 and W14562-91) of PspA polypeptides from different pneumococcal strains can be used to divide the strains into several lamilies based on sequence homologies. PspA polypeptides, or Iraquents of them, can be used in vaccines to protect animals against S. pneumoniae infection and hence for the prevention of diseases such as offits media, meningitis, bacteraemia and pneumonia. The sequence of the 3' half of the PspA alpha-helical region and the immediate 5' tip of the coding sequence are likely to be the critical sequences for predicting PspA cross-reactions and vaccine
                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                            18 TPAPSTIPGPRRGSGPETFTFDPLPEPAAAPAGRPSASRGHRKRSRRVLYPRVVRRQLPV 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neural Mena+ protein; mammalian Ena; Enabled protein; Evl protein; cytoskeleton; cell morphology; cell adhesion; cell differentiation; cell growth; cell motility; mouse.
                                                                                                                                                                                                                                                                                                                                                                             78 EEPNPAKRILFILILTIVFCQILMAEEGVPAPI,P---PEDAPNAASIAPTPVSPVLEP 131
                                                                                                                                                                                                                                                                                                                                                                                                           143 papkpa------papkpapapkpap-apapkpap-papkpekpaekp 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This protein comprises novel murine neural Mena+. Its amino acid sequence was deduced from a CDNA clone (see V02998) obtained from
                                                                                                                                                                                                                                                                                44;
                                                                                                                                                                                                                                              Score 101; DB 18; Length 183; Pred. No. 0.033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Detection of modulators of Mena and Ena-VASP-like genes and - used in control of cytoskeletal dynamic events in normal abnormal cell morphology, adhesion, motility, growth and
                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                              32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Soriano P, Wehland J;
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                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "encoded by GGN"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                                                                                                                                                                              12.38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse neural Mena+ protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Certler FB, Niebuhr K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WP1; 1998-101197/09.
                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                 183 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-JUL-1998
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                                                                                                                                                                  composition.
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                                                                                                                                                                                                   Sednence
                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W37151;
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                                                                                                                                                                                                                                                                                Matches.
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c a mouse brain cDNA library. Neural Menai contains an exon that introduces 244 amino acids between amino acids 238 and 239 of mammalian Ena (Mena, see W37148). Two other Lasoforms, neural Mena++ (see W37153), are also disclosed. Unlike Mena, neural Mena isoforms exhibit neural Mena++ (see W37153), are also disclosed. Unlike Mena, neural Mena isoforms exhibit neural tissue-specific distribution. Based on the disclosed Mena and EVI genes (see also V02996-97) and proteins (see also W37148-49), a variety of methods and compositions are provided for screening, isolating and characterising endogenous and exogenous factors, drugs and therapeutic agents useful to evaluate and/or control cytoskeletal dynamic events involved in normal and abnormal cell morphology, adhesion, mothlity, growth and/or differentiation. A method of detecting a modulator of Mena activity/expression is
                                                                                                                                                                                                                                                                                                                                                                                                                                                57 GHRKRSRRVLYPRVVRRQLPVEEPNPAKRLLFLLTIVFCQILMAEEGVPAPLPPEDAPN 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     452 cgsqaspppgtplastpsskpsvlpspsaga-----pasaetplnpelgdssase 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Detection of modulators of Mena and Ena-VASP-like genes and proteins - used in control of cytoskeletal dynamic events in normal and abnormal cell morphology, adhesion, motility, growth and
                                                                                                                                                                                                                                                                                                                                               Indels 46; Gaps
                                                                                                                                                                                                                                                                                                                                                                               2 CHSRSCHPTMT-ILQAPTPAPSTIPGPRRGSGPEIFTFDPLPEPAAAP----AGRPSASR 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Enabled protein; Ev1 protein; thesion; cell differentiation;
                                                                                                                                                                                                                                                                                                              Length 783;
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                                                                                                                                                                                                                                                                                                                                              51;
                                                                                                                                                                                                                                                                                                              DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Soriano P, Wehland J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cytoskeleton; cell morphology; cell adhesion; cell growth; cell motility; mouse.
                                                                                                                                                                                                                                                                                                                            0.21;
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                                                                                                                                                                                                                                                                                                                                              11; Mismatches
                                                                                                                                                                                                                                                                                                              Score 100;
Pred. No. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neural Mena++ protein; mammalian Ena;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 4; Page 60-63; 77pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117 ----AASLAPTPVSPVLEPFNLTSEP 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W37152 standard; Protein; 787
                                                                                                                                                                                                                                                                                                              12.2%;
26.0%;
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                                                                                                                                                                                                                                                                                                              Query Match 12.29
Best Local Similarity 26.09
Matches 38; Conservative
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                                                                                                                                                                                                                                                             783 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse neural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W09801755-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-JUL-1996;
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Nomo sapiens.
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                                                                                                                                                                                                                                                         Seguence
                                                                                                                                                                                                                         claimed.
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Y68732
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This protein comprises novel murine neural Mena++. Its amino acid sequence was deduced from a cDNA clone obtained from a mouse brain cDNA library. Two other isoforms, neural Mena+ (see W37151) and neural Mena+ (see W37151) and neural Mena+ (see W37151) and neural Mena+ (see W37148), are also disclosed. Unlike mammalian Ena (Mena, see W37148), neural Mena isoforms exhibit neural clissue-specific distribution. Based on the disclosed Mena and Evl. (see Specific distribution. Based on the disclosed Mena and Evl. (see Specific distribution. Based on the disclosed Mena and Evl. (see Specific distribution. Based on the disclosed Mena and Evl. (see Specific distributions are provided for screening, solating and characterising endogenous and exogenous factors, isolating and characterising endogenous and exogenous factors, cytoskeletal dynamic events involved in normal and abnormal cell morphology, adhesion, motility, growth and/or differentiation. A complete of detecting a modulator of Mena activity/expression is
                                                                                                                                                                                                                                                                                                                                                                                         456 cgsqaspppgtplastpsskpsvlpspsaga-----pasaetplnpelgdssase 505
                                                                                                                                                                                                                                                                                                                                                                                                                            57 CHRKRSRRVLYPRVVRRQLPVEEPNPAKKLLFLLLTIVFCQ1LMAEEGVPAPLPPEDAPN 116
                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                            2 CHSRSCHP"MT-ILQAPTPAPSTIPGPRRCSGPEIFTFUPLPRPAAAP----AGRPSASR 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neural Mena+++ protein; mammalian Ena; Enabled protein; Evl protein; cytoskeleton; cell morphology; cell adhesion; cell differentiation; cell growth; cell motility; mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Detection of modulators of Mena and Ena-VASP-like genes and proteins used in control of cytoskeletal dynamic events in normal and abnormal cell morphology, adhesion, motility, growth and
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                                                                                                                                                                                                                                                                                                                                 46;
                                                                                                                                                                                                                                                                                              12.2%; Score 100; DB 19; Length 787; 26.0%; Pred. No. 0.21; Live 11; Mismatches 51; Indels 4.
                                                                                                                                                                                                                                                                                                                              51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wehland J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GBFB ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH. (HUTC-) HUTCHINSON CANCER RES CENT FRED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          506 -----pylqaasqpaesptpqglvl---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 4; Page 63-65; 77pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117 ---- AASLAPTPVSPVLEPFNLTSEP 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         539 gpayasalppppppppppppppppp 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA.
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Matches 38; Conserv
                                                                                                                                                                                                                                                787 AA;
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This protein comprises novel murine neural Mena++. Its amino acid sequence was deduced from a CDNA clone obtained from a mouse brain CDNA library. Two other isoforms, neural Mena+ (see W37151) and neural Mena, see W37152), are also disclosed Unlike mammalian can (Mena, see W37148), neural Mena isoforms exhibit neural cissue-specific distribution. Based on the disclosed Mena and Evl genes (see also V02996-98) and proteins (see also W37148-49), a variety of methods and compositions are provided for screening, isolating and characterising endogenous and exogenous factors, isolating and characterising endogenous and exogenous factors, cutys and therapeutic agents useful to evaluate and/or control cytoskeletal dynamic events involved in normal and abnormal cell morphology, adhesion, motility, growth and/or differentiation. A method of detecting a modulator of Mena activity/expression is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identifying modulators of nuclear receptors, useful e.g. as anticancer and anti-inflammatory agents, according to their effect on binding between the receptor and high-mobility group protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         471 cgsqaspppgtplastpsskpsvlpspsaga-----pasaetplnpelgdssase 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57 GHRKRSRRVI.YPRVVRRQLPVEEPNPAKRLLFLLI.TIVFCQILMAEEGVPAPLPPEDAPN 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 CHSRSCHPTMT-ILQAPTPAPSTIPGPRRGSGPEIFTFUPLPEPAAAP----AGRPSASR 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Retinoic acid receptor; RAR; high mobility group protein; HMG protein; nuclear receptor; antiproliferative; anti-inflammatory; antipsoriasis; anticancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents a high mobility group (HMG)-Y/R HMG sequences that interact with retinoic acid receptors (RARs)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Amino acid sequence of high mobility group (HMG)·Y/R protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 100; DB 19; Length 802;
; Pred. No. 0.21;
11; Mismatches 51; Indels 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117 ----AASLAPTPVSPVLEPFNLTSEP 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     554 gpayasalppppppppppppppppppppppp 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Y68732 standard; Protein; 168 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   12.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 12.2%
Best Local Similarity 26.0%
Matches 38; Conservative
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                                                                                                                                                                                                                                                                                                                                                             802 AA;
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ligand dependent manner to induce gene expression can be identified using the method of the invention. The specification describes a method for identifying compounds that modulate a nuclear receptor. The method comprises incubating a polypeptide containing presence of second polypeptide containing the nuclear receptor-binding part of a INW protein, and detecting any alteration in binding between the two polypeptides. The method is useful for identifying potential antipoliferative, anti-inflammatory, antipsoriasis and anticancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identifying modulators of nuclear receptors, useful e.g. as anticancer and anti-inflammatory agents, according to their effect on binding between the receptor and high-mobility group protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein.
                                                                                                                                                                                                                                                                                                                                                                     76 -PVFEPNPAKRLLFLLLTIVFCQILMAEEGVPAPLPPEDAPNAASLAPTPVSPVLEPFNL 134
                                                                                                                                                                                                                                                                                                                                                                                                           ----aplpp----- 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents a high mobility group (HMG)-R protein HMG sequences that interact with retinoic acid receptors (RARs) in a ligand dependent manner to induce gene expression can be identified using the method of the invention. The specification describes a method for identifying compounds that modulate a nuclear receptor. The method comprises incubating a polypeptide containing a
                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                        ppkepsevptpkr...----prgrpkgsknwrrrkrrasrrsprrrss 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Retinoic acid receptor: RAR; high mobility group protein; HMG protein; nuclear receptor; antiproliferative; anti-inflammatory; antipsoriasis; anticancer.
                                                                                                                                                                                                                                                                                                       17 PTPAPSTIPGPRRGSGPEIFTFDPLPEPAAAPAGRPSASRGHRKRSRRVLYPRVVRRQL-
                                                                                                                                                                                                                                                                          41;
                                                                                                                                                                                                                                       Length 168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Amino acid sequence of high mobility group (HMG)-R protein.
                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                        52;
                                                                                                                                                                                                                                         DB 21;
                                                                                                                                                                                                                                       Score 98.5; DB
Pred. No. 0.05;
                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                       135 TSEPSDYALDI,STFLQQHPAA 155
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27.7%;
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                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                     168 AA;
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liquad-binding region of nuclear receptor with test compound in presence of second polypeptide containing the nuclear receptor-binding part of a HMG protein, and detecting any alteration in binding between the two polypeptides. The method is useful for identifying potential antiproliferative, anti-inflammatory, antipsoriasis and anticancer
                                                                                                                                                                                                                                                                                                                                         81 rrrssdpcvppaphwrssfllgldsf....-aplpp...-ppplpgah 119
                                                                                                                                                                                                                                                                                                           RRQL--PVEEPNPAKRLLFLLLTIVFCQILMAEEGVPAPLPPEDAPNAASLAPTPVSPVL 129
                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                              12 TILQAPTPAPSTIPGPRRGSGPETFTFDPLPEPAAAPAGRPSASKGHRKRSKKVLYPRVV 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This protein is encoded by gene 036 (see T91708), which was identified by differential display analysis as being expressed at a higher level in normal colon tissues than in cancerous colon tissues. Gene 036 is a candidate tumour suppressor gene. A correlation was found between an increase in the expression level of gene 036 and a decrease in a colon cell's tumour potential. Hence, methods that increase the level of expression of gene 036 may inhibit or slow the progression to tumours and cancer. e.g. colon cancer. The 036 protein is used in claimed methods for treating a patient suffering from a disorder associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene 036 product differentially expressed in colon tumour cells.
                                                                                                                                                                                                             41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene 036 with reduced or amplified expression in tumour cells used, optionally with genes 097, 030 and 056 or their protein products, for diagnosis and treatment of colonic cancer
                                                                                                                                                                          DB 21; Length 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                colon cancer; differential expression; gene
                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human; diagnosis; gene therapy; tumour suppressor
                                                                                                                                                                                        Pred. No. 0.083;
; Mismatches 56;
                                                                                                                                                                      11.7%; Score 96.5; 27.4%; Pred. No. 0.0
                                                                                                                                                                                                                                                                                                                                                                                                          120 hhhrlwppppsstcaltttlhstpaa 145
                                                                                                                                                                                                                                                                                                                                                                          130 EPFNLTSEPSDYALDLSTFLQQHPAA 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W25790 standard; Protein; 739 AA
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                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MILL-) MILLENNIUM PHARM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1997-470615/43.
                                                                                                                                                                      Query Match
Best Local Similarity
Matches 40; Conserv
                                                                                                                       179 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Colon tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W09733551-A2
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                                                                                                                       Sequence
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or inhibit the formation of Ras-Sos complex are useful in the treatment of cancer. The present sequence represents a Drosophila

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13;

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The specification describes a crystal complex comprising at least a Son of sevenless Sos contacting region of a Ras protein and at least a Son of sevenless (Sos) protein catalytic region fragment, that effectively diffracts rays. Ras and Sos form a tight complex. Sos does not impede the binding sites for the nucleotide base and the ribose of GTP or GDP and thus the Ras-Sos complex maintains a structure that permits and thus the Ras-Sos complex maintains a structure that permits of uncleotide release and rebinding. The crystals are used for the of more than 5.0 Angstrom. The crystals are used for the crimination of the atomic coordinates of the complex to a resolution of three-dimensional coordinates obtained from the crystals, is useful for identifying an agent that stabilizes the Ras-Sos complex. The crystals are also useful for identifying agents that inhibit the crystals are also useful for identifying agents that inhibit the growing a crystal of a protein-ligand complex. Agents that stabilize
                                                                                                                                                                            7;
                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel crystals comprising a Ras-Son of sevenless complex, useful for screening drugs useful in cancer treatment
                                                                                                                                                                                                                                                                                   93
                                                                                                                                                                                                               16 APTPAPSTIPGP----RRGSGPEIFTFDPLPEPAAAPAGRPS-----ASRGHR---- 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Amino acid sequence of a Drosophila Son of sevenless (Sos) protein.
                                                                                                                                                                                                                                                                                   60 -KRS-----RRVLYPRVVRRQLPVEEPNPAKRLLFLLL-------
insufficient expression of gene 036 protein, and for identifying compounds that modulate 036 protein activity. Such compounds are useful in the diagnosis, prevention and treatment of tumours and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cole P, Kuriyan J;
                                                                                                                                                                                                                                                                                                                                                          92 -----TIVECQIIMAEEGVPAPLPPEDAPNAASIAP-TPVSPVLEPFNLTSEP 138
                                                                                                                                                                                                                                                                                                                                                                              53;
                                                                                                                                       11.6%; Score 95.5; DB 18; Length 739; 27.0%; Pred. No. 0.5; ive 14; Mismatches 60; Indels 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Son of sevenless: Sos; crystal; Ras-Sos complex; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bar-Sagi D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 169-175; 224pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Y68821 standard; protein; 1596 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Boriack-Sjodin A, Margarit SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-US16348.
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                                                                                                                                                             1 Similarity 27.09
47; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein coordinate data.
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                                                                                          739 AA;
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1465 plpisp----aassstttspltpamspmspnipshpvestsssyahglrmryggygth 1519
                                                                                                                                                                                         Transcription factor; probe; reverse transcription; PCR; primer; expression vector; E.coli; COS cell; ras; cancer cell multiplication; polyoma virus; transformation.
                                                                                                                                                                         62 SRRV-----LYPR----VVRRQLPVE-----EPNPAKRLLFLLL1/11VFCQ11,MAEEGV 105
                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ETS transcription factor activated by ras - may be used in the study of cancer cell proliferation and the proliferation of the polyoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The amino acid sequence of the novel ETS transcription factor family
                                                                                                                            4 SRSCHPTMTILQAPTPAPSTIPGPRG--SGPEIFTFDPLPEPAAAPAGRPSASRGHKKR 61
                                                                                                                                                                                                                        106 PAPLPPEDAPNAASLAPT--PVSPVLEPF--NLTSEP----SDYALDLSTFLQQ----H
                                                                                                     45;
                                                                             Length 1596;
                                                                                                                                                                                                                                                                                                                                                                                                                               Protein sequence of PEA3-beta -an ETS transcription factor.
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                                                                                                    68;
                                                                               DB 21;
                                                                              11.6%; Score 95.5; D
28.3%; Pred. No. 1.2;
ive 19; Mismatches
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Misc-difference 500
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                                                                                                                                                                                                                                                                                                                                                            AA.
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                                                                                            Best Local Similarity 28.3%
Matches 52; Conservative
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                                              1596 AA;
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Misc-difference 84
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member - PEA3-beta. The gene was isolated from a HepG2 cell line cDNA library. The probe for the screening was prepared by reverse transcription on HepG2 mRNA followed by PCR using primers 03170-1, to produce a probe of 170-200 bp. The screening isolated the full length sequence of the transcription factor. The gene was inserted into the expression vectors pBluescript KS and pcDV1 for expression of the protein in E.coli and COS7 cells, respectively. The FTS transcription factor has specificity for and is activated by ras. It is useful as a reagent in studies for the elucidation of the mechanism of cancer cell multiplication or polyoma virus transformation of cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     162 hapaagpvqqv--gpapaphslpep----gpqqqtf-avprpphqplqmp-----kmm 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 RRVLYPRVVRRQLPVEEPNPAKRLLFILLTIVFCQILMAEEGVP------ 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 HSRSCHPTMTILQAPTPAPSTIPGPRRGSGPEIFTFDPLPEPAAAPAGRPSASRGHRKRS 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 94.5; DB 16; Length 520; Pred. No. 0.42; 13; Mismatches 62; Indels 57;
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Bust Local Similarity 22.4%
Matches 38; Conservative 1.
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BE275966 601120727
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AA41066 2130909.r
AW960290 ES7372361
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AB0073 yv90g11.r1
BE878459 601487866
AA144404 zc66e09.r
AW465331 BP230018B
BE751344 203178 MA
BE751016 201294 MA
BE750116 201294 MA
BE75116 AV683186
AV683186 AV683186
BF043065 BP250026B
AV693060 AV693060
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BE735733 601304556
W39753 2c80b07.r1
BE939840 RC6-UT001
AV54384 AV594384
W47587 2c35b02.r1
BF025858 601670012
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AN356940 EST65572
AM356940 EST65572
AM367127 MRC-HF015
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Similar to SW:EXI_HUMAN P46695 RADIATION-INDUCIBLE IMMEDIATE-EARLY
GENE IEX-1 ;, mRNA sequence.
AI824906
EST
                                                      AI824906 wb03e06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A1876358 uk74a05
AA833402 ub58b04
                                   Description
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SUMMARIES
                                                                                                                                                            147 W52268
11 AA743819
142 H80073
137 BFR7
                                                    A1824906
B1384949
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ANATOGG6
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3 AW465331

35 BE751344

35 BE750116

39 BF040186

39 BF045952

7 AV617905
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AA833402
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VERSION
KEYWORDS
                    Result
                                8
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Inda E361543"
/clone="inda E361543"
/clone="ib="NIH_MGC_20"
/tissue_type="melanotic melanoma"
/lab_host="bH10B (phage resistant)"
/note="Organ: skin; Vector: pOTB7; Site_1: xho1; Site_2: EcoR1; cDNA made by oligo-dr priming. Directionally cloned into EcoR1/Xho1 sites using the following 5' adaptor: GGCACGAG(G). Size_reslected 5500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                         National Institute (MGC)

National Institute (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert_Strausbergenih.gov
Tissue Procurement: ArcC/OCTD/OTP

CDNA Library Arrayed by: The J.M.A.G.E. Consortium (LLNL.)

UNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL. at: image:llnl.gov

Plate: LLCM284 row: p column: 24

High quality sequence stop: 540.
                                                                                                                                                                    Euteleostomi;
           601276496F1 NIH_MGC_20 Homo sapiens cDNA clone 1MAGE:3617543 5',
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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NIH-MGC http://www.ncbi.nlm.nlh.gov/MGC/
                                                     BE384949
BE384949.1 GI:9330314
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                                      mRNA sequence.
                                                                                                                                             Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                         Sequencing Center
information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ô
                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
Tel: (30) 496-1550
mail: Robert_Strausbergfaith.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 411)
                                                                                                       NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 others
                                                                                                                                                                                                                                                                                                                                            CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consorttum/LLNL at:
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/lab_host="DH108"
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                                                                                                                                                                                                                                                                                                                                                                                                                                  www-bio.llnf.gov/bbrp/image/image.html
Insert Length: 557 Std Error: 0.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="NCI_CGAP_GC6"
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Location/Qualifiers
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                                                                                                                                                    Tumor Gene Index
Unpublished (1997)
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Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Tel: (301) 496-1550

Tel: (301) 496-1550

Tissue Procurement: ATCC/CTUD/OTP

CDNA Library Arrayed by: The L.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov

Plate: LLCM276 row: g column: 24

High quality sequence stop: 747.

Location/Qualifiers

I. 951

Location/Qualifiers

I. 951

Alborne="MAGC-20"

/clone="Ib="MIHAGC-20"

/clo
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NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                         BE383865.1 CI:9329230
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Matches 258; Conservative
mRNA sequence.
BE383865
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/uz.ret_range:2007534"
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/lab_host="DH10B (phage-resistant)"
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(Stratagene) and Superscript II RT (Life Technologies)."
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                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert_Strausberg@hlh.gov
Tissue Procurement: ATC/DCTD/DTP

Tissue Procurement: ATC/DCTD/DTP

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM72 row: e column: 07

High quality sequence start: 7

High quality sequence stop: 699.
                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 761s)
NIH-WGC http://www.ncbi.nlm.nih.gov/MGC/.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"/db_xref="taxon:9606"
DE275966
BE275966.1 GI:9150928
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Best Local Similarity 99.67
Matches 257; Conservative
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Eukaryota; Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 916)

S NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.

S NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.

I Unpublished (1999)

L Contact: Robert Strausberg Anh. D.

Tel: (301) 496-1550

Email: Robert_Strausberg Anh. G.E. Consortium (LLNL)

Thissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov f column: 08

High quality sequence stop; 659.

Location/Qualifiers

I. column: Incertion/Qualifiers

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/db_xref="taxon:9606"
/db_xref="taxon:9606"
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/lab_host="DH10B (phage_resistant)"
/note="Organ: uterus, vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sali; Cloned unidirectionally. Primer: Oligo dT:
Average insert size 2.1 kb.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
Memaalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 603)
NIH-MGC http://www.ncbi.nlm.nlh.gov/MGC/.
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Matches 250; Conservative
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Homo sapiens
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/clone_lib="NIH_MGC_70"
/clone_lib="NIH_MGC_70"
/lab_host="phi0B (phage-resistant)"
/note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dr. ste_2: Sal1; cloned unidirectionally. Primer: Oligo dr. archaologies.
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                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Verlebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 762)
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                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CLone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.h column: 09
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                                                                                                                                                             NIH-MGC http://www.ncbl.nlm.nih.gov/MGC/.
National Institutes of Health, Mammalian Gene Collection (MCC)
Unpublished (1999)
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99.6%; Pred. No. 8.9e-55;
.ive 0; Mismatches 1; Indels
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/db_xref="taxon:9606"
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                                                                                    Homo sapiens
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9 Gaps

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JOURNAL
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/clone_inacasisted
/clone_inb="NrH_MGC_14"
/clone_ib="NrH_MGC_14"
/tissue_type="renal cell adenocarcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: kidney; Vector: poTB7; Site_1: xhol; Site_2:
Coorgan: kidney; Vector: poTB7; Site_1: xhol; Site_2:
Cloned into EcoRI/Xhol sites using the following 5'
adaptor: GGCACCAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vertebrata; Euteleostomi;
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Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
                                    Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert Strausbergenih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The L.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM18 forw: j column: 24
High quality: Sequence stop: 579.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA410666 463 bp mRNA EST 18-MAY-1997 2t30g09.rl Soares ovary tumor NbHOT Homo sapiens CDNA clone IMAGE:723904 5' similar to SW:GL96_MOUSE P46694 IMMEDIATE EARLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117 GTCCGGCCCAGCTGCCAGTCGAGGAACCGAACCAGCCAAAAGGCTTCTCTTTCTGCTG 236
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  Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95.1%; Score 245.4; DB 106;
llarity 99.2%; Pred. No. 1.7e-52;
Conservative 0; Mismatches 1;
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Mammalia; Eutheria; Primates;
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  National Institutes of Unpublished (1999)
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ses 257; Conserv
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AW960290 S85 bp mRNA EST 01-JUN-2000
EST372361 MAGE resequences, MAGF Homo sapiens CDNA, mRNA sequence.
AW960290
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                               CCAGAGGACGCCCCTAACGCCGCATCCCTGGCGCCCACCCCTGTGTCCCCCGTCTCGAG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                             61 CICACCATCGICTTCTGCCAGATCCTGATGGCTGAAGAGGGTGTGCCGGCGCCCCTGCCT 120
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                                                                                                                                                                                                                                                                                                                                                                                          Length 463;
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                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="fob8:593521"
/db_xref="taxon:9606"
/clone="IMAGE:723904"
/clone="IMAGE:723904"
/clone=lib="Soares ovary tumor NbHOT"
                                                                                                                                                                                                                                                                                                                                                                                         Score 244.6; DB 7;
Pred. No. 2.6e-52;
0; Mismatches 4;
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0
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                                                                                                                                                                                                                                                                                                                                                                                          94.88;
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453 CAACACCCGGC 463
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                                                 Gay, C., Holt
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NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
National institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                         colon tumor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausbergenih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 585) Hegde, P., Ol,R., Abernathy,K., Dharap,S., Gaspard,R., Gay,,I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and Quackenbush,J.
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                                                                                                     in a model of
                                                                                             Assessment of gene expression patterns in a model metastasis using a 19,200 element cDNA microarray Unpublished (2000)

The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Fax: 301 838 3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                      // Organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="MAGE resequences, MAGF"
/note="vector: pBluescriptsKm"
190 c 148 g 113 t
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Pred. No. 1.2e-51;
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96.1%;
                                                                                                                                                                                                                                                  Email: johnq@tigr.org
Plate: 144
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BE563592
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Best Local Similarity
Matches 248; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                      134
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                                                 AUTHORS
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/dboar interpression in the control in the contro
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1 (bases I to 447)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.

The WashU-Marck EST Project
Unpublished (1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       446
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                                      information can
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Pred. No. 2.6e-50;
Mismatches 2; Indels
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution info-
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM382 row: k column: 02
High quality sequence stop: 692.

1. 910
1. 810
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447 GCAACACCGGAC 458
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Best Local Similarity
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/Organism="Homo sapiens"
/db_xref="GDB:1256850"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone_11B="Soares_senescent_fibroblasts_Nb;iss"
/tissue_type="senescent fibroblast"
/lab_host="belloB (ampicillin resistant)
/note="vector: p77730 (pharmacia) with a modified
polylinker V_TYPE: phagemid; Site_1: Not I; Site_2: Eco RI
ist strand cDNA was primed with a Not I - oligo(dT)
                                                                                                                                                                                                                                                                                                                                                     AA743819 513 bp mRNA EST 23-JAN-1998 ob01d04.s1 NC1_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1322407 3' similar to SW:IEX1_HUMAN P46695 RADIATION-INDUCIBLE IMMEDIATE-EARLY GENE IEX.1; mRNA sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 513)
NC1-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
                                                            This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length; 3171 Std Error: 0.00 Seq primer: mob. REGATT High quality sequence stop: 401.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    202 GTCCGCCCCGC-TGCCAGTCGAGGAACCGAACCCAGCCAAAAGGCTTCTCTTTTTGCGTG 260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     180 GCCC"TTAATCTGACTTCGGAGCCCTCGGACTACGCTCTGGACCTCAGCACTTTCCTCCA 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GTCCGGCGCCAGCTGCCAGTCGAGGAACCGAACCCAGCCAAAAGGCTTCTTCTTCTGCTG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5,
   Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 223; DB 147; Length 447; Pred..No. 7.9e-47; 0; Mismatches 0; Indels 2,
Park Parkway, Box 8501, St.
                                                   Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA743819.1 GI:2784635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86.4%;
99.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 86.4
Best Local Similarity 99.2
Matches 245; Conservative
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AA743819/C
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1 (bases 1 to 212)

Hillierri., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston The WashU-Werck EST Project
Unpublished (1995)
  Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97 GAGGGTGTGCCGGCGCCCCTGCCAGAGGACGCCCCTAACGCCGCATCCCTGGCGCCC 156
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yv80911.rl Soares melanocyte 2NbHM Homo sapiens-cUNA clone
IMAGE:249092 5' similar to SP:S33363 S33363 GLY96 PROFEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          157 ACCCCTGTGTCCCCCGTCCTCGAGCCCTTTAATCTGACTTCGGAGCCCTCGGACTACGCT
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                                                                                                                unknown library type
Inscrt Length: 834 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 384.
Location/Qualifiers
1. 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 217.2; DB 1:
Pred. No. 2.4e-45;
); Mismatches 3
                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:132407"
/clone_lib="NCI_CGAP_Kid3"
/lab_host="DH10B"
            Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Wilson RK
Washington University School of
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98.6%;
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Matches 219; Conserv
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H80073
  National
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/Lissue_type="melanocyte"
/lab.host="DH108 (ampicillin resistant)"
/lab.host="DH108 (ampicillin resistant)"
/note="Vector: pT713D (Pharmacia) with a modified
polylinker; Site_1: Not I: Site_2: Eco RI: 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5' Trace Argander Confector Confect
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NH-WGC http://www.ncbi.nlm.nih.gov/WGC/.
National Institutes of Health, Mammalian Gene Collection (WGC)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                                                                                                                                                                    This clone is available royalty-free through LLNI, ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    160 CCTGTGTCCCCCCGTCCTCGAGCCCTTTAATCTGACTTCGGAGCCCTCGGACTAAGGCTCTG 219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100 GGTGTGCCGCCCCCCCCGCCTCCAGAGGACGCCCCTAACGCCGCATCCCTGGCCCCCACC 1.59
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   St. Louis, MO 63108
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Pred. No. 2.2e-42;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
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/clone_lib="Soares melanocyte 2NbHM"
/sex="Male"
Forest Park Parkway, Box 8501,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               220 GACCTCAGCACTTTCCTCCAGCAACACCCGG 250
                                                                                                              Email: est@watson.wustl.edu
High quality sequence stops: 192
                                                                                                                                                                                                                                                                                               Seq primer: M13RPl
High quality sequence stop: 192
Location/Qualifiers
                                                                                                                                                                                    Source: IMAGE Consortium, LLNL
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Best Local Similarity 97.6%;
Matches 206; Conservative (
                                   Tel: 314 286 1800
Fax: 314 286 1810
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/db_xref="taxon:966"

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/tissue_
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1 (bases I to 504)

1 (bases I to 504)

Krizman, D., Rucaba, T., Lacy, M., I.e. N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Walfe, T., Waterston, R. and Wilson, R.

Conpublished (1997)

Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA143404 504 bp mRNA EST 08-NOV-1997
2066609.rl Stratagene pancreas (#937208) Homo sapiens cDNA cione
IMAGE:591880 5' similar to SW:GL96_MOUSE P46694 IMMEDIATE EARLY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59 TGC-TCACCATCGTCTTCTGCCAGATCCTGATGGCTGAAGAGGGTGTGCCGGCGCCCCTG 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          118 CCTCCAGAGGAC-GCCCCTAACGCCGCATCCCTGGC-GCCCACCCCTGTGTCCCCCGTCC 175
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Email: Robert_Strausberg@nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LENL)
DNA Sequencing by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Colone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov c column: 17
Plate: LLCMG60 row: c column: 17
High quality sequence stop: 645.
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Pred. No. 1e-41;
0: Mismatches 0;
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98.1%; Pred. No. 15
0; Mismatches
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AA143404 GI:1712791
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Tal: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1695 Std Error: 0.00
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 392.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 GCTCACCATCGTCTTCTGCCAGATCCTGATGCCTGAAGAGGGTGTGCCGGCGCCCCTGCC 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 rccagaggacgcccraacgccgcarccragcccccacccrrgrgrcccccgrccrcda 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCCCTTTAATCTGACTTCGGAGCCCTCGG----ACTACGCTCTGGACCTCAGCACTTTCC 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GTCCGGCGCCAGCTGCCAGTCGAGGAACCGAACCC.AGCCAAAAGGCTTCTTCTGCCT 59
                                                                                                                                                                                                                                                                                                                                                                                                         Score 197.8; DB 2; Length 504;
Pred. No. 2e-40;
0; Mismatches 19; Indels 5;
                                                                                                                                                              /organism="Homo sapiens"
/db_xref="CDB:4623266"
/db_xref="Laxon:9606"
/db_xref="Laxon:9606"
/clone="InhaE:591880"
/lab_host="SOLR cells (Ranamycin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                          76.78;
90.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCCAGCAACACCCGGC 481
                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 76.7
Best Local Similarity 90.7
Matches 233; Conservative
                                                                                                                                                                                                                                                                                                                                                 80
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ORIGIN
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                                                                                                                                     FEATURES
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Search completed: January 30, 2001, 18:47:28 Job Lime: 28459 sec

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by RNA polymerase II, the RNA polymerase which transcribes messenger RNA. RNA polymerase II transcription proceeds in vitro upon addition of several nuclear fractions designated TFIIA, B, D, E, F, H, I and J to RNA polymerase II holoenzyme. Fraction TFIII has been shown to contains a TBP and other TAFs. Purification of IFIID and separation of its components reveals 7 proteins ranging in size from 30-250 kD. Serum raised against the TFIID fraction allowed cloning of the correspector lambda-gtll expression libraries.
                                                                                                                                                                                                                                                                                                                               154 CCCACCCCTGTGTCCCCCGTCCTCGAGCCCTTTAATCTGACTTCGGAGCCCTCGGACTAC 213
                                                                                                                                                                                                                                                                   GAAGAGGGTGTGCCGGCGCCCCTGCCTCCAGAGGACGCCCCTAACGCCGCATCCCTGGCG 153
                                                                                                                                                                                                                                                                                                                                                                                                        747 AGATCTCGCCGGCGCGGTGCTCTCGCTCTTAACCTCCTGACCACGCCCCCCAGAT 688
                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                  34 CCAGCCAAAAGGCTTCTTTTTGTGCTCACCATCGTCTTCTGCCAGATCCTGATGGCT 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids encoding human TATA-binding protein associated factor
                                                                                                                                                                                         DB 17; Length 1120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TATA-binding protein associated factor; TAF; nuclear protein; RNA polymerase transcription; TATA-binding protein; TBP; initiation; ds.
                                                                                                                                                                                                                         Indels
                                                                                                                                          Sequence 1120 BP; 307 A; 291 C; 312 G; 210 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TATA-binding protein associated factor, dTAFII40 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tanese
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                                                                                                                                                                                      13.0%; Score 33.6; DE
51.0%; Pred. No. 2.2;
tive _ 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
80..916
/*tag= a
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Wang E, Weinzlerl ROJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          687 CCGCCGAGCTGCCCACCGTTTTC
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93US-0087119.
96US-0646715.
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T79601 standard; cDNA; 1120
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Best Local Similarity
Matches 104; Conserv
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Tjian R,
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(TAR) polypeptide, dTAFI140 (mol. weight 40kD). TAF peptides derived from dTAFI130 alpha, dTAFI130 beta, dTAFI140, dTAFI160, dTAFI130 beta, dTAFI140, dTAFI160, dTAFI180.

dTAFI1110, dTAFI1150, and dTAFI1250, their human equivalents and nucleic acids encoding them, are used to modulate transcription, initiation. TAFS are nuclear proteins involved in RNA polymerase I, II and III transcription. The peptides act by binding to a different TAF, an activator, or TBP (TATA-binding protein) or competitively inhibiting association of a TAF domain with another compound, typically a protein like TBP or another TAF, an activator,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAAGAGGGTGTGCCGGCGCCCCTGCCTCCAGAGGACGCCCCTAACGCCGCATCCCTGGCG 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        154 CCCACCCCTGTGTCCCCCGTCCTCGAGCCCTTTAATCTGACTTCGGAGCCCTCGGACTAC 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              747 AGATCTCCGCCGCCGGTGCTCTCGCTCTTAACCTCCTGACCACCGCCCCCCAGAT 688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34 CCAGCCANAAGGCTTCTCTTTTTGCTGCTCACCATCGTCTTCTGCCAGATCCTGATGGCT
  (TAF) peptide(s) - for production of recombinant peptide(s), used for modulating transcription of TAFs
                                                                                                                                                                                                                                                                                                                                                                                                                                Score 33.6; DB 18; Length 1120; Pred. No. 2.2;
                                                                                                  179601 encodes Drosophila TATA-binding protein associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                 Sequence 1120 BP; 307 A; 291 C; 312 G; 210 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66
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                                                            Example 1; Column 61-64; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   687 CCGCCGGAGCTGCCCACCGTTTTC 664
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Best Local Similarity 51.0
Matches 104; Conservative
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Surface molecule 4F2. Antisense DNA or RNA, antibodies, antibody fragments, and peptide and non-peptide antagonists to LAT1 are useful as anticancer agents. The present sequence encodes human LAT1, which is specifically claimed in the present invention.
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                                                                                                                                                                          8 GCCAGCTGCCAGTCGAGGAACCGAACCCAGCCAAAAGGCTTCTTTTTTCTGCTGCTCACCA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The TATA-binding protein associated factor dTAF1140 (including specific antibodies and fusion products) are used in drug screening, diagnostics and therapeutics. They are used in the development of specific biochemical assays for screening compounds that agonise or antagonise selected transcription factors involved in regulating gene expression associated with human pathology.
                                                                                                                                                                                                                                                                      672
                                                                                                                                                                                                                                    TCGTCTTCTGCCAGATCCTGATGGCTGAAGAGGGTGTGCCGGCGCCCCCTGCCAG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   screening;
                                                                                                                                                    ·;
                                                                                                                                                                                                                                                                  ccglgaaclgctacagcgtgaaggcngcnacncgggtccaggatgcctttgccgccg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TATA-binding protein associated protein factors - and corresponding nucleotide sequence and deriv. antibodies, useful in screening, diagnostics and therapeutics
                                                                                                                   13.1%; Score 33.8; DB 21; Length 4539; llarity 53.0%; Pred. No. 2.6; Conservative 2; Mismatches 53; Indels 0;
                                                                      Sequence 4539 BP; 765 A; 1450 C; 1297 G; 998 T; 29 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein associated factor; dTAFII40; ss; s therapeutic; gene transcription regulation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                TATA-binding protein-associated factor dTAFI140 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tanese
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 89-92; 180pp; English.
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80..913
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Weinzierl ROJ;
                                                                                                                                                                                                                                                                                                                                       070728 standard; cDNA; 1120 BP.
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93US-0087119.
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Wang E, We
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                                                                                                                                 Local Similarity
es 62; Conserv
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30-JUN-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diagnostic;
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Tjian R,
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Matches
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GAAGAGGGTGTGCCGGCGCCCTGCCTCCAGAGGACGCCCCTAACGCCGCATCCCTGGCG 153
                                                                                                                                         154 CCCACCCCTGTGTCCCCCCGTCCTCGAAACCTTGAACTTCGGAGCCCTCGGACTAC 213
                                                                                                                                                           This is the nucleotide sequence encoding the Drosophila TATA-binding protein (TBP) associated factor (TAF) designated TAFI160. The protein is a component of the TFIID fraction required for reconstituting RNA polymerase II in vitro transcription activity. The encoded protein has an estimated mol. wt. of 60 kD by SDS-PAGE.

The invention relates to purified proteins involved in transcription
                                                  93
                             Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Screen for cpds, that bind human TATA-binding process associated factor - by testing ability to bind to polypeptide fragments of the factor, useful as (ant)agonists of transcription factors involved in
                                                                                                                                                                                                                                                                                                                                                                         Drosophila; TATA-binding protein; TBP associated factor; TFIID; RNA polymerase II; transcription; messenger RNA; nuclear fraction; holoenzyme; lambda-gtll; expression library; ds.
                                             34 CCAGCCAAAAGGCTTCTCTTTTCTGCTCACCATCGTCTTCTGCCAGATCCTGATGGCT
                                                                                                          Drosophila TATA-binding protein associated factor dTAFII60 gene.
                          -
   Length 1120;
                         Indels
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 DB 15;
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80..916
/*tag* a /product Drosophila TAFII60
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Score 33.6; DI
Pred. No. 2.2;
                         0; Mismatches
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                                                                                                                                                                                                       214 GCTCTGGACCTCAGCACTTTCCTC 237
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Wang E, Weinzierl ROJ;
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 13.0%;
51.0%;
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93US-0013412.
93US-0087119.
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            Similarity
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Query Match
Best Local Simi
Matches 104;
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28-JAN-1993;
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1201 GICCAGGGCCACCATITGAACCAGGAGCCCTGGAGGICCAACTICACCCTIAGCACCAG 1142
                                                                            CCAGAGGACGCCCTAACGCCGCATCCCTGGCGCCCACCCCTGTGTCCCCCCGTTCTTCGAG 180
                                                                                                                                                                   181 CCCTTTAATCTGACTTCGGAGCCCTCGGACTACGCTCTGGACCTCAGCACTTTCCTCCAG 240
                                                                                                                                                                                     1 GTCCGCCGCCAGCTGCCAGTCGAGGAACCCAACCCAAAAGGCTTCTCTTTTCTGCTG 60
                                                           61 CTCACCATCGTCTTCTGCCAGATCCTGATGGCTGAAGAGGGTGTGCCGGCGCCCTGCCT
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                                                                                                                                                                                                                        241 CAACACC 247
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                                                                                                                                                                                                                                           961 TTTCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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02-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                               A08372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Key
5'UTR
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                                                                                                                                                                                        2539 AGGATGGTGCACCCTCTGTCCCTAGGGACCCCTTTGTGGCCAGATGCCTGACCCCCA 2480
                                                                                                                                                                         98 AGGGTGTGCCGGCCCCTGCCTCCAGAGGACGCCCCTAACGCCGCATCCCTGGCGCCCA 157
                                                                                                                                                     Gaps
attack, neurological disorders, e.g. neuroblastoma, glioblastoma or cancers, or to promote apoptosis in cells, or treat refractory epilepsy. They can also be used for screening test substances for 1B1 biological activity. IB1 producing cells can be used therapeutically to produce IB1 in a subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1 describes the determination of the presence of a mutation in the pro-alphal(III) gene. Primers used in PCR are given in 030834-48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kit for detecting genetic pre-disposition for vascular aneurysms - contains primer to amplify portions of Type III procollagen DNA and detects mulation in standard procollagen DNA
                                                                                                                                                     .
0
                                                                                                                          Length 2953;
                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3690 BP; 771 A; 1031 C; 1152 G; 736 T; 0 other;
                                                                            Sequence 2953 BP; 620 A; 906 C; 840 G; 587 T; 0 other;
                                                                                                                                                  32;
                                                                                                                          DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label - Type_III_procollagen
                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                         ss.
                                                                                                                      13.5%; Score 34.8;
62.8%; Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Mutation; pro-alphal(III); primer; PCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kuivaniemi SH, Prockop DJ, Tromp GC;
                                                                                                                                                                                                                                              2479 CCCCAGCCTGCCTTCCCCAGCCCC 2454
                                                                                                                                                                                                                              158 CCCCTGTGCCCCGGTCCTCGAGCCC 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
103..3690
                                                                                                                                                                                                                                                                                                                                                                                                         Type III procollagen (prior art).
                                                                                                                                                                                                                                                                                                          030849/c
ID Q30849 standard; cDNA; 3690 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UYJE-) UNIV JEFFERSON THOMAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92WO-US03866.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 1A-F; 44pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 46.2%;
Matches 114; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91US-0696607
                                                                                                                                                                                                                                                                                                                                                                              24-MAR-1993 (first entry)
                                                                                                                                   Best Local Similarity 62.8
Matches 54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1992-398878/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; R28916.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-MAY-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9219754-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-NOV-1992
                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                    030849;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Key
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The present invention describes a cell surface protein which is an L-type amino acid transporter-1 (LAT1), which mediates the transport of neutral amino acids, leucine, isoleucine, propylalamine, methionine, tyrosine, tryptophan, value and histidine, into the cell independently of sodium ions. The LAT1 protein conjugates with the cell membrane
                                                                             Human L-type amino acid transporter 1 nucleotide sequence SEQ ID NO:1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neutral amino acid transporter protein which conjugates with cell membrane protein 4F2 and operates independently of sodium ions is useful for screening potential cancer proliferation inhibitors -
                                                                                                      L-type amino acid transporter 1; LAT1; 4F2hc; 4F2 heavy chain; neutral amino acid transporter; tumour; cancer; proliferation; cell membrane surface 4F2 molecule; anticancer;.ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 9; Page 125-132; 189pp; Japanese.
                                                                                                                                                                          Location/Qualifiers
1..65
                                                                                                                                                                                                                                                                                                                                                                                                                         (NISC-) JAPAN SCI & TECHNOLOGY CORP.
                                                                                                                                                                                                                                                     "I.AT1"
A08372 standard; cDNA; 4539 BP.
                                                                                                                                                                                                         /*tag= a
66..1589
/*tag= b
/product= "1
1590..4474
/*tag= c
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                                                    12-JUL-2000 (first entry)
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Gaps

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Indels

Length 3690;

DB 13;

Score 34.2; DB 13; Pred. No. 1.9; 0; Mismatches 133;

166 TCCCCCGTCCTCGAGCCCTTTAATCTGACTTCGGAGCCCTCGGACTACGCTCTGGACCTC

683 CCCCCCNTCGCCNNCNCCCNCCCT 652 226 AGCACTTTCCTCCAGCAACACCCGGCCGCCTT

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A00010 to A02716 represent polynucleotides isolated from cDNA libraries constructed from human colon cancer cell lines. The present invention also describes a method of detecting differentially expressed genes correlated with a cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample derived from a cell suspected of being cancerous, where detection of the differentially expressed gene product is correlated with a cancerous state of the cell from which the test sample was derived. The polynucleotides sequences can be used in a method for detecting differentially expressed genes correlated with a cancerous state of a mammalian cell. The polynucleotides can also be used as probes for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     detecting and mapping related genes. They can be used in diagnosis and prognosis of diseases and disorders (e.g. identification of pre-metrastatic cancerous states, stages of cancer, or responsiveness of cancer to therapy). This is particularly for breast cancer, oestrogen receptor-positive breast cancer, oestrogen receptor-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polynucleotide library used to determine cancerous states of mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Labat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sudduth-Klinger J;
                                                                                                                                                                                                                                 Human colon cancer cell line polynucleotide sequence SEQ ID NO:2475.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J, Innis MA, Garcia PD, Sudduth-Klinger. Randazzo F, Kennedy GC, Pot D, Kassam A; Crkvenjakov R, Dickson M, Drmanac S, Lab. Garcia V, Jones LW, Stache-Crain B;
                                                                                                                                                                                                                                                                                               Human; colon cancer; tumour; diagnosis; gene expression product; probe; detection; cancerous state; metastasis; identification; breast cancer; oestrogen receptor-positive breast cancer; therapy; oestrogen receptor-negative breast cancer; lung cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          negative breast cancer, lung cancer, and colon cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1000 BP; 21 A; 53 C; 574 G; 22 T; 330 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 994; 1097pp; English.
                                  A02484 standard; cDNA; 1000 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-0085426.
98US-0085537.
98US-0085696.
98US-0105234.
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                                                                                                                                                                         (first entry)
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Reinhard C, Giese K, F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CHIR ) CHIRON CORP. (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-126369/11.
                                                                                                                                                                      19-MAY-2000
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15-MAY-1998;
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                                                                                                        A02484;
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A02484,
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This cDNA sequence includes an open reading frame encoding rat islet-brain 1 (IBI, see W80601), a transcriptional activator that is involved in the control of the GIUT2 and insulin genes by interacting with homologous cis-regulatory elements of the GLUT2 and insulin gene promoters. IBI cDNA was isolated from a rat of interacting with homologous cis-regulatory elements of the GLUT2 cand insulinoma INS-1 CDNA using GTI1 oligonucleotides conferentiated insulinoma INS-1 CDNA using GTI1 oligonucleotides capon of the GLUT2 promoter. IBI is abundantly expressed in the region of the GLUT2 promoter. IBI is abundantly expressed in the caporcatic islets in the brain. Human IBI polymotleotide (see W80602) and polypeptide (see W80602) are also claimed. IBI polymotleotide (see W80602) are also claimed. IBI colympaptides, nucleic acids, agonists and antagonists can be used in the treatment or diagnosis of diabetes, neuromal disabilities or cancers, to inhibit cells from undergoing apoptosis, to treat dementia, parkinsonism, Alzhelmer's disease, neuronal disabilities such as speech disorders and memory alteration, autoimmume diseases
                                                                                                                                                                              IBI; islet-brain 1; transcription factor; rat; diabetes; dementia; Parkinson's disease; Alzheimer's disease; epilepsy; neuroblastoma; glioblastoma; apoptosis; cancer; autoimmune disease; systemic lupus erythematosus; myocardial infarction; ischaemia; diagnosis; therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated transcription factor islet-brain 1 - used to develop products for treating e.g. diabetes, neurodegenerative disorders, cancers, autoimmune disease, heart disease or epilepsy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to develop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         affecting the CNS such as systemic lupus erythematosus, diabetes, heart diseases such as myocardial infarct and ischemia or brain
                                                                                                                                                Rat transcription factor islet-brain 1 (181) cDNA.
                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 13; Fig 1A; 111pp; English.
                                     ВР
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97GB-0006731.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98WO-GB00972
                                   V62462 standard; cDNA; 2953
                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (KIDD/) KIDDLE S J.
(NICO/) NICOD P.
(WAEB/) WAEBER G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bonny C, Waeber G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB; W80601.
                                                                                                                                                                                                                                                                                                                                                                                                                      WO9844106-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-APR-1997;
                                                                                                                 15-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-OCT-1998
                                                                                                                                                                                                                                                                                                         Rattus sp
                                                                           V62462;
RESULT 10
                     V62462/c
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6

Indels

84;

0; Mismatches

Conservative

Best Local Similarity Matches 68; Conserv

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Query Match

106 ccediccccrecriccadaddacecccraaceccerarccredceccccccred 165

14.0%; Score 36.2; DB 21; Length 1000; 44.7%; Pred. No. 0.42;

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Equilibrative nucleoside transport protein; iENTP; NBMPR; transport; nitrobenzylmercaptopurine riboside; antiviral, antitumour; screening; inhibitor; drug; knockout mice; cancer; chemotherapy; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New equilibrative nucleoside transport protein insensitive to nitrobenzylthio-purine riboside - useful for, e.g. identifying specific therapeutic nucleoside analogues and in gene therapy to protect transduced cells against ablative chemotherapy
                                                                                                                                                      Nucleotide sequence of intron 3 of 1ENTP gene.
                                                                                                                                                                                                                                                                                    adenosine deaminase; factor VIII; intron; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SJUD-) ST JUDE CHILDREN'S RES HOSPITAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 88; 114pp; English.
V69706 standard; DNA; 170 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98US-0058389.
97US-0838845.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98WO-US07283
                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Crawford CR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1998-594576/50.
                                                                                                                                                                                                                                                                                                                                                                                            WO9846749-A1.
                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-APR-1998;
                                                                                                       08-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-APR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                22-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Belt JA,
                                                      v69706;
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Sequences V69704 to V69715 represent introns of the gene encoding an equilibrative nucleoside transport protein (iENTP), which is insensitive to introbenzylmercaptopurine riboside (NBMFR). Cells transformed with a construct containing the iENTP nucleic acid can be used to produce the protein recombinantly. IENTP is used to identify specific ligands (protein recombinantly. IENTP is used to identify specific ligands constructly antiviral and antitumour nucleoside analogues that are preferentially provides all available transport activity are used. Contain provides all available transport activity are used, as to identify permeants of iENTP and (b) to screen specific inhibitors of identify permeants of iENTP and (b) to screen specific inhibitors of is identify permeants of iENTP and (b) to screen specific inhibitors of as probes, primers, antisense molecules, and ribozymes for therapy or diagnosis, and knockout mice in which both alleles encoding iENTP contain an inactivating defect are also useful for drug screening. Contain an inactivating defect are also useful for drug screening. Contain an inactivating defect are also useful for drug screening. Contain an inactivating defect are also useful for drug screening. Contain an inactivating defect are also useful for drug screening. Contain an inactivating defect are also useful for drug screening. Contain an inactivating defect are also useful for drug screening. Contain an inactivating defect are also useful for drug accenting that land and the inactivation of the inactivat
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Sequence 170 BP; 18 A; 77 C; 42 G; 33 T; 0 other;

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101 GTGTGCCGGCGCCCTGCCTCCAGAGGACGCCCTAACGCCGCATCCCTGGCGCCCACCC 160
                                                                  .;
o
Score 37.6; DB 19; Length 170;
Pred. No. 0.12;
0; Mismatches 29; Indels 0
                                                                                                  161 CTGTGTGCCGGTCCTCGAGCCCT 184
                                                                                                                 14.6%;
65.5%;
          Best Local Similarity 65.5
Matches 55; Conservative
Query Match
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242235/c

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This invention describes novel polypeptide fragment sequences (I) and their encoding nucleic acids (II) which are highly expressed in normal bladder tissue and have cytostatic activity. (II) are used for recombinant expression of (I) and to isolate complete genes. (I) are used to identify agents suitable for the treatment of bladder tumours, to directly treat this form of cancer (including expression from gene of therapy vectors), or are used in a preparation for cancer treatment. (I) is also used for the generation of specific antibodies. (II) are identified by assembling ESTS (expressed sequence tags) from a particular cusume type before comparison of expression patterns. This allows a caduces the number of fallures because of ESTS from different libraries representing different parts of the same unknown gene distorting the estimated frequency of occurrence in a particular tissue. 24112-242248 crepresent EST fragments derived from a human normal bladder tissue cDNA xx
                                                                                                                                                                                                                                                                                                                                                                                             <u>:</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180 TGTTGCTGGAGCTGCTGCTGCTGCTGCTGAACATGGTG-GCTCGCCTCCCCGGGGG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 TCACCATGGTCTTCTGCCAGATCCTGATGGGTGAAGAGGGTGTGCCGGCGCCCCTGCCTC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122 CAGAGGACGCCCCTAACGCCGCATCCCTGGCGCCCACCCCTGTGTCCCCCGGTCCTCGAGC 181
                                                                                                                                                                                                                                                                                                                                                                                         Dahl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         240 TGCTGCTGCAATTGCTGCTGCTGCTGCTGCTGCTGTAACTGCTGGAGCTGCTGCTGCTGC 181
                                                                                                                                treatment; EST; expressed sequence tag; cytostalic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 TCCGGCGCCCAGCTGCCAGGGAACCGAACCCAGCCAAAAGGCTTCTCTTTCTGCTGC 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polypeptides and their nucleic acids, useful for treatment of bladder tumour and identification of therapeutic agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ];
                                                                                                                                                                                                                                                                                                                                                                                        Pilarsky C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1526;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1526 BP; 365 A; 523 C; 437 G; 201 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 GGGCGGCTCCGGCGCCTCCCGGCTGCTACTCCG 16
                                                                                              Human normal bladder tissue cDNA derived EST 114.
                                                                                                                                                                                                                                                                                                                                                                                  Hinzmann B, Schmitt A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (META-) METAGEN GES GENOMFORSCHUNG MBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 3; Page 234; 366pp; German.
      Вр.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Р-РЅDВ; Y60556, Y60557, Y60558.
 Z42235 Standard; cDNA; 1526
                                                                                                                                                                                                                                                                                                                 98DE-1018620.
                                                                                                                                                                                                                                                                                  98DE-1018620
                                                                 (first entry)
                                                                                                                                                 therapy; ss.
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Matches 114; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-602416/52.
                                                                                                                                Human; bladder;
                                                                                                                                                                                                              DE19818620-Al
                                                                 31-JAN-2000
                                                                                                                                                   cancer; gene
                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                 Rosenthal A,
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                                                                                                                                                                                                                                                                                                         (INCY-) INCYTE PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   be used for gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                     136..165
                                                                                                                    /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                    Hillman JL, Yue H,
                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-256994/22.
P-PSDB; Y70474.
                                                                                                                                                                                                                                                 03-SEP-1999;
                                                                                                     misc_binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Simi
Matches 76;
                                                                                                                                                                                                                    16-MAR-2000
                            sig_peptide
                                                          mat_peptide
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V69706
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        anti-arteriosclerotis; hepatofropis; anti-leukaemis; anti-inflammatory; immunomodulatory; anti-asthmatis; anti-anaemis; anti-idabetis; diagnosis; anti-sclerotis; dermatological; neuroprotective; anti-epileptis; cancer; anti-ralandamer's; anti-Parkinsonian; cerobroprotectuve; ophthalmological; hypotensive; gene therapy; prevention; treatment; arteriosclerosis; cell proliferative disorder; autoimmunofunflammatory; diabetes mellitus; neurological; vision; reproductive; smooth muscle; ss.
                                                                                                                                                                                                                                                                                                                                                           alleles encoding lEMP contain an inactivating defect are also useful for drug screening. Cells that have been transduced with lEMP nucleic acid acry vivo are used particularly, for cancer chemotherapy. Vectors in which the lEMTP gene is linked to a heterologous gene (e.g. encoding adenosine deaminase and factor VIII) can be used for gene therapy.
                                                                                                                                                                                                 encodes an equilibrative nucleoside transport procein (IENTP), which is insensitive to nitrobertylmercaptopurine riboside (NBMPR), Cells transformed with a construct containing the IENTP nucleic acid can be used to produce the protein recombinantly. IENTP is used to identify specific ligands (particularly antiviral and antitumour nucleoside anialogues that are preferentially transported into cells) and to raise activity are used: (a) to identify permeants of IENTP and (b) to screen specific inhibitors of iENTP (potential drugs) Fragments of the iENTP nucleic acid are used, as probes, primers, antisense molecules, and ribosymes for therapy or dlagnosis, and knockout mice in which both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100 GGTGTGCCGGCGCCCCTGCCTCCAGAGGACGCCCCTAACGCCGCATCCCTGGCGCGCCCACC 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cyclic nucleotide-associated protein-2; CNAP-2; human; cytostatic;
                                                                                  New equilibrative nucleoside transport protein insensitive to nitrobearzylthio-purine riboside – useful for, e.g. identifying specific therapeutic nucleoside analogues and in gene therapy to protect transduced cells against ablative chemotherapy
                                                                                                                                                                                      This represents the 5' UTR (untranslated region) of the DNA that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 38.6; DB 19; Length 6354; Pred. No. 0.14; 0; Mismatches 29; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human cyclic nucleotide-associated protein-2 (CNAP-2) cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6354 BP; 1322 A; 1797 C; 1873 G; 1355 T; 7 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product "Human CNAP-2 protein"
(SJUD-) ST JUDE CHILDREN'S RES HOSPITAL.
                                                                                                                                                           Example 3; Pages 76-79; 114pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                            Patel DH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 65.9%;
Matches 56; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             251683 standard; cDNA; 4228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..4014
                            Belt JA, Crawford CR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           251683;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
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The present sequence is the cDNA encoding human cyclic nucleotide associated protein-2 (CNAP-2), identified in Incyte clone 3149674, that is isolated from ADRENONO4 CDNA library. It is expressed in nervous, reproductive, cardiovascular and haematopoietic/immune tissues. CNAP sequences may be used for prevention, treatment and diagnosis of diseases associated with altered CNAP expression such as, call proliferative disorders (e.g. arteriosclerosis, cirrhosis, leukaemia, lymphoma and cancer of the breast, prostate, lung and brain), autoimmune/ inflammatory disorders (e.g. asthma, anaemia, diabetes mellitus, multiple sclerosis and psoriasis), neurological disorders (e.g. epilepsy, alzheiner's/Parkinson's disease and strokes), vision disorders (e.g. conjunctivitis, glaucoma, cataracts and retinitis pigmentosa), creproductive disorders (e.g. infertility, uterine fibroids, ectopic pregnancies and impotence) and smooth muscle disorders (e.g. anaphylactic shock, Kearns-Sayre syndrome and hypertension). It can also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1185 ctccgacttcgacatggcctatgagcgtggccggatctccgtgtccctgcaggaaggc 1244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         135 TAACGCCGCATCCCTGGCCCCCACCCCTGTGTCCCCCGTCCTCGAGCCCTTTAATCTGAC 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for preventing,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75 CTGCCAGATCCTGATGGCTGAAGAGGTGTGCCGGCGCCCCTGCCTCCAGAGGACGCCCC 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated cyclic nucleotide associated proteins useful for preventing, diagnosing and treating cell proliferative, autoimmune/inflammatory, neurological, vision, reproductive and smooth muscle disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tang YT;
                                                                                                                                                                                                                                                                                                                                             /bound_molety- "Primer or Probe" /note- "Useful for amplification or hybridisation
/note= "Shares 24% identity to Aquifex pyrophilus esterase 28LC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patterson C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                      /*tag= c
/product= "Mature CNAP-2 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14.8%; Score 38.2; DB 21; 54.7%; Pred. No. 0.17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            195 TTCGGAGCCCTCGGACTAC 213
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Shaw D;

Kelly M,

Howells D,

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93WO-GB01467
                                                                                                                                                                                                                                                                                                         (MEDI-) MEDICAL RES COUNCIL,
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                                                                                                                                                                                                                                                                                                                                                          Hadfield KM,
                                                   Homo sapiens,
                                                                                                                                                                                                     13-JUL-1993;
                                                                                                                                                                                                                                                      13-JUL-1992;
                                                                                                 WO9401548-A.
                                                                                                                                                    20-JAN-1994.
                                                                                                                                                                                                                                                                                                                                                       Gross J, Ha
Sibson DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9846749-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-APR-1998;
11-APR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                 Human; secreted protein; expressed sequence tag; EST; haematopoiesis;
tissue growth; activin; inhibin; chemotaxis; chemokinesis; haemostatic;
receptor; ligand; thrombolytic; anti-inflammatory; cadherin; anti-tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents a human expressed sequence tag (EST). The polynucleotide, which is a secreted EST, and the encoded protein are predicted to have useful biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, immune stimulating or suppressing activity, haematopolesis regulating activity, tissue growth activity, haematopolesis regulating chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/chemothactic/ch
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polynucleotides encoding human secreted proteins - derived from e.g. human blood, kidney, foetal lung, placenta, testes, brain, ovary, pituitary, retina and colon cDNA libraries.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 193 BP; 35 A; 39 C; 68 G; 51 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lavallie ER,
Treacy M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 164; 618pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     235 CTCCAGCAACACCCGGCCGCCTTC 258
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15-FEB-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GEMY ) GENETICS INST INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J, Jacobs K,
Spaulding V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human genome fragment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 84, Conserva
                                                                                                                                                                               gene therapy; ss.
                                                EST clone BY66.
                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                              WO9845436-A2.
                                                                                                                                                                                                                                                                                                                                                                                  10-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                     10-APR-1997;
                                                                                                                                                                                                                                                                                                                                    5-0C'r-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Agostino MJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Racie LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           077534;
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Equilibrative nucleoside transport protein; iENTP; NBMPR; transport; nitrobenzylmercaptopurine riboside; antiviral; antitumour; screening; inhibitor; drug; knockout mice; cancer; chemotherapy; gene therapy; adenosine deaminase; factor VIII; UTR; untranslatede region; ds.
                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                 2 TCCGGCGCCAGCTGCCAGTCGAGGAACCCAACCCAAAAGGCTTCTTTTTTGTGCTGC 61
                                                                                                               Human nucleic acid fragments, isolated from brain, adrenal tissue, the placenta or bone marrow comprise any of: (A) a sequence selected from (Q76401-Q77613), (B) an allelic variation of a
                                                                                                                                                                 sequence as described in (A), or (C) a sequence complementary to (A) or (B).
                                 New nucleic acid fragment encoding gene products \boldsymbol{\cdot} can be used for genetic analysis and mapping
                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                     Score 44; DB 15; Length 297;
Pred. No. 0.0026;
3; Mismatches 15; Indels
                                                                                                                                                                                                                                                 Sequence 297 BP; 66 A; 117 C; 61 G; 52 T; 1 other;
                                                                               Claim 1; Page 575-576; 616pp; English.
                                                                                                                                                                                                                                                                                                17.1%; Scor
77.9%; Pred
ative 0; }
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    V69699 standard; DNA; 6354 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5' UTR sequence of iENTP DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98WO-US07283
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97US-0838845
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WPI; 1994-035056/04.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         diabetic retinopathy; fibroproliferative disorder; artherosclerosis; TGF-beta signalling pathway; TGF, Transforming growth factor; pancreatic cancer; anglogenesis; inflammation; fibrosis; tumour growth; vascularisation; cytostatic; antidiabetic; opthalmological; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTCACCATCGTCTTCTGCCAGATCCTGATGGCTGAAGAGGGTGTGCCGGCGCGCCCCTGCCT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Fchd605 is a novel human gene that is up-regulated in monocytes treated with oxidised low density lipoproteins (LDL). Differential display was used to detect genes that are differentially expressed in monocytes treated so as to simulate the conditions under which foam cells develop during atherogenesis. Both fchd605 and fchd602 (see T94470) are up-regulated under the disease condition of treatment with oxidised LDL. The fchd605 gene product (see W16006) has sequence similarity to mouse gly96. The discovery of the up-regulation of these 2 genes provides a fingerprint profile, e.g. markers for the study of cardiovascular diseases, including atherosclerosis, ischemial/repertusion, hypertension, restenosis and arterial inflammation. Methods are provided for the diagnosis,
                                                                                                                                                                                                                                                             monitoring in clinical trials, screening for therapeutically effective compounds, and treatment of cardiovascular diseases based on discoveries regarding the expression patterns of novel genes (chd531 (see T94467), fchd540 (see T94468), fchd545 (see T94469),
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                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 258; DB 18; Length 1228; 100.0%; Pred. No. 1e-60;
                                       for diagnosis, drug screening and treatment of cardiovascular disease, e.g. atherosclerosis, restenosis, hypertension, etc
                          New genes differentially expressed in cardiovascular disease
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                                                                              Claim 1; Fig 5; 163pp; English.
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P-PSDB; W36006
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cardiovascular diseases by novel human genes which are differentially expressed in different cardiovascular disease states. Compositions which can modify TGF-beta signalling pathway are identified by screening. These are used therapeutically to treat fibroproliferative and oncogenic disorders, especially TGF (Transforming growth factor)-beta related disorders, including diabetic retinopathy, artherosclerosis, pancreatic cancer, angiogenesis, inflammation, fibrosis, tumour growth and vascularisation. The present sequence is fch6605 gene which is upregulated in monocytes treated with oxidised LDL (low density lipoprotein) can be used to design cardiovascular disease treatment strategies. Depending on whether the up-regulation has a pathogenic or decrease the activity of the protein product of the gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identifying substances for ameliorating symptoms of fibroproliferative diseases or oncogenic related disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          211 giccggcgccagctgccagicgaggaaccgaacccagccaaaaggciictititigcig 270
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100.0%; Pred. No. 1e-60;
ive 0; Mismatches 0;
                                                       /product= "fcdh605 protein"
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ID V89271 standard; cDNA; 193
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Best Local Similarity 100.
Matches 258; Conservative
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January 30, 2001, 21:29:29 ; Search time 77.57 Seconds (without alignments) 1249.465 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                       258
1 GTCCGGCGCCAGCTGCCAGT.....AGCAACACCCGGCCGCCTTC 258
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    480022 seqs, 187831343 residues
                                                                                                                                                                                                                                                                                            US-08-799-910-9_COPY_211_468
                                                                                                        Ом nucleic - nucleic search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Description	Human Fchd605 gene	Nucleotide sequenc EST clone BY66. H	Human genome fragm 5' HTR sequence of	Human Cyclic nucle	Human normal bladd	Rat transcription	Type III procollag Human L-type amino
RIES	, , , ,						
SUMMARIES	T94471	V89271	Q77534 V69699	Z51683 V69706	Z42235 A02484	V62462	A08372
	18	20	15	21	20	19	21
% Query Match Length DB	1228	193	297 6354	4228 170	1526	2953	4539
% Query Match	100.0	32.6	17.1	14.8	14.1	13.5	13.1
Score	258	86	44 38.6	38.2 37.6	36.4 36.2	34.8	33.8
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
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| 187 | em_gst1;* |
| 188 | em_gst1;* |
| 189 | em_gst1;* |
| 180 | em_gst1;* |
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Result No. 1	Match Match	Length DB 755 11	1D 1D 1D 1D 1D 1D 1D 1D 1D 1D	Description BE383865 60127319 BE275966 60112073 BE821346 60149373 BE88213386 60149373 BE563592 60133470 BE910077 60150214 AWAG62348 h125c073 AW662348 h125c073 AW662348 h125c073 AW662348 h125c073
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BE383865 951 bp mRNA EST 21-JUL-2000 601273192F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614255 5', mRNA sequence.
BE383865
BE383865.1 GI:9329230
EST. human.

RESULT 1 BE383865 LOCUS DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

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us-08-799-910-9.rst

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Location/Quailiners

(reganism="Homo sapiens"

/ Organism="Homo sapiens"

/ Clone="IMAGE:3614255"

/ Clone="IMAGE:3614255"

/ Clone="IMAGE:3614255"

/ Clone="Lib="NIH_MGC_20"

/ Tissue_type="melanotic melanoma"

/ Tab_host="DH10B (phage-resistant)"

/ Note="Organ: skin; Vector: poTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/Xhio; Vector: poTB7; Site_1: XhoI; Site_2: GCARI/Xhio; Vector: poTB7; Site_1: XhoI; Site_2: Alab made by oligo-dT priming. Directionally cloned into EcoRI/Xhio; Alab site, Size-selected >500bp for average insert size 1: Rkb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of Carifornia, Berkeley) using ZAP-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies)."
           Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria: Primates; Catarrhini; Hominidae; Homo.

Eutheria: Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 951)

National Institutes of Health, Mammalian Gene Collection (MGC)

In Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert Strausbergenih.gov

Tissue Procurement: ATCC/DTD/DTP

CONA Library Preparation: Ling Hong/Rubin Laboratory

CONA Library Arrayed by: The 1.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the T.M.A.G.E. Consortium/LLNL at: image.llnl.gov

Plate: LLCM276 row: g column: 24

High quality sequence stops: 747.

Location/Qualifiers
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60.9%; Score 748.2; DB 10
Best Local Similarity 91.5%; Pred. No. 4.8e-180;
Matches 848; Conservative 0; Mismatches 73;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 765)
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15 (Contact: Robert Strausberg, Ph.D.
16 (Contact: Robert Strausberg, Ph.D.
17 (Contact: Robert Strausberg, Ph.D.
18 (Contact: Robert Strausberg, Ph.D.
19 (Contact: Robert Straibution: MGC clone distribution information can be found through the I.M. G.E. Consortium/LLNL at: Image.llnl.gov
19 (Robert Strausbergener)
19 (Robert Strausbergener
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/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2: EcoR1; cDNA made by oligo-dT priming. Directionally cloned into EcoR1/XhoI sites using the following 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BE275966 765 bp mRNA ES'F 13-JUL-2000
601120727F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2967534 5'
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/db_xref="taxon:9606"
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BE275966
BE275966.1 GI:9150928
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adaptor: GCCACCAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
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CDNA clone IMAGE:3895736 5
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                                                                                                  106; Length 765;
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Mammalia: Eutheria: Primates; Catarrhini; Hominidae;
Il (bases I to 762)
NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
National Institutes of Health, Mammalian Gene Collect
                                                                                                                       Indels
                                                                                                Score 621.4; DB 10
Pred. No. 9.2e-148;
0; Mismatches 1;
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601493736F1 NIH_MGC_7
                                                                                             Ouery Match 50.6
Best Local Similarity 99.4
Matches 655; Conservative
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="lib="NIH_MGC_70"
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/lab_host="DH10B (phage-resistant)"
/note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.1 kb. Library constructed by Life Technologies."
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CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LI.NI.)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LicMG74 row: h column: 09
High quality sequence stop: 613.
Location/Qualifiers
1. 762
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8
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Pred. No. 2.2e-143;
0; Mismatches 38; Indels
                Ph.D.
             Contact: Robert Strausberg, Ph.D
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue_Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                   193
                                                                                                                                                                                                                                                                                                                                                                                   49.2%;
ilarity 93.9%;
Conservative (
                                                                                                                                                                                                                                                                                                                                 288
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Best Local Similarity
Matches 705; Conserv
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JOURNAL,
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/do_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="lib="NIH_MGC_31"
/clone=lib="NIH_MGC_31"
/tissue_type="leiomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
8 Average insert size 2.1 kb. "
137 c 268 g 134 t
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Futheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 916)
NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
Mational institutes of Health, Mammalian Gene Collection (MGC)
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CGCCCCAGCGCCTCTCGCGGGCACCGAAAGCGCAGCCGCAGGGTTCTCTAACCCTCGAGTG 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Afrausberg@nih.gov
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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Pred. No. 9.4e-140;
0; Mismatches 30; Indels 8
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High quality sequence stop: 659.
Location/qualifiers
1. 916
                                                                                                                                                                   720 ATTACTTATGCTCTAATAATATAGGTAT 750
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BE882130.1 GI:10330906
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Best Local Similarity 94.7%;
Matches 676; Conservative
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                                                                                                                                                                                                                                                                                                                    mRNA sequence.
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JOURNAL
                                                                                                                                                                                                                                                                                                                                  ACCESS10N
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Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550
Email: Robert Strausberg@nih.gov
Telssue Procurement: DCTD/DTP
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM186 row: j column: 24
High quality sequence stop: 579.
High quality sequence stop: 579.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HEZ/3386 603 bp mRNA EST 13-JUL-2000
601143493F1 NIH_MGC_14 Homo sapiens CDNA clone IMAGE:3507191 5'
BE273386
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1 (bases 1 to 603)

NIH-MGC http://www.ncbi.ulm.nih.gov/MGC/.
National Institutes of Health, Mammallan Gene Collection (MGC)
Unpublished (1999)
                                                                                                    CTCACCATCGTCTTCTGCCAGATCCTGATGGCTGAAGAGGGTGTGCCGGCGCCCCTGCCT
                                                        240 CTCACCATCGTCTTCTGCCAGATCCTGATGGCTGAGAGGGTGTGCCGGCGCCCTGCCT
                                                                                                                                                                CCCTTTAATCTGACTTCGGAGCCCTCGGACTACGCTCTGGACCTCAGCACTTTCCTCCAG
                                                                                                                                                                                              360 CCCTTTAATCTGACTTCGGAGCCCTCGGACTACGCTCTGGACCTCAGCACTTTCCTCCAG
                                                                                                                                                                                                                            CAACACCCGGC - CGCCTTCTAACTGTGACTCCCCGCACTCCCCAAAAAGAATCCGAAAAA
                                                                                                                                                                                                                                         510 CCACAAAGAAACACCAGGCGTACCTGGTGCGCGAGAGCGTATCCCCAACTGGGACTTCCG
                                                                                                                                                                                                                                                                                                                                                   570 AGGCAACTTGAACTCAGAACACTACAGCGGAGACGCCACCCGGTGCTTGAGGCGGGACCG
                                                                                                                                                                                                                                                                                                                                                                 630 AGGCGCACAGAGACCGAGGCGCATAGAGACCGAGGCACAGCCCAGCTGGGGCTAGGCCCG
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AUTHORS
TITLE
JOURNAL
COMMENT
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cloned into EcoRI/Xhol sites using the following 5' adaptor: GGCAGGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDMA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
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                                                                                                                                                                                               GTCCTGAGATCTTCACCTTCGACCCTCTCCCGGAGCCGCAGGGGCCCCTGCCGGGGGCCC 154
                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                           CCAGCGCCTCTCGCGGGCACCGAAAGCGCAGCGCAGGGTTCTCTACCCTCGAGTGGTCC 214
                                                                                                                                                                                                                                                                                                                                  CCATCGTCTTCTGCCAGATCCTGATGGCTGAAGAGGGTGTGCCGGCGCCCCCTGCCTCCAG 334
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                                                                                                                                                    CACCCGCCCCTTTTAACTGTGACTCCCCGCACTCCCCAAAAAGAATCCGAAAAACCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGGARGCCCCTAACGCCGCATCCCTGGCGCCCACCCCTGTGTCCC -CCGTCCTCGAGCCC
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 810)
                                                                                                             DB 106; Length 603;
                                                                                                                                     Indels
                                                                                                          48.0%: Score 589.4; DB 106
ilarity 99.7%; Pred. No. 1.3e-139;
Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mRNA sequence.
BE563592
BE563592.1 GI:9807312
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||GCA 603
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                                                                                                                                601;
                                                                                                           Query Match
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DEFINITION
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BE563592
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3688825"
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Site_2: EcoR1; CubA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAGCGG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin
(University of California, Berkeley) using ZAP-CDNA synthesis Rit (Stratagene) and Superscript II RT (Life Technologies).
Technologies).
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61 CCCTCCACCATCCCGGGACCCCGGGGGGTCCTGAGGATCTTCACCTTCGACCCT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 CTCCCGGAGCCCGCAGCGGCCCCTGCCGGGCGCCCCCAGCGCCTCTCGCGGGCACCGAAAG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117 CTCCCGGAGCCCGCAGCGGCCCCTGCCGGGCCCCCAGCGCCTCTCGCGGCCACGAAAG 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   420 CTACGCTCTGGACCTCAGCACTTTCCTCCAGCAACACCCGGCCGCCTTCTAACTGTGACT
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. 3e-139;
                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                               47.9%; Score 588;
92.1%; Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 753; Conserv
                                                                                                                                                                                                                                                                                                                                                                                Query Match
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   TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                   BASE COUNT
ORIGIN
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1. .585
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/clone="IMAGE:3903754"
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/tlssue_type="epithelioid carcinoma"
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/note="Organ: pancreas; Vector: pCMV-SPOR76; Site_1: Not1; Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 585)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: ATC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCMG95 row: f column: 11
High quality sequence stop: 585.
High quality sequence stop: 585.
Location/Qualifiers
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National Institutes of Health, Mammalian Gene Collection (MGC)
   597
                               594
                                                             653
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                                                                                                                                                                                                                                                                                                                                                         BE910077 585 bp mRNA EST 29-SEP-2000
601502143F1 NIH_MGC_70 Homo sapiens CDNA clone IMAGE:3903754
GGAGACGCCACCC - - GGTGCTTGAGGCGGGACCGAGGCGCA - CAGAGACCGAGG - CGCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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11arity 100.0%; Pred. No. 1.7e-138;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                               GAGATGTGTACGTAATATTTTAACTTATGCAAGG 811
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                       mRNA sequence.
BE910077
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nes 585; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             131
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Matches
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TITLE
JOURNAL
COMMENT
                                                             598
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LOCUS
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Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (Dases 1 to 586)

NoT-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

L Unpublished (1997)

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Tel: (301) 496-1550

Email: Robert Strausberg@nih.gov

Tel: (301) 496-1550

Email: Robert.Strausberg@nih.gov) for further information.

Seq primer: -400P from Gibco

High quality sequence stop: 471.

Location/Qualifiers

1. 586

//clone="Image: 2907365"

//clone="Image: 2907365"

//clone="Image: Soares_NFL_T_GBC_S1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note-"Organ: pooled; Vector: pT7:3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell
                                                                                                                                                                                                                                                                                                                                                            TCTGGTGGTGGGTCGTAAGTTTAGGAGGTGACTGCATCCTCCAGCATCTCAACTCCGTCT 1023
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                                                                                                                     TGCTCCTAATTAATATTTATGTATTTATGTAGGTCCTCCTAGGTGATGTGAATGTGTA
                                                                                                                                                                              CGTAATATTTTAACTTATGCAAGGGTGTGAGATGTTCCCTCTGCTGAAATGCAGG
                                                                                                                                                                                             844 TCTCTTGGTATTTATTGAGCTTTGTGGGACTGGTGGAAGCAGGACACCTGGAACTGCGGC
                                                                                                                                                                                                                                                      AW340002 586 bp mRNA EST 31-J4 hc91d03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2907365 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /lab_host="DH108"
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NCI_CGAP_GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of 11.M.A.G.E. clones 297480-302087, 682632-687239, 72408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaido. " 187 c 110 g 134 t.
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clone IMAGE:2973324 3',
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia: Eutheria; Primates: Catarrhini; Hominidae; Homo.
1 (bases 1 to 598)
NCI-CGAP http://www.ncbi.nlm.nih.gov/nciogap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1101 GGCTGGCTGCCAGGTAGAGGCTTGGGGGTTGGTGGCGCTGTCACGGAGCGACTGTCGAGAT 1160
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hi25c07.x1 NC1_CGAP_Co14 Homo sapiens cDNA
                                                                                                                                                                        47.3%; Score 581.2; DB 89
.99.5%; Pred. No. 1.5e-137;
                                                                                                                                                                                                     0; Mismatches
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AUTHORS
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Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: Robert_Strausbergenih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
Emmert-Buck, M.D., Ph.D.
CUNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Jennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml
Seq primer: -40UP from Gibco
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/clone="IMAGE:2973324"
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/tissue_type="moderately-differentlated adenocarcinoma"
/lab_host="DH10B"
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Pred. No. 3.9e-137;
0; Mismatches 9; I
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/lasue_type="epithelioid carcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT. Average Insert size 1.1 kb. Library constructed by Life Technologies."
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                                                                                                                                        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                   A EST 24-AUG-2000 . sapiens cDNA clone IMAGE:3895736 3',
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NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can l
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                             Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert_Strausberg@nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 567.2; DB 110; Length 614;
Pred. No. 5.7e-134;
0; Mismatches 8; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Plate: LLCM674 row: h column: 09
High quality sequence start: 12
High quality sequence stop: 613.
Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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                   BE621600 614 bp mRNA
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BE621600.1 GI:9892540
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98.2%;
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AW956285 588 bp mRNA EST 01-JUN-2000
EST368355 MAGE resequences, MAGD Homo sapiens CDNA, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray Unpublished (2000)

Contact: John Quackenbush
The Institute for Genomic Research
712 Medical Center Dr., Rockville, MD 20850, USA
713 130 838 3528
Fax: 301 838 0208
                                                                                                                                                                                                         1059 TGAGATCCGTGAGATCCTTCCATCTTCTTGAAGTCGCCTTTAGGGTGGCTGCGAGGTAGA 1118
                                                                                                                                                                                                                                                                                        1119 GGGTTGGGGGTTGGTGGCCTGTCACGGAGCGACTGTCGAGATCGCCTAGTATCTTCTGTG 1178
                                                                                                                          ATCCTCCAGCATCTCAACTCCGTCTGTCTACTGTGTGAGACTTCGGCGGACCATTAGGAA 1058
                                                                                                                                           194 ATCCTCCAGCATCTCAACTCCGTCTGTCTGTGTGAGACTTCGGCGGACCATTAGGAA 135
                                                              TGGGGCTAGGCCCGGTGGGAAGGAGACGTCGTTAATTTATTCTTATTGCTCCTAATTA 735
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AAGCAGGACACCTGGAACTGCGGCAAAGTAGGAGAAAATAGGGGAGGATCTCGGGTGGG 255
                                                                                                                                                                                                                                                  75
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                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                              556 AACTGGGACTTCCGAGGCAACTTGAACTCAGAACAACTACAGGGGAGACGCCACCCGGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGAGGACGTCCCGGCTGGGATGAAGTCTGGTGGTGGGTCGTAAGT"I"TAGGAGGI'GACT'GC
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98.3%; Pred. No. 1.5e-132;
tive 0; Mismatches 9; I
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="MAGE resequences, MAW
/note="Vector: pbluescriptsKm"
a 117 c 187 g 149 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 588)
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Plate: 90
Seg primer: Reverse.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 548)
NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert Strausbergenin.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from Glbco
High quality sequence stop: 466.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AATCTGACTTCGGAGCCCTCGGACTACGCTCTGGACCTCCAGCACTTTCCTCCAGCAACAC 456
                                                                                                                                                                                                                                            ATCGTCTTCTGCCAGATCCTGATGGCTGAAGAGGGTGTGCCGGCGCCCCCTGCCTCCAGAG 336
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                                                                                                                                             337 GACGCCCTAACGCCGCATCCCTGGCGCCCACCCCTGTGTCCCCCCGTCCTCGAGCCCTTTT
                                                                                                                                                                GAAACACCAGGCGTACCTGGTGCGCGAGGCGTATCCCCAACTGGGACTTCCGAGCCAAC
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                   Pred. No. 2.3e-131;
); Mismatches 21;
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0
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AW263252.1 GI:6640068
             . 5%;
           Best Local Similarity 95.5
Matches 596; Conservative
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AW263252/c
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1 (bases I to 617)

1 (bases I to 617)

1 (bases I to 617)

2 (bases I to 617)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Zoquang Han
Chinese National Human Genome Center at Shanghai
201203, P. R. China
7e1: 86-21-50801919(ex.45)
Email: hanzg@chgc.sh.cn
                                                                                                                                                                                                                                                                                                                                                     1035
                                                                                                                                                                                                                                                                                                                                                                                                                     AGACTICGGCGGACCATTAGGAATGAGATCCGTGAGATCCTTCCATCTTCTTGAAGTCGC 1095
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mRNA sequence.
                                                                                                                                                                                                                                                                GAAATGGGGAGGACTCGGGTGGGGAGGACGTCCCGGTGGGATGAAGTCTGGTGGTGGTGG 975
                                                                                                                                                                                                  915
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                                                                                                             ATATTTATATGTATTTATGTACGTCCTCCTAGGTGATGGGGATGTGTACGTAATTTAT
                                                         TATTGAGCTTTGTGGGACTGGTGGAAGCAGGACACCTGGAACTGCGGCAAAGTAGGAGAA
                                                                                                                                                                                                                                                                                                                                           DB 38; Length 617;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITIAGGGTGGCTGCGAGGT-AGAGGGTTGGGGGGTTGGTGGGCTGTCA 1142
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AV690660 GKC Homo sapiens cDNA clone GKCBAA04 5',
AV690660
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/dev_stage="Adult"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="GKC
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                                                           /lab_host="DH108"
/note="Organ: pooled: Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell: NCI_CGAP_GCBI) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I:M A.G.E. clones 297480-302087, 682632-687239, 726408-728911, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. "

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                                                                                                                                                                                                                                                                                                                                                                                                                                          TGTACGTAATATTTATTTTAACTTATGCAAGGGTGTGAGATGTTCCCTCTGCTGTAAATG
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                                                                                                                                                                                                                                                                                  44.4%; Score 544.8; DB 88
99.6%; Pred. No. 2.8e-128;
tive 0; Mismatches 2;
                                               /clone_lib="Soares_NFL_T_GBC_S1"
            /organism="Homo sapiens"
/db_xref="taxon:9606"
                                    /clone="IMAGE:2700722"
                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA sequence.
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/Organism="Homo sapiens"
/Organism="Homo sapiens"
/Organism="Homo sapiens"
/Organism="1000
//Organism=13800248"
/Clone_lib="NIH_MGC_69"
/Lissue_type="large_cell_carcinoma, undifferentiated"
/Issue_type="large_cell_carcinoma, undifferentiated"
/Inb_host="Dupp (phage-resistant)
//Orde="Organ: lung; Vector: pCWV-SPORT6; Site_]: NotI;
Site_2: Sal]; Cloned unidirectionally. Primer: Oligo dT.
Site_2: Sal]; Cloned unidirectionally. Primer: Oligo dT.
#PAPERGE INSERT SIZE 1:1 kb. Library constructed by Life
                                                                                          Euteleostomi;
                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert Strausbergenih.gov
Tissue Procurement: DCTD/NTP/Gazdar
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM660 row: c column: 17
High quality sequence stop: 645.
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                                                                                                                                1 (bases 1 to 1070)
NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                               Hominidae;
                                                                                       Vertebrala;
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                                                                                                               Catarrhini;
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95.6%; Pred. No. 3.3e-127;
ative 0; Mismatches 17;
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Mammalia; Eutheria; Primates;
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GI:10327235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 521)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausbergenin.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 662 Std Error: 0.00 Seq primer: -40UP from Gibco
High quality sequence stop: 456.

1.0521
                                                                      A1800828 521 bp mRNA EST 19-DEC-1999 wg13f12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMACE:2365007 3', mRNA sequence.
                     GGACCGAGGCGCACAGAGACCGAGGCGCATAGAGACCGAGGCACAGCCCAGCTGGGGCTA
                                                                                                                                             TATGTATTTATGTACGTCCTCCTAGG - - - - TGATGGAGATGTGTACGTAATATTTTT
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Pred. No. 8.3e-122;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2365007"
/clone=lib="Soares_NSF_F8_9W_OT_PA_P_S1"
                                                                                                                                                                                                                                           AACTIATGCAAGGGTGTGAGATGTTCCCTCT-GCTGTAAATGCAGG 843
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Unpublished (1997)
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Best Local Similarity 99.8
Matches 520; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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Job time: 28456 sec
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Sequence 2393, Ap Sequence 9722, Ap Sequence 9724, Ap Sequence 10214, Ap Sequence 9719, Ap Sequence 2888, Ap Sequence 2888, Ap Sequence 2393, Ap Sequence 1703, Ap Sequence 2393, Ap Sequence 1703, Ap Sequence 2984, Ap
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Sequence 4785, Ap
Sequence 430, App
Sequence 1025, Ap
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14935, Ap
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Sequence 429, App
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Sequence 2355, A
Sequence 4785, A
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1 GTCCGGCGCCAGCTGCCAGT......AGCAACACCCGGCCGCCTTC 258
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/cgn2_6/ptodata/2/pna/US6017_COMB.seq:
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                                             GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
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61 CICACCATCGTCTTCTGCCAGATCCTGATGGCTGAAGAGGGTGTGCCGGCGCCCCTGCCT 120
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APPLICANT: Shyjan, Andrew W.
APPLICANT: McCarthy, Sean A.
APPLICANT: McCarthy, Sean A.
APPLICANT: Monahan, John
APPLICANT: Monahan, John
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.1182-001
CURRENT FILING DATE: 2000-08-28
PRIOR APPLICATION NUMBER: 60/151,062
PRIOR FILING DATE: 1999-08-27
                                                                                  Indels
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                                                Score 258; DB 24;
Pred. No. 7.5e-52;
Mismatches 0;
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100.0%; Pred. No. 7.5e-52;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 9708
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 356
LENGTH: 521
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                                             100.08;
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Best Local Similarity 100.0
Matches 258; Conservative
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Best Local Similarity 100.
Matches 258; Conservative
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; ORGANISM: Homo sapiens
US-09-644-869-356
US-09-726-805-429
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                                                            APPLICANT: Labat. Ivan APPLICANT: Labat. Ivan APPLICANT: Stache Crain, Birgit APPLICANT: Stache Crain, Mark APPLICANT: Dickson, Mark APPLICANT: Dickson, Mark TITLE OF INVEWTION: Novel Nucleic Acid Sequences Obtained TITLE OF INVEWTION: From Various Libraries FILE REFERENCE: 774

CURRENT APPLICATION NUMBER: US/09/528,409

CURRENT FILING DATE: 1999-03-19

NUMBER OF SEQ ID NOS: 116231

SOFTWARE: Hy-Patent.pl Version 3.1
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APPLICANT: Gearing, David P.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.2017-001
CURRENT APPLICATION NUMBER: US/09/726.805
CURRENT FILING DATE: 1999-11-30
PRIOR FILING DATE: 1999-11-30
NUMBER OF SEQ ID NOS: 2158
SOFTWARE: FastSEQ for Windows Version 4.0
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100.0%; Score 258; DB 19;
Best Local Similarity 100.0%; Pred. No. 7.4e-52;
Matches 258; Conservative 0; Mismatches 0;
               ; Sequence 88514, Application US/09528409; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 429, Application US/09726805 GENERAL INFORMATION:
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OTHER INFORMATION: n = A,T,C or G
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                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
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LOCATION: (1)...(453)
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ORGANISM: Nomo sapiens
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LENGTH: 506
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Indels

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Mismatches Pred. No.

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Best Local Similarity
Matches 258; Conserv
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                                                                                                                                                 APPLICANT: BONDAZI, VIVIEN

APPLICANT: BONDAZI, VIVIEN

TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS, AND

TITLE OF INVENTION: USES THEREOF

FILE REFERENCE: CLO00456

CURRENT APPLICATION NUMBER: US/60/196,718

CURRENT FILING DATE: 2000-04-13

NUMBER OF SEQ ID NOS: 7494

SOFTWARE: ESECREC for Windows Version 4.0

SEP UD NO 2355

LENGTH: 521
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GENERAL INFORMATION:
APPLICANT: HOLIZMAN:
APPLICANT: Gearing, David P.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREFOR
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
CURRENT APPLICATION NUMBER: US/09/699,998
CURRENT APPLICATION NUMBER: US/0162,362
PRIOR FILING DATE: 1999-10-29
PRIOR FILING DATE: 1999-10-29
SOFTWARE: FastSED for Windows Version 4.0
SEQ ID NO 4785
LENGTH: 529
                                                                                                                                                                                                                                                                                                                                                                   Length 521;
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7.5e-52;
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                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 258;
100.0%; Pred. No. 7
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US-09-699-998-4785
; Sequence 4785, Application US/09699998
                                                                                                                  Sequence 2355, Application US/60196718
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 258; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sapiens
                      241 CAACACCCGGCCGCCTTC
                                    451 caacaccoggccgccttc
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US-09-699-998-4785
                                                                                                        US-60-196-718-2355/c
                                                                                                                                                                                                                                                                                                          TYPE: DNA
CRGANISM: HUMAN
US-60-196-718-2355
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61 CTCACCATCGTCTTCTGCCAGATCCTGATGGCTGAAGAGGGTGTGCCGGCGCCCCTGCCT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GTCCGGCGCCAGCTGCCAGTCGAGCACCCAGCCAAAAGGCTTCTCTTTCTGCTG 60
                                           182 gtccggcgccagctgccagtcgaggaaccgaacccagccaaaaggcttctttttgctg 241
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                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GEALING, David P.
APPLICANT: GEALING, Samantha J.
APPLICANT: GEALING, Samantha J.
APPLICANT: Busfield, Samantha J.
APPLICANTION: HUMBER: US/09/396,885
CURRENT APPLICATION NUMBER: 60/106,444
PRIOR PILING DATE: 1998-10-30
PRIOR APPLICATION NUMBER: 60/126,842
PRIOR FILING DATE: 1999-103-30
PRIOR PILING DATE: 1999-03-30
NUMBER: OF SEQ ID NOS: 5360
SOFTWARE: EASLEED for Windows Version 3.0
SEQ ID NO 430
LENGTH: 617
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100.0%; Pred. No. 7.6e-52;
tive 0; Mismatches 0;
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LOCATION: (1)...(617)
OTHER INFORMATION: n = A,T,C or
                                                                                                                                                                                                                                                                 422 caacacccggccgccttc 439
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Best Local Simi
Matches 258;
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Length 529;

23;

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100.0%; Score 258;

Ouery Match

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US-09-699-998-9797
                                   Query Match
Best Local :
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ORGANISM:
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Sequence 14935, Application US/09698010

GENERAL INFORMATION:
APPLICANT: Williamson, Mark
APPLICANT: Shyjan, Andrew W.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
FILE REPRENCE: 1600.2029-001
CURRENT FILING DATE: 2000-10-27
FRICK PROR APPLICATION NUMBER: 05/09/698,010
PRIOR PRILING DATE: 1999-10-29
NUMBER OF SEQ ID NOS: 15684
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 673
                                                                                                                                 APPLICANT: Gearing, David P.
APPLICANT: Gearing, David P.
APPLICANT: Gearing, Douglas A.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A
TITLE OF INVENTION: HUMAN MAMMARY EPITHELIUM LIBRARY
FILE REFERENCE: 1600.1086-001
CURRENT APPLICATION NUMBER: 92/09/522,303
CURRENT APPLICATION NUMBER: 60/123,393
EARLIER APPLICATION NUMBER: 60/123,393
EARLIER PILING DATE: 1999-03-08
NUMBER OF SEQ (D NOS: 1353
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 657
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100.0%; Score 258; DB 19;
Best Local Similarity 100.0%; Pred. No. 7.6e-52;
Matches 25%; Conservative 0; Mismatches 0;
                                                                                                       Sequence 1025, Application US/09522303 GENERAL INFORMATION:
                   346 caacaccggccgcttc 363
241 CAACACCCGCCGCCTTC 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 CAACACCGGCCGCCTTC 258
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ORGANISM: Homo sapiens

US-09-522-303-1025
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; ORGANISM: HOMO SapienS
US-09-698-010-14935
                                                                                        US-09-522-303-1025
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329 ctcaccatcgtcttctgccagatcctgatggctgaagayggtytgccggccctgcct 388
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                                                      1 GTCCGGCGCCGCCTGCCAGTCGAGGAACCGAACCCAAAAGGCTTCTCTTTTTTCTGCTG 60
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                                                                                                              61 CICACCAICGICITCIGCCAGAICCIGAIGGCIGAAGAGGGGIGIGGGGGGGGCCCTGCCI
                                                                                                                                                                      121 CCAGAGGACGCCCTAACGCCGCATCCCTGGCGCCCACCCCTGTGTCCCCCGTCCTCGAG
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         Length 673;
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100.0%; Pred. No. 7.7e-52;
Live 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 9797, Application US/0969998
GERERAL INFORMATION:
APPLICANT: Holtzman, Douylas A.
APPLICANT: Holtzman, Douylas A.
APPLICANT: Gearing, David B.
TITLE OF INVENTION: THERFERD
TITLE OF INVENTION: THERFERD
FILE REFERENCE: 1600.2008-001
CURRENT APPLICATION NUMBER: 05/09/699,998
FILE REFERENCE: 1600.2008-001
CURRENT APPLICATION NUMBER: 05/162,362
PRIOR FILING DATE: 1999-10-29
NUMBER OF SEQ ID NOS: 10905
SOFTWARE: FastSEQ for Windows Version 4.0
EDGTH: 673
                                  Indels
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100.0%; Score 258; DB 23; 100.0%; Pred, No. 7.7e-52;
                                Mismatches
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         Similarity 100.
58; Conservative
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Best Local Similarity 100.
Matches 258; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Homo sapiens
US-09-699-998-9797
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Indels

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RESULT 12
US-09-721-588-4548
Sequence 4548, Application US/09721588
Sequence 4548, Application US/09721588
GENERAL INFORMATION:
APPLICANT: GEATING, David P.
APPLICANT: Willeval, Jean-Luc
TILLE OF INVENTION: THEREFOR
TITLE OF INVENTION: THEREFOR
TITLE OF INVENTION: THEREFOR
FILL REPERBENCE: 1600-2046-001
CURRENT APPLICATION NUMBER: US/09/721,588
CURRENT PI).ING DATE: 2000-11-22
CURRENT PI).ING DATE: 60/167,381
PRIOR PELICATION NUMBER: 60/167,381
PRIOR FILLING DATE: 1999-11-24
NUMBER OF SEQ ID NOS: 5410
SOFTWARE: FastSEO for Windows Version 4.0
SOFTWARE: 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 258; DB 24; Best Local Similarity 100.0%; Pred. No. 7.7e-52; Matches 258; Conservative 0; Mismatches 0;
Mismatches
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     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-721-588-4548
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US-09-726-787-2982
           Matches
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Sequence 250, Application US/09716473
Sequence 250, Application:
APPLICANT: Williamson, Mark
APPLICANT: Williamson, Mark
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREFOR
TITLE OF INVENTION: THEREFOR
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
CURRENT APPLICATION NUMBER: US/09/716,473
CURRENT FILING DATE: 1999-11.19
PRIOR FILING DATE: 1999-11.19
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                100.0%; Score 258; DB 24; Length 673; 100.0%; Pred. No. 7.7e-52; tive 0; Mismatches 0; Indels 0
                                                                                APPLICANT: Gearing, David P.
APPLICANT: Gearing, Sean A.
APPLICANT: McCarthy, Sean A.
APPLICANT: McCarthy, Sean A.
APPLICANT: McCarthy, Sean A.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.2005-001
CURRENT APPLICATION NUMBER: US/09/710,286
CURRENT FILING DATE: 2000-11-10
PRIOR PILING DATE: 1999-11-04
NUMBER OF SEQ ID NOS: 4115
SEQ ID NO 3772
LENGTH: 673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 258; DB 24;
Pred. No. 7.7e-52;
                                                            Sequence 3772. Application US/09710286
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                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0
Matches 258; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
US-09-716-473-2500
                                                                                                                                                                                                                                                                                      ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-710-286-3772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                        ; Sequence 3772, Appli
; GENERAL INFORMATION:
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SEQ 1D NO 2500
LENGTH: 673
                                        RESULT 10
US-09-710-286-3772
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Gaps

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Length 673; Indels

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121 CCAGAGGACGCCCCTAACGCCGCATCCCTGGCGCCCCACCCCTGTGTCCCCCGTCCTCGAG 180
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                                                                                                                                                                                                                                                           CCCITIPAATCIGACTICGGAGCCCICGGACTACGCICTGGACCTCAGCACTITCCICCAG 240
                                                                                                                                                                                                                                                                              61 CTCACCATCGTCTTCTGCCAGATCCTGATGGCTGAAGAGGGTGTGCCGGGGCCCCTGCCT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTCCGGCGCCAGCTGCCAGTCGAGGAACCGAACCCAGCCAAAAAGGCTTCTTTTCTGCTG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GTCCGGCGCCAGCTGCCAGTCGAGGAACCGAACCCAGCCAAAAGGCTT/CTCTTGCTG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCAGAGGACGCCCCTAACGCCGCATCCCTGGCGCCCACCCCTGTGTCCCCCGTCCTCGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 10469, Application US/0969998

GENERAL INFORMATION:
APPLICANT: HOLTAMA:
APPLICANT: HOLTAMA:
APPLICANT: Gearing, David P.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.2008-001
CURRENT APPLICATION NUMBER: US/09/699,998
CURRENT FILING DATE: 2000-10-30
PRIOR APPLICATION NUMBER: 60/162,362
PRIOR FILING DATE: 1999-10-29
           Indels
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Pred. No. 7.8e-52;
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100.0%; Pred. No. 7.8
ive 0; Mismatches
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Matches 258; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: DNA
; ORCANISM: Homo sapiens
US-09-699-998-10469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 15
US-09-699-998-10469
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                                                                                                                                                                                                                                                                                                                                                                   Length 673;
                            APPLICANT: Gearing, David P.
APPLICANT: Holtzman, Douglas A.
TITLE OF INVENTION: MOYEL NUCLEIC ACID MOLECULES AND USES:
TITLE OF INVINION: THEFEOR
FILE REFERENCE: 1600.2010.001
CURRENT APPLICATION NUMBER: US/09/726,787
CURRENT FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: 60/168,132
PRIOR FILING DATE: 1999-11-30
NUMBER OF SEQ ID NOS: 3241
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2982
LENGTH: 673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE 1778, Application US/0969998

GENERAL INFORMATION:
APPLICANT: Holtzman, Douglas A.
APPLICANT: Gearing, David P.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES.
TITLE OF INVENTION: THEREFOR
TITLE OF INVENTION: THEREFOR
FILE REFRENCE: 1600.2008-001
CURRENT APLICATION NUMBER: US/09/69,998
PRIOR FILING DATE: 2000-10-30
PRIOR FILING DATE: 1999-10-29
NUMBER OF SEQ ID NOS: 10905
SOFTWARE: FaatSeQ for Windows Version 4.0
LENGTH: 706
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Pred, No. 7.7e-52;
Sequence 2982, Application US/09726787
GENERAL INFORMATION:
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COTHER INFORMATION: n = A,T,C ous-09-699-998-1778
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ORGANISM: Homo sapiens
US-09-726-787-2982
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ORGANISM: Homo sapiens
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Best Local Similarity
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ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5876949ris
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               148 CTGCCCCCCCCCCCTGTGTCCCCCGTCCTCGAGCCCTTTAATCTGACTTCGGAGCCCTCG 207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Martinis, Susan A. APPLICANT: Sassanfar, Mandana APPLICANT: Sassanfar, Mandana APPLICANT: Kim, Sunghoon APPLICANT: Lee, Sang Ho APPLICANT: Lee, Sang Ho APPLICANT: Schimmel, Paul R. TITLE OF INVENTION: RECOMBINANT MYCOBACTERIAL METHIONYL-TRNA TITLE OF INVENTION: SYNTHETASE GENES, TESTER STRAINS AND ASSAYS NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2; Length 4362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches 110; Indels
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Two Militia Drive
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COMPUTER: IBM PC COMPUTEDLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordberfect 6.0
CURRENT APPLICATION UATA:
APPLICATION UNBER: US/08/455,073A
FILING DATE: 31-MAY-1995
CLASSIFICATION: 530
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49.5%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/08584226
Patent No. 5798240
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                             NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: UPP
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (215) 568-3100
TELEPHONE: (215) 568-3439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4362 base pairs
                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 49.59
Matches 109; Conservative
                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: double
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220..2118
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ADDRESSEE: Hamilton,
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                                                                                                       19103
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; LOCATION;
US-08-455-073A-1
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591 CCGGGGATTCTATCTGACGGGGACGGATGAGCACGGCCTGAAGGTGGCGCAGGCCGCG 532
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                                                                                                                               SOFTWARE: DISTRICT TO CURRENT APPLICATION DATA: PC 208/584,226
FILING DATE: US/08/584,226
FILING DATE: US/08/584,226
FILING DATE: US/08/584,226
FILING DATE: US/08/584,226
FILING DATE: US/08/305,766
FILING DATE: 13-SEP-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
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0; Mismatches
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                                                                                                                                                                                                                                                                                          TORNEY/AGENT AND THE NAME: BIOOK, David E. REGISTRATION NUMBER: 22,592
                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12.3%;
                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                      ZIP: 02173-4799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 48.19
Matches 90; Conservative
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STATE: Massachusetts
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Compositions And Methods
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Pred. No. 4.1;
0; Mismatches 110; Indels
                                   APPLICANT: OOSLTA, Ben A. TITLE OFF INVENTION: Diagnosis of the Fragile X Syndrome NUMBER OF SECUENCES: 14 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: PAPLICATION NUMBER: US/07/705,490 FILING DATE: 19910708 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Gideon Dreyfuss
APPLICANT: Mixiko C. Siomi
APPLICANT: Yan Zhang
TITLE OF INVENTION: Fragile X Related Proteins, C
TITLE OF INVENTION: Of Making And Using The Same
CORRESPONDENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    208 GACTACGCTCTGGACCTCAGCACTTTCCTCCAGCAACACC 247
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STREET: 1301 McKinney, Suite 5100
                                                                                                                                                                                                                             COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5876949
                                                                                                                                                                                                                                                                                                                                                                                                                                                        32,714
                    Slephen T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: D-TELECOMMUNICATION INFORMATION:
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TELEX: 762829
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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ilarity 49.5%;
Conservative
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NAME: Paul, Thomas D.
REGISTRATION NUMBER: 32,7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 3765 base pairs
NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 713/651-5246
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STATE: Texa_
COUNTRY: U.S.A.
77010-3095
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Best Local Similarity
Matches 109; Conserv
                                                                                                                                                    Houston
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US-07-705-490-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    154 CCCACCCTGTGTCCCCCGGTCCTCGAGCCCTTTAATCTGACTTCGGAGCCCTCGGACTAC 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Weinzierl, Robert O.J.
TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS,
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING TAFS AND METHODS OF USE
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34 CCAGCCAAAAGGCTTCTCTTTTTGCTGCTCATCGTCTTCTGCCAGATCCTGATGGCT 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1120;
                                                                                                  ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT STREET: 4 Embarcadero Center, Suite 3400 CITY: San Francisco STATE: California
                                                                                                                                                                                                          COMPUTER FRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,715
FLING DATE: US-MAY-1996
CLASSIFICATION: 435
PRIOR APPLICATION UNBER: US/08/188,582
FILING DATE: 28-JAN-1994
ATTORNEY/AGENT IMPORMATION:
NAME: OSMEN REGISTRATION
NAME: OSMEN REGISTRATION
TELECOMMUNICATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: 36,627
TELECOMMUNICATION INDERER: A-57650-2/AJT/RAO
TELECOMMUNICATION INCREMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 33.6; DI
Pred, No. 1.2;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     214 GCTCTGGACCTCAGCACTTTCCTC 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 51.0%;
Matches 104; Conservative
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Nelson, David L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1120 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDS
80..913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                               94111-4187
                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; NAME/KEY;
; LOCATION;
US-08-646-715-8
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APPLICANT:
APPLICANT:
                                                                                                                                                                             COUNT'RY:
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Gaps

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94 GAAGAGGGTGCCGGCGCCCTGCCTCCAGAGGACGCCCCTAACGCCGCATCCCTGGCG 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34 CCAGCCAAAAGGCTTCTCTTTCTGCTGCTCACCATCGTCTTCTGCCAGATCCTGATGGCT 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          154 CCCACCCTGTGTCCCCCGTCCTCGAGCCCTTTAATCTGACTTCGGAGCCCTTCGGACTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 1120;
                            NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
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                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,582
FILING DATE: 28-JAN-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66
                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: A-57650-2/AJT/RAO TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 33.6; DB Pred. No. 1.2; 0; Mismatches
                                                                                                                                                                                                                                     PC-DOS/MS-DOS
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                                                                                                                                                     Sequence 8, Application US/08646715
Patent No. 5637686
GENERAL INFORMATION:
APPLICANT: Tjian, Robert
                                                                                                                                                                                                                                                                                                    FILING DATE: 28-JAN 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard REGISTRATION NUMBER: 36,627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dynlact, Brian D.
Hoey, Timothy
Ruppert, Siegfried
Tanese, Naoko
                                                                                                                                                                                                                                                                                                                                                                                                                                     (415) 781-1989
(415) 398-3249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 1120 base pairs
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Matches 104; Conservative
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Comai, Lucio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: double
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: CDNA
                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; NAME/KEY;
; LOCATION;
US-08-188-582-8
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                                                                                                                                        COUNTRY:
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                                                                               GENERAL INFORMATION:
APPLICANT: Waeber, G
APPLICANT: Nicod, P
TITLE OF INVENTION: Transcription Factor Islet-Brain 1 (1B1)
NUMBER OF SEQUENCES: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 2953;
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                                                                                                                                                                                                                                                                                                                     COMPUTE:: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
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Pred. No. 0.69;
0; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/859,201
FILING DATE: 20-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                      GB 9706731.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 03-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9709920.4
FILING DATE: 15-MAY-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2479 CCCCAGCCTGCCTTCCCCAGCCC 2454
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Patent No. 5534410
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Comai, Lucio
APPLICANT: Comai, Lucio
APPLICANT: Tilan, Robert
APPLICANT: Tilan D.
Segfried
                                                 Sequence 1, Application US/08859201
Patent No. 5880261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: LUADN CSCTF
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: ME
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                              750 Arimo Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 13.5%;
Best Local Similarity 62.8%;
Matches 54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 2953 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                   Luann Cserr
                                                                                                                                                                                                           STREET: 750 Arimo Aven
CITY: Oakland
STATE: California
COUNTR: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 20-MAY-1
PRIOR APPLICATION DATA:
APPLICATION NUMBER: C
                                                                                                                                                                          CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
         RESULF 10
US-08-859-201-1/c
                                                                                                                                                                                               ADDRESSEE:
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LOCATION:
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Gaps

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Wang, Edith

APPLICANT: APPLICANT: APPLICANT:

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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A 'NITROBENZYLMERCAPTOPURINERIBOSIDE (NBMPR)-INSENSITIVE, EQUILIBRATIVE, NUCLEOSIDE THANSPORT PROTEIN, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF
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                                                                                                                                                                                             -AGAGGACGCCCTAAACGCCGCATCCCTGGCGCCCACCCCTGTGTCCCCCGGTCC 175
                                                                                                                                                                                                                                                                176 TCGAGCCCTTTAATCTGACTTCGGAGCCCTCGGACTACGCTCTGGACCTCAGCACTTTCC 235
                                                                                                                                                                                                              Gaps
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                                                                                                                                  Length 2847;
                                                                                                                                                               56; Indels
                                            genomic sequence)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
                                                                                                                            Score 39.4; DB 4;
Pred. No. 0.04;
0; Mismatches 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/058,389A
FILING DATE: April 9, 1998
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Belt, Judith A. APPLICANT: Crawford, Charles R. APPLICANT: Crawford, Charles R. TITLE OF INVENTION: (NUMPR).INSENTITLE OF INVENTION: (NUMPR).INSENTITLE OF INVENTION: (NUMPR).INSENTITLE OF INVENTION: USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5, Application US/09058389A Patent No. 6130065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Jackson Esg., David A. REGISTRATION NUMBER: 26,742 REFERENCE/DOCKET NUMBER: 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               relecommunication information:
Telephone: 201-487-5800
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                                                                                                                                                               , vative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hackensack
: New Jersey
RY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                     236 TCCAGCAAC 244
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US-09-058-389A-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER:
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TITLE OF INVENTION: A NITROBENZYLMERCAPTOPURINERIBOSIDE.
TITLE OF INVENTION: (NBMPR)-INSENSITIVE, EQUILIBRATIVE, NUCLEOSIDE TRANSITITLE OF INVENTION: PROTEIN, NUCLEIC ACIDS ENCODING THE SAME AND METHODS TITLE OF INVENTION: USE
                                                                                         2461 GGTGAGAGGCCTGCCTGGCCCTCTGCCCGAGGCAGCTTCATTGAGGCCTCC 2520
                                                                   100 GGTGTGCCGGCGCCCTGCCTCCAGAGGACGCCCTAACGCCGCATCCCTGGCGCCCACC 159
                                            Gaps
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         Length 6354;
 Score 38.6; DB 3; Length 6. Pred. No. 0.079; 0; Mismatches 29; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NOTE: US/09/058,389A FILING DATE: April 9, 1998 CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.064;
29;
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Pred. No. 0.06.
0; Mismatches
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                                                                                                                                                             2521 CCTGCGCCCCTGCCTCCAGCCCT 2545
                                                                                                                                                                                                                                                                    Sequence 13, Application US/09058389A
Patent No. 6130065
                                                                                                                                          160 ccrdrgrcccccgrccrcdAgcccr 184
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                                                                                                                                                                                                                                                                                                                      Belt, Judith A.
Crawford, Charles R.
Patel, Divyen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 CTGCGCCCCTGCCTCCAGCCCT 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
15.0%;
65.9%;
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                                     56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                170 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 65.5
Matches 55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          201-343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /desc
                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New Jersey
: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hackensack
                Best Local Similarity
Matches 56; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                     INFORMATION:
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DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: US
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                                                                                                                                                                                                                                             US-09-058-389A-13
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CITY: H
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Gaps

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116 TGCCTCCAGAGGACGCCCCTAACGCCGCATCCCTGGCGCCCACCCCTGTGTCCCCCGTCC 175
                                                                                                                                                                                                                               505 TGAGTCCAGAGGGTGTTGCCAGGAGCTCCTCCTCCCTTCCCCTCCCCACTCTCCCGGGTC 564
                                                                                                                                                                                                                                                                             176 TCGAGCCCTTTAATCTGACTTCGGAGCCCTCGGACTACGCTCTGGACCTCAGCACTTTCC 235
                                                                                                                                                                                                                                                                                                  Length 2847;
                                                                                                                                                     56; / Indels
        /note= "HUMDAFC1 (Promotor and 5'
end of Exon 1, genomic sequence)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05920
FILING DATE: 19920714
                                                                                                              DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Sims, Peter J.
APPLICANT: Bothwell, Alfred L.M.
APPLICANT: Elliott, Elleen A.
APPLICANT: Elliott, Elleen A.
APPLICANT: Madri, Joseph
APPLICANT: Madri, Joseph
APPLICANT: Mollins, Scott
APPLICANT: Rollins, Scott
APPLICANT: Squinto, Stephen
TITLE OF INVENTION: Universal Donor Cells
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                        15.3%; Score 39.4; DB
56.6%; Pred. No. 0.04;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E. Kilpatrick & Cody
1100 Peachtree Street, Suite 2800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: Georgia
COUNTRY: 0.5.
ZIP: 30309-4530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GenBank HUMDAF; HUMDAFC1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application PC/TUS9205920 GENERAL INFORMATION:
APPLICANT: Sims, Peter J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
ATTORREY/AGENT INFORMATION:
NAME: PABDE, PATCHE 1, RECISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMRETECOMMUNICATION INFORMATION:
TELEPHONE: 404-815-650
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INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
IFMGTH: 2847 BASSE PAIRS
                                                                                                        Ouery Match
Best Local Similarity 56.6'
Matches 73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLONE: Human DAF CDNA
      CTHER INFORMATION:
CTHER INFORMATION:
US-08-483-433-2
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HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 1100 PORTY: Atlanta STATE: Georgia
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ORIGINAL SOURCE:
ORGANISM: HOM
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                                                                 116 TGCCTCCAGAGGACGCCCCTAACGCCGCATCCCTGGCGCCCACCCCTGTGTCCCCCGTCC 175
                                                                                                                                               176 TCGAGCCCTTTAATCTGACTTCGGAGCCCTCGGACTACGCTCTGGACCTCAGCACTTTCC 235
                                                                                                                                                                     Hest Local Similarity 56.6%; Pred. No. 0.04;
Matches 73; Conservative 0; Mismatches 56; Indels
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTENE Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,433
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                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Sims et al.
TITLE OF INVENTION: Universal Donor Cells
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSE: Patrea L. Pabst
STREET: 2800 One Allantic Center
STREET: 1201 West Peachtree Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIBRARY: GenBank HUMDAF; HUMDAFC1
CLONE: Human DAF cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 800
PRIOR APPLICATION DATA:
-APPLICATION NUMBER: 08/087,007
FILING DATE: JULY 1,1993
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/906,394
FILING DATE: JUNE 29, 1992
CLASSIFICATION: 800
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: Sequence 2, Application US/08483433

: Patent No. 6100443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFRENCE/DOCKET NUMBER: OMRE
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-873-8794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 2: SEQUEDNCE CHARACTERISTICS: LENGTH: 2847 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature LOCATION: 1.819
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MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U.S.
ZIP: 30309-3450
                                                                                                                                                                                                                                 236 TCCAGCAAC 244
                                                                                                                                                                                                                                                                        625 TACTCCACC 633
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STATE: Georgia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
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182 CCTTTAATCTGACTTCGGAGCCCTCGGACTACGCTCTGGACCTCAGCACTTTCCTCCAGC 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : Kilpatrick & Cody
1100 Peachtree Street, Suite 2800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Bell, Leonard
APPLICANT: Squinto, Stephen
TITLE OF INVENTION: Universal Donor Cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: Georgia
COUNTRY: U.S.
2.IP: 30309-4530
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/087,007
FILING DATE: 19930701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sims, Peter J.
Bothwell, Alfred L.M.
Elliott, Elleen A.
Flavell, Richard A.
Madri, Joseph
Rollins, Scott
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                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/08087007
Patent No. 5705732
Patent No. 5705732 5684223
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ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea 1, 284
REGISTRATION NUMBER: 31, 284
REFERENCE/DOCKET NUMBER: OMRI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-815-6500
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                                                                                                                                                                                                           242 AACACCGGCCGCCTTC 258
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TYPE: nucleic acid
STRANDEDNESS: single
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COCATION: 1.819
OTHER INFORMATION: /not
COTHER INFORMATION: end
US-08-087-007-2
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TELEFAX: 404-815-6555
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human DAF CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: SIMS,
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGA.
MOLECULE TYPE: CD
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ORGANISM: Hon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
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APPLICANT:
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181 CCCTTTAATCTGACTTCGGAGCCCTCGGACTACGCTCTGGACCTCAGGACTTTCCTCCAG 240
                             391 ccctttaatctgacttcggagcctcggactacgctctggacctcagcacttcctccag 450
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16.7%; Score 43; DB 1; Length 7218;
Best Local Similarity 7.4%; Pred. No. 0.0054;
Matches 19; Conservative 139; Mismatches 99; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKINER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                            Sequence 14, Application US/08232463
Patent No. 5670367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                           241 CAACACCCGGCCGCCTTC 258
                                                                                                                                        7218 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (703)683-4109
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INFORMATION FOR SEQ 1D NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pTZgpt-F1s
                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 22313-0299
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                                                                                                                                                                                                                                                                               US-08-232-463-14
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15.3%; Score 39.4; DB 1; Length 2847;

Query Match

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NAME/KEY:
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ORGANISM: P
                                                                                         Ouery Match
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                                              Length 1228;
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                                       Score 258; DB 3;
Pred. No. 1.2e-60;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7853-067-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FASTEM: DOS
SOFTWARE: FASTEGO VETSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,495
FILING DATE:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/799,910
                                                                                                                                                                                                                                                                                                                                                                             Sequence 9, Application US/08944495; Patent No. 6087477; GENERAL INFORMATION:
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                                         100.0%;
100.0%;
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REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 78:
TFLECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                         451 CAACACCGGCCGCCTTC 468
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INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                               258
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ATTORNEY/AGENT INFORMATION:
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TYPE: nucleic acid
                                                             Matches 258; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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                                                  Similarity
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US-08-826-246-9
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US-08-944-495-9
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APPLICANT: FALB, Dean A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: COMPOSITIONS AND DIAGNOSIS OF CARDIOV...S: ULAR DISBASE
FILE REFERENCE: 7853-126
CURRENT APPLICATION NUMBER: US/09/126,640A
CURRENT FILING DATE: 1998-07-30
EARLIER APPLICATION NUMBER: 08/799,910
EARLIER APPLICATION NUMBER: 09/799,910
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-02-13
EARLIER FILING DATE: 1997-02-13
EARLIER FILING DATE: 1997-02-13
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                                                                                                       Score 258; DB 3;
Pred. No. 1.2e-60;
0; Mismatches 0;
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SOFTWARE: FastSEQ for Windows Version 4.0
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Patent No. 6099823
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Matches 258; Conservative
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Best Local Similarity 100.
Matches 258; Conservative
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            COCATION: 1...468 COTHER INFORMATION: US-08-944-495-9
Coding
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Sequence 2
Sequence 4
Patent No.
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Patent No. 6048709
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: THE TREATMENT AND DIAGNOSIS OF
TITLE OF INVENTION: CARDIOVASCULAR DISEASE
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
US-08-450-562-22

PCT-US95-07201-43

US-08-329-704-1

US-08-472-604-1

US-08-486-117-1

US-08-486-117-1

US-08-85-337A-2

US-08-865-337A-2

US-08-92-137-3

US-08-92-137-3

US-08-92-137-3

US-08-92-137-3

US-08-92-137-3

US-08-92-060-4

US-08-176-090-4

US-08-460-900-4

US-08-85-11
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REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-078-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)7909090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/826,246
FILING DATE: 28-MAR-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/799,910
FILING DATE: 13-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/011/787
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
ANDEL COMPUTER: 16-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: PENNIE & EDMONDS LLP
1155 Avenue of the Americas
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TELEFAX: (212)8699741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
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    TYPE: nucleic acid STRANDEDNESS: both
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STREET: 11
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US-08-826-246-9
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      LENGTH:
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Sequence 13, Appli
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1 GTCCGGCCCCAGCTGCCAGT.....AGCAACACCCGGCCGCCTTC 258
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Seguence 2, A
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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/pcTUS_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/pcTUS_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/pcTUS_COMB.seq:*
                      GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
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US-09-058-389A-13
US-08-859-201-1
US-08-188-582-8
US-08-646-715-8
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US-09-018-576-2
US-09-018-576-11
US-09-248-137-2
US-09-248-137-1
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PCT-US92-05920-2
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US-08-455-073A-1
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US-09-320-878-19
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-08-681-811-2
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JS-08-087-007-2
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Maximum Match 100%
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length: 2000000000
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unclassified.

RS Sibson,D.R. and Hadfield,K.M.

HUMAN NUCLEIC ACID FROMENTS ISOLATED FROM BRAIN, ADRENAL TISSUE,

PLACENTA OR BONE NARROW AND THEIR USE

NAL PALENT: EP 0587279-A 16-MAR-1994;

MEDICAL LEC 0587279-A 16-MAR-1994;

MEDICAL Location/Qualifiers

Jocation/Qualifiers

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17.14: Score 44; DB 81; Length 297;
Best Local Similarity 77.94; Pred. No. 4.3;
Matches 53; Conservative 0; Mismatches 15; Indels
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Search completed: January 30, 2001, 19:24:37 Job time: 25963 sec

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Sibson, Dr. and Gross, J.
HUMAN NUCLEIC ACID FRAGMENTS, ISOLATED FROM BRAIN ADRENAL TISSUE,
PLACENTA OR BONE NARROW
PATENT: WO 9401548-A 20-JAN-1994;
MEDICAL RES COUNCIL (GB); SIBSON DAVID ROSS (GB)
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 Score 139.2; DB 62;
Pred. No. 2e-21;
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A75448 GI:6065525
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A78427 GI:6090092
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117 c 61 g 55
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Best Local Similarity 77.9%;
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Mus musculus clone RP23-329K24, *** SEQUENCING IN PROGRESS ***, 59
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 187868)
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Web site: http://www.hgsc.bcm.tmc.edu/
                                                                                                                                                                                                                                   58.0%; Score 149.6; DB 1.75.6%; Pred. No. 2.7e-23; ive 0; Mismatches 54
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Matches 204; Conservative
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Sequencing vector: M13: L08821
Chemistry: Dye-primer Bodipy: 82% of reads
Chemistry: Dye-terminator Big Dye: 18% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 13377 bases at least 040
Consensus quality: 169668 bases at least 020
Estimated insert size: 166938; sum-of-contigs estimation
Consignation 2.3x in 020 bases; sum-of-contigs estimation
                                                                                                                              NOTE: This is a 'working draft' sequence. It currently consists of 59 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as arbitrary. On the exact sizes of the apps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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in length

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COMMENT

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2 (bases 1 to 1938)
Charles, C.H., Yoon, J.K., Simske, J.S. and Lau, L.F.
Genomic structure; cDNA sequence, and expression of gly96, a growth
factor-inducible immediate-early gene encoding a short-lived
glycosylated protein
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Submitted (29-JUL-1992) L. Lau, University of Illinois College of
Med., Dept. of Genetics, M/C 669, 808 South Wood Street, Chicago,
IL 60612, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92875 GTCCGGCGCCAGCTACCAACCGAGGAACCCAACATTGCCAAGAGGGTCCTCTTTCTCCTG 92934
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Rodentia; Sciurognath1; Muridae; Murinae; Mus.
1 (bases 1 to 1938)
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                     119938: gap of unknown length
129876: contig of 10038 bp in length
142943: gap of unknown length
143343: contig of 13267 bp in length
161164: contig of 17821 bp in length
161264: app of unknown length
180316: contig of 18052 bp in length
180416: gap of unknown length
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48714 c 48138 g 51580 t 3296 others
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Pred. No. 4.7e-24;
0; Mismatches 53; Indels
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Location/Qualifiers
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/db_xref-"taxon:10090"
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house mouse.
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                                                                                                                                                                                                     Consensus quality: 139878 bases at least 040
Consensus quality: 165603 bases at least 030
Consensus quality: 177139 bases at least 030
Consensus quality: 177139 bases at least 030
Consensus quality: 177139 bases at least 030
Estimated insert size: 183300; agarose-fp estimation
Estimated insert size: 200576; sum-of-contigs estimation
Quality coverage: 3.48 in Q20 bases; sum-of-contigs estimation
* NOTE: This is a "working draft' sequence. It currently
* consists of 30 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
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                                                           Web site: http://www.jgi.doe.gov
                                                                                                                                                Center clone name: RPCI-23_128D3
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Center: Joint Genome Institute
Center Code: JGI
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/protein_id="AAB36278.1"
/db_xref="G1:1488385"
/tb_xref="G1:1488385"
AAPAGRESCSRGHEKSRRYLYPRVVRQLPVEEDRPAKRIJFLLTTUFCQILMAE
ECVRAPLPPEDAPNAASLAPTPVSPVLEPFNLTSEPSDYALDLSTFLQQHPAAR"
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                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 1223)
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                                                                                                                                                                                                                  GenBank staff at the National Library of Medicine created thisentry [NCBI gibbsq 177109] from the original journal article. This sequence comes from Fig. 2A.

Location/Qualifiers
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Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-SEP-1996
                                                                                                                                       Kondratyev, A.D., Chung, K.N. and Jung, M.O.
Identification and characterization of a radiation-inducible
glycosylated human early-response gene
cancer Res. 56 (7), 1408-1502 (1996)
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Pred. No. 1.5e-46;
0; Mismatches 1; Indels
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 Partial, 1223 nt]
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99.68;
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Matches 257; Conservative
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Mus musculus clone RP23-128D3, WORKING DRAFT SEQUENCE, 30 unordered
Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

1 (bases 1 to 1758)

Schafer, H., Trauzold, A., Siegel, E.G., Folsch, U.R. and Schmidt, W.E. PRG1: a novel early-response gene transcriptionally induced by pituitary adepylate cyclase activating polypeptide in a pancreatic carcinoma cell line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (15-JUL-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata, Vertebrata, Euteleostomi,
Sciurognathi, Muridae, Murinae, Mus.
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                                                                                                                                     Trauzold,A.
Direct Submission
Submitted (05-MAR-1996) A. Trauzold, Laboratory of Molecular GastroenterAlogy-1st Dept. of Medicine, University of Kiel, Schittenhelmstrasse 12, Kiel, D-24105, FRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  169 CCCGTCCTCGAGCCCTTTAATCTGACTTCGGAGCCCTCGGACTACGCTCTGGACCTCAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                              Score 154.4; DB 11;
Pred. No. 2.5e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              51;
                                                                                                                                                                                                               Location/Qualifiers

1. 1758
/organism="Rattus norvegicus"
/db_xref="taxon:10116"
/cell_line="AR4-2J"
590. .1279
                                                                                            Cancer Res. 56 (11), 2641-2648 (1996)
96221139
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DOE Joint Genome Institute.
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Unpublished
2 (bases 1 to 203476)
DOE Joint Genome Institute.
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590. .1279
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76.78;
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/db_xref="GDB:738998"
complement(114300. .114430)
/note="WI-18721;The location is between each flanking site
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/note="stSG4264;The location is between each flanking site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hirakawa, Japan Science and Technology Corporation (JST), Advanced Databases Department: 5-3, Yonbancho, Chiyoda-ku, Tokyo 102-0081, Japan (Email:mikatckyo.jst.go.jp, URL.http://www.alis.tokyo.jst.go.jp/, Tel:81-3-5214-8491, Fax:81-3-5214-8470)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Japan Science and Technology Corporation (JST)
5-3, Yonbancyo, Chiyoda ku, Tokyo, 102-0081 Japan
5-7 For further infomation about this sequences, please visit our
sequence archive Web site (http://www-alis.tokyo.jst.go.jp/HGS/top.
html) or send email to webmaster@www-alis.tokyo.jst.go.jp.
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Shinas,. Tamlya,G., Oka,A. and Inoko,H.
Homo sapiens 2,229,817bp genomic DNA of 6p21.3 HLA class 1 region
Published Only in DataBase (1999) In press
(pases 1 to 200000)
Hirakawa,M., Yamaquchi,H., Imai,K. and Shimada,J.
Direct Submission
Submitted (21-SEP-1999) to the DDBJ/EMBI/GenBank databases. Mika
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/standard_name="D6S2115"
/note="SHGC-13451;The location is between each flanking
site of por animers."
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HLA Class I region,
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Phone:+81-463-93-1121, Fax:+81-463-94-8884,
The sequence is submitted by Human Genome Sequencing in ALIS
project of JST
                                                         61120 CCAGAGGACGCCCCTAACGCCGCATCCCTGGCGCCCACCCTGTGTCTCCCCGGTCGTCGAG
                                                                                                                                           CCAGAGGACGCCCCTAACGCCGCATCCCTGGCGCCCCACCCCTGTGTCTCCCCCCGTCTCTCGAG
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/db_xref="taxon:9606"
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/db_xref="GDB:4566033"
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/map="6p21.3"
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AUTHORS
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/db_xref="cDB-1581086"
//db_xref="cDB-1581086"
complement(153977. .154114)
/note="SGC34551;The location is between each flanking site
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            117236. .117362
/note="SGC34396,The location is between each flanking site
of PCR primers."
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IEX-1=radiation-inducible immediate-early gene [human, placenta,
                                                                                                                  /note="SHGC-10364; The location is between each flanking
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flanking site of PCR primers."
/db_xref="GDB:580497"
188925. .188989
/note="pml216;The location is between each
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ilarity 100.0%; Pred. No. 2.4e-47;
Conservative 0; Mismatches 0;
                                                                                                                                                                  complement(117961, .118093)
/note="SGC32809;The location is
of PCR primers."
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142184. 142339
/note=*KIAAA0170;The location is
of PCR primers."
/db_xref="GDB:4586652"
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                                                                                                                                                                                                                                                                                                      complement(142215. .142343)
/note="WI-15445; The location is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="GDB:594325"
complement(197650. .197804)
/note="cda01e04;The location
of pcR primers"
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/standard_name="D6S1376"
                                                                                   .117836)
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48336 c 49153 g 50053
                                                                                                 /standard_name="D6S2041"
                                                                 /db_xref="GDB:4580073"
complement(117712. .11
                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="GDB:4582352"
complement(165191, .16
/db_xref="GDB:4574312"
                                                                                                                                                  /db_xref="GDB:735115"
                                                                                                                                  site of PCR primers.
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Shiina, T., Tamiya, G., Oka, A., Takishima, N., Yamagata, T.,
Rikkawa, E., Iwata, K., Tomizawa, M., Okuaki, N., Kuwano, Y.,
Watanabe, K., Fukuzumi, Y., Itakura, S., Sugawara, C., Ono, A.,
Yamazaki, M., Tashiro, H., Ando, A., Ikemura, T., Soeda, E., Kimura, M.,
Bahram, S. and Inoko, H.
Molecular dynamics of MHC genesis unraveled by sequence analysis of
the 1,796,938-bp H.A. class I region
Proc. Natl. Acad. Sci. U.S.A. 96 (23), 13282-13287 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shina, T. and Takishima, N. Shina, T. and Takishima, N. Direct Submission

Direct Submission

Submitted (29-Jan.1999) to the DDBJ/EMBL/GenBank databases. Takashi Shina, Tokai University School of Medicine, Department of Molecular Life Science 2; Bohseidal, Isehara, Kanagawa 259-1193, Japan (E-mail:tshina@is.icc.u-tokai.ac.jp, Tel:81-463-93-1121, Fax:81-463-94-8884)

Location/Qualifiers
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Homo sapiens genomic DNA, chromosome 6p2l.3, HLA class I region,
clone:876L4, complete sequence.
                                                                                                                                                                        61 CTCACCATCGTCTTCTGCCAGATCCTGATGGCTGAAGAGGGTGYGCGGGGGCCCCTGCCT 120
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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42609, 42802
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72609, 43370
/rpt_family="MIR"
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20862. 21002
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21566. 2187
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19178. 19451
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121	CCAGAGAGGCCCCTAACGCCGCATCCCTGGCGCCCCTGTGTCCCCCGTCCTCGAG 180	
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241	CAACACCGGCGGCTTC 258	
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ORGANISM FERENCE AUTHORS	~	
TTLE TOURNAL REMARK	Geraghty, D. E. Large scale sequence analysis of the human MHC class I r Unpublished (1998) Fred Hutchinson Cancer Research Center	•
9 9 2 9	The Clinical Research Division 1100 Fairview Ave. N., P.O. Box 19024 Seattle, WA 98109-1024	
TITLE	nome	
EMARK	40	
MENT	sion: AC006049)	
	Sequence Quality Assessment: This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality zero. Ouality levels above 40 are expected to have less than 1 error in 10,000 bp. Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.	,
	Double stranded (DS) coverage: 58.8% DS or two chemistry coverage: 99.5% Single stranded regions: 2	
	Sequence Validation: This sequence has been validated by Multiple Complete Digest Mapping. Comparison of the experimentally derived map digest fragments with sequence-predicted fragments is given below.	

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PVSEVLEPFNLTSEPSTALDLSTFILQOHFAAF"
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                                10-NOV-1998
                   AF071596 1693 bp DNA PRI 10-NOV-1998
Homo sapiens apoptosis inhibitor (IEX-1L) gene, complete cds.
AF071596
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Submitted (10-JUN-1998) Tumor Immunology, Dana Farl
Institute, 44 Binney Street, Boston, MA 20115, USA
Location/Qualifiers
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RESULT

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/translation="MCHSRSCHPTMT1LQAPTPAPST1PGPRRGSGPE1FTFDPLPEP
AAAPAGRPSASRGHRKRSRRVLYPRVVRRQLPVEEPNPAKRLI.FLLLT1VFCO11.MAE
EGVPAPLPPEDAPNAASLAPTPVSPVLEPFNLTSEPSDYALDLSTFLQQHPAAF"
                                                                                                                                                                                                                                                                                              and
                                                                                                                                                                                                                                                      revised by [4]
2 (bases 1 to 508)
Schaefer, H., Trauzold, A., Lettau, P., Kalthoff, H., Foelsch, U.R. an Schmidt, W.E.
CDNA cloning and sequencing of a novel human early response gene and characterization of its expression in pancrealic carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (23-SEP-1997) H.Schaefer, Trauzold, Laboratory of
Molecular Gastroenterology, 1st Dept.of Medicine, University of
Kiel, Schittenhelmstrasse 12, Kiel, D-24105, FRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 (bases 1 to 1864)
Schafer, H., Diebel, J., Arlt, A., Trauzold, A. and Schmidt, W.E.
The promoter of human p22/PACAP response gene 1 (PRG1) contains
functional binding sites for the p53 tumor suppressor and for
06 - NOV - 3998
                                                                                                              Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Butheria;
Primates; Catarrhin1; Hominidae; Homo.
1 (bases 1 to 1864)
                                                                                                                                                                                                         Molecular
of Kiel,
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Location/Qualifiers
1. 1864
/Organism="Homo sapiens"
/db_rref="taxon:966"
/cell_iine="818-4"
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                                                                                                                                                                                 Direct Submission
Submitted (05-MAR-1996) A. Trauzold, Laboratory of
Gastroenterology, 1st Dept.of Medicine, University
Schittenhelmstrasse 12, Kiel, D-24105, FRG
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Pred. No. 6.3e-47;
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/db_xref="SWISS-PROT:P46695"
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/gene="PRG1"
563. .801
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3 (bases 1 to 1864)
Schaefer, H.
1864 bp
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/trānslation="MCHSRSCHPTWTILQAPTPAPST1PGPRRGSGPE1FTFUPLPEP
AAAPAGREGASRGHRKSRRYSLPSSGEYRRSGHSRCALPWSHWGTTRLQSLDLTCLL
FCLPLVRRQLPVEEPNYARLLFLLITTTVFCQILMAEEGVPAPLPPEDAPNAASLAPT
PVSFVLEPFNLTSPAALDLSTFLQQHPAAF"
393 c 369 g 285 L
                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniala; VerLebrata; Eutleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1309)

Wu,M.X., Ao,Z., Prasad,K.V.S., Wu,R. and Schlossman,S.F.

IEX-1L, an apoptosis inhibitor involved in NF-kappaB-mediated cell survival
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCAGAGGACGCCCTAACGCCGCATGTCTGGCCGCCCACCCCTGTGTCCCCCCGTCCTCGAG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA PRI 21-AUG-1998 protein (IEX-1L) mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                      Ao.2. and Wu.M.X.
Direct Submission
Submitted (17-DEC-1997) Tumor Immunology, Dana Farber Cancer Institute, 44 Binney Street, Boston, MA 02115, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18.1 CCCTTTAATCTGACTTCGGAGCCCTCGGACTACGCTCTGGACCTCAGCACTTTCCTCCAG
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ilarity 100.0%; Pred. No. 6.7e-47;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="type II membrane protein"
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/protein_id="AAC33558.1"
/db_xref="GI:3449376"
                                                                                                                                                                                                                                                                                      Science 281 (5379), 998-1001 (1998)
98369175
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/db_xref="taxon:9606"
1. 1309
/gene="IEX-1L"
                                                                                                        ... Joyne7 1309 bp
Homo sapiens anti-death
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                241 CAACACCGGCCGCCTTC 258
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AAAPAGRPSASRGHRKRSRRVLYPRVVRRQLPVEEPNPAKRLLFLLITIVFCQILMAE
EGVPAPLPPEDAPNAASLAPTPVSPVLEPFNLTSEPSDYALDLSTFLQQHPAAF"
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ilarity 100.0%; Pred. No. 6.8e-47;
Conservative 0; Mismatches 0;
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/db_xref="taxon:9606"
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/citation=[3]
/replace="g"
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/replace="t"
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/gene="dif-2"
/citation=[3]
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AC011578 Homo sapi
AC074092 Homo sapi
AC083783 Homo sapi
AL147951 Anopheles
AF102818 Mus muscu
AF005029 Halobacte
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AC069342 Homo sapi
AL147283 Anopheles
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Kumar,R., Pittelkow,M.R. and Warner,G.M.
Direct Submission
Submitted (11-AUG-1998) Nephrology Research, Mayo Clinic, 200 1st
Street SW, Rochester, MN 55905, USA
Location/Qualifiers
                                      AJ1004832 Homo sapi
                                                                            U80602 Mus musculu
                                                           Streptomy
                                                                   AC069521 Homo sap
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AC026986 Homo s
AL355502 Homo s
AC026758 Oryza s
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AP000030 Homo
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Identification and characterization of a radiation-inducible
glycosylated human early-response gene
Cancer Res. 56 (7), 1498-1502 (1996)
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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AP000212 H
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Ultraviolet Radiation in Human Keralinocyles
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Eukaryoca; Metazoa; Chordata; Vertebrata; Manumalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.

1 (bases 1 to 1230)

1 (bases 1 to 1230)

1 (bases 1 to 1230)

1 (facentiation and characterization of a novel monocyte/macrophage differentiation-dependent gene that is responsive to lipopolysaccharide, ceramide, and lysophosphatidylcholine Blochem. Blophys. Res. Commun. 235 (1), 4-9 (1997)
/translation="MCHSRSCHPTWT1LQAPTPAPST (PGPRRCSGPELFTFDPLPE)
AAAPAGRPSASRGHRKRSKRVLYPRVVRRQLPVEEPNPAKRLLFLLT1VFCQ1LMAR
EGVPAPLPPEDAPNAASLAPTPVSPVLEPFNLTSEPSDYALDLSTFLQQHPAAF"
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Submitted (11-AUG-1997) A. Pietzsch, Institute for Clinical
Chemistry and Laboratory Medicine, University of Regensburg,
Franz Josef-Straus-Allee II, 93053 Regensburg, FRG
3 (bases 1 to 1230)
Kondratyev.A.D., Chung.K.N. and Jung.M.O.
Identification and characterization of a radiation-inducible
glycosylated human early-response gene
Cancer Res. 56 (7), 1498-1502 (1996)
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Best Local Similarity 100.0%; Pred. No. 8.3e-47;
Matches 258; Conservative 0; Mismatches 0;
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    /organism="Homo sapiens"

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January 30, 2001, 19:23:39; Search time 1900.13 Seconds (Without alignments) 694.889 Million cell updates/sec
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1 GTCCGCCCCCACCTGCCAGT.....AGCAACACCCGGCCGCCTTC 258
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44: em_htg8:* 45: em_htg9:* 47: em_htg9:* 48: em_htg9:* 48: em_hum4:* 48: em_hum4:* 50: em_hum5:* 51: gb_pt5:* 52: gb_pt7:* 53: gb_pt7:* 54: gb_htg1:* 55: gb_htg1:* 56: gb_htg1:* 56: gb_htg1:* 56: gb_htg1:* 56: gb_htg1:* 56: gb_htg1:* 66: gb_htg1:* 67: gb_htg1:* 67: gb_htg1:* 67: gb_htg1:* 66: gb_htg1:* 67: gb_htg1:* 67: gb_htg1:*	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	AF083421 Homo sapi	Y14551 Homo sapien	AF039067 Homo sapi	AF071596 Homo sapi	X96438 H.sapiens P	ACO06165 Homo sapi	AB023051 Homo sapi	AP000512 Homo sapi	S81914 IEX-1=radia	X96437 R.norvegicu	AC074150 Mus muscu	X67644 M.musculus	AC022301 Mus muscu	A75448 Sequence 11	A78427 Sequence 11	AC011820 Homo sapi	166494 Sequence 14	AL356812 Streptomy	U40656 Myxococcus	283863 Mycobacteri	M64356 Ĥuman decay
ID	AF083421	HSDIF2	AF039067	AF071596	HSPRG1	AC006165	AB023051	AP000512	581914	RNPRG1	AC074150	MMGLY96	AC022301	A75448	A78427	AC011820	166494	SC1B2	MXU40656	MTCY159	HUMDAFC1
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% Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	99.4	29.8	58.6	58.0	54.0	17.1	17.1	16.7	16.7	15.6	15.4	15.3	15.3
Score	258	258	258	258	258	258	258	258	256.4	154.4	151.2	149.6	139.2	44	44	43.2	43	40.2	39.8	39.6	39.4
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              ·1 others
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1 (bases 1 to 297)
Sisson, D. R. and Gross, J.
HUMAN NUCLEIC ACID FROMENTS, ISOLATED FROM BRAIN ADRENAL TISSUE,
PLACENTA OR BONE NARROW
PATCHL: WO 9401548-A 20-JAN-1994;
MEDICAL ERS COUNCIL (18B): SIBSON DAVID ROSS (GB)
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              ATGTGTCACTCTCGCAGCTGCCACCCGACCATGACCATCCTGCAGGCCCCGACCCCGGCC
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Sequence 1134 from Patent WO9401548.
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Submitted (29-JAN-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jun 13, 2000 this sequence version replaced gi:8248590.

Center: Baylor College of Medicine
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                                                                                                                                                                                             1359 GAGAGAACGTATCCCAAACTGGGATTTCTAAGGCAACGCTAACTCAGAACACTACCGCCA 1418
                1192 TGGGCCCATTACTGGGCCCCGGGTCCTGGAGCCTTGAACCTGACCTGGAGTCCTGGGA 1251
                                                                                                                                   540 GCGAGAGCGTATCCCCAACTGGGACTTCCGAGGCAACTTGAACTCAGAACACTACAGCGG 599
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Mus musculus clone RP23-329K24, *** SEQUENCING IN PROGRESS **
                                                           360 GCCCCCACCCTGTGTCCCCCGTCCTCGAGCCCTTTAATCTGACTTCGGAGCCCTCGGA
                                                                                                                    CTACGCTCTGGACCTCAGCACTTTCCTCCAGCAACACCCGGCCGCCTTCTAACTGTGACT
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312 TGTGCCGGCGCCCCTGCCTCCAGAGGACGCCCCTAACGCCGCATCCC
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Contact: hgsc-help@bcm.tmc.edu
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HTG; HTGS_PHASE1.
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Chemistry: Dye-brimer Bodipy: 82% of reads
Chemistry: Dye-terminator Big Dye: 18% of reads
Assembly program: Phrap; version 0.990129
Consensus quality: 133377 bases at least Q00
Consensus quality: 159061 bases at least Q00
Consensus quality: 169068 bases at least Q00
Estimated insert size: 166938; sum-of-contigs estimation
Quality coverage: 2.3x in Q20 bases; sum-of-contigs estimation
                                                                                                            arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                       NOTE: This is a 'working draft' sequence. It currently consists of 59 contigs. The true order of the pieces is not known and their order in this sequence record is
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of 7086 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93036 TGCGCCCATTACTGCGCCCCCGGTCCTCGAGCCTTTGAACCTGAGCTTGGAGTCCTCGGA 93095
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                                                                                                                                                                                                                                                                                                                                                                                                                               CCCTCCACCATCCCGGGACCCCGGGCGGGCTCCGGAGATCTTCACCTTCGACCCT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          480 CCCCCCACTCCCCAAAAAAAATCCGAAAAACCACAAAAAACACACCAGGCGTACCTGGTGC
                                                                                                                                                                                                                                                                                                                              Length 203476;
                                                                                                                                                                                                                                                                                                                                                    0; Mismatches 144; Indels 134;
                                                                                                                                                                                                                                                            /clone_lib="RPCI mouse BAC library 23"
a 48714 c 48138 g 51580 t 3296 others
                                                 contig of 10713 bp in length
gap of unknown length
contig of 10038 bp in length
gap of unknown length
                                                                                                   contig of 13267 bp in length
gap of unknown length
contig of 17821 bp in length
                                                                                                                                                       in length
                                                                                                                                                                                 contig of 23060 bp in length
of 6164 bp in length
unknown length
of 7637 bp in length
                                                                                                                                                                                                                                                                                                                          DB 70;
                                                                                                                                          gap of unknown length
contig of 19052 bp in
gap of unknown length
                                      unknown length
                                                                                                                                                                                                                                                                                                                           17.1%; Score 210.6; DB 7(62.4%; Pred. No. 2.1e-38;
                                                                                                                                                                                                                     /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="RP23-128D3"
contig
gap of contig
contig
                                                                                                                                                                                            Location/Qualifiers
                                                                                                                             161164: 0
161264: 0
180316: 0
                                      109025:
                                                                119838:
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                                                  119738
                                                                                                                                                                                                                                                                                                                                        al Similarity 62.4
461; Conservative
95025
101189
101289
108926
109026
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161265
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ORIGIN
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growth
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Direct Submission

Submitted (29-JUL-1992) L. Lau, University of Illinois College of

Med., Dept. of Genetics, M/C 669, 808 South Wood Street, Chicago,

IL 60612, USA

2. (basses 1 to 1938)

Charles, C.H., Yoon, J.K., Simske, J.S., and Lau, L.F.

Genomic structure, CDNA sequence, and expression of gly96, a grow dator-inducible immediate-early gene encoding a short-lived

glycoxylated protein
                93203 GAGAGAACGTATCCCAAACTGGGATTTCTAAGGCAACGCTAACTCAGAACACTACCCCCA 93262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 CCCTCCACCATCCCGGGACCCCGGGGGCTCCGGTCCTGAGATCTTCACCTTCGACCCT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 CTCCCGGAGCCCGCAGCGGCCCCTGCCGGGCGCCCCCAGCGCCCTCTCGCGGGCCACCGAAAG 180
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540 GCGAGAGCGTATCCCCAACTGGGACTTCCGAGGCAACTTGAACTCAGAACATACACTACAGGG 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       712 ATGIGCCACTCGCGCAACCATCICCACATGACTGGCCTGAGGGCCCCTTCTCCAGCT 771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAGGCTTCTCTTTCTGCTGCTCACCATCGTCTTCTGCCAGATCCTGATGGCTGAAGAGGC 311
                                                                                                                                                                                                11-MAR-1993
                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1938)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ATGTGTCACTCTCGCAGCTGCCACCCGACCATGACCATCCTGCAGGCCCCGACCCGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1938;
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                                                                                                                                                                                                ROD
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Pred. No. 6.4e-38;
0; Mismatches 145;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
/strain="BALB/c"
/db_xref="taxon:10090" .
525 c 503 g 520
                                                                                                                                                                                                                                                              gly96 gene; glycosylated protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oncogene 8 (3), 797-801 (1993)
93173526
                                                                                                                                                                                                mRNA
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                                                                                         93263 AGAGACCGCGGGTCCTG 93281
                                                                                                                                                                                     M.musculus gly96 mRNA.
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62.2%;
                                                                        618
                                                                                                                                                                                                                                             X67644.1 GI:287803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 62.27
Matches 460; Conservative
                                                                  600 AGACGCCACCCGGTGCTTG
                                                                                                                                                                                                                                                                                                     Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           390
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ACCESSION
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ORIGIN
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AUTHORS
TITLE
JOURNAL
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TITLE
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MEDLINE
FEATURES
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                                                                                                                                                                                                                                               VERSION
KEYWORDS
SOURCE
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Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

1 (bases 1 to 1758)
Schafer, H., Trauzold, A., Siegel, E.G., Folsch, U.R. and Schmidt, W.E. PRGI: a novel early-response gene transcriptionally induced by pituitary adenylate cyclase activating polypeptide in a pancreatic carcinoma cell line
                                                                                                                                                             1042 CGGCGGACCATFAGGAATGAGATCCGTGAGATCCTTCCATCTTGTAGAGTCGCTTTAG 1101
                                                                                                                                                                                                                             1102 GGTGGCTGCGAGGTAGAGGGTTGGGGGTTGGTGGGGCTGTCACGGAGCGACTGTCGAGATC 1161
                                                                                              61 CCTCCACCATCCCGGGACCCCGGCGGGGTCCGGGGTCCTGAGATCTTCACCTTCGACCT 120
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                                                59 GGGAGGACTCGGGTGGGGGAGGACGTCCCGGCTGGATGAAGTCTGGTGGTGGTGGTCGTAA 118
                                                                                                             238 GGTGGCTGCGANGTANAGGGTTGGGGGGTTGGTGGTGGCTGTCACNGAGCGACTATCGACATC 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 CTCCCGGAGCCCGCAGCGGCCCCTGCCGGGCGCCCCAGCGCCTCTCGCGGGCACCGAAAG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (05-MAR-1996) A. Trauzold, Laboratory of Molecular Gastroenterology, 1st Dept.of Medicine, University of Kiel, Schittenhelmstrasse 12, Kiel, D-24105, FRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         178 CGGCGGACCATTAGGAATGAGATCCGTGGATCCTTCCATCTTCTTGAAGTCGCTTTAN
GCTTTGTGGGACTGGAGGAGCAGGAC - CCTGGAACTGCGGCAAAGTAGGAGAAG - AATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 11, Length 1758;
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                                                                                                                                                                                                                                                                                            1162 GCCTAGTAGTTCTGTGAACACAAATAAAATTGATTTACTGTC 1204
                                                                                                                                                                                                                                                                                                              298 GCCTANTATGTTCTGTGAACACAAATAAAATTGATTTACTGTC 340
                                                                                                                                                                                                                                                                                                                                                                                                              ROD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 242.4; DB 11;
Pred. No. 1.3e-45;
0; Mismatches 181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Rattus norvegicus"
/db_xref="taxon:10116"
/cell_line="AR4-2J"
590 .1279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cancer Res. 56 (11), 2641-2648 (1996) 96221139
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R.norvegicus PRG1 gene.
X96437
X96437.1 GI:1515318
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590, 1270
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62.1%;
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Matches 589; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Norway rat.
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
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Best Local 3
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ACCESSION
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ORIGIN
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TITLE
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                                                                                              982
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SOURCE
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                                                                                                                                                                                420
                                                                                                                                                             241 AACCCAGCCAAAAGGCTTCTCTTTCTGCTGCTCACCATCGTCTTCTGCCAGATCCTGATG 300
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CCCTCCACCATCCCGGGACCCCGGGGGGCTCCGGTCCTGAGATCTTCACCTTCGACCTT 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cloning of ARE-containing genes by AU-motif-directed display Genomics 54 (2), 278-286 (1998) 99047534
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Pred. No. 1.4e-58;
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Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 343)
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HOMO Sapiens partial MRNA; ID YG40-2.
AJ227914
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/cell_type="T lymphocyte"
/cell_line="T122.12"
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Best Local Similarity 97.1%;
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                                            832 GYGCGCTGCCCTGGAGTCACTGGGGAACGACCCGACTCCAGAGGCCTCGACCTGACCTGT
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/product="radiation-inducible immediate early response gene IEX1"
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EGVPAPLPPEDAPNASLAPTPVSPVLEPFNLTSEPSDYALDLSTFLQQHPAAF"
                                                         neug342] 477 bp mRNA PR1 02-SEP-1998
Homo Sapiens radiation-inducible immediate early response gene 1EX1
(TEX1) mRNA, complete cds.
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Kumarr, K. Kobayashi, T., Warner, G.M., Wu, Y., Salisbury, J.
Lingle, W. and Pittelkow, W.R.
A Novel Immediate Early Response Gene, IEX-1 Is Induced Ultraviolet Radiation in Human Keratinocytes
Oppublished
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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Kondratyev.A.D., Chung,K.N. and Jung,M.O. Identification and characterization of a glycosylated human early-response gene Cancer Res. 56 (7), 1498-1502 (1996)
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Pred. No. 3.1e-98;
0; Mismatches 0;
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Kumar,R., Pittelkow,M.R. and Warner,G.M.
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/codon_start=1
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/db_xref="taxon:9606"
/cell_type="keratinocyte;
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/replace="g"
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Primates; Catarrhini; Hominidae; Homo.
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Direct Submission
Submitted (05-MAR-1996) A. Trauzold, Laboratory of
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/db_xref="Sunss-prot: p46695"
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AAAPAGRPSASRGHPRKRSRRVLYPRVVRRQLDVEEPNRAKRLLFLLITIVFCCILMAE
EGVPAPLPPEDAPNAASLAPTPVSPVLEPFNLTSEPSDYALDLSTFLQQHPAAF"
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                                                              Foelsch, U.R. and
Castroenterology, 1st Dept.of Medicine, University of Kiel, Castroenternelmstrasse 12, Kiel, D-24105, FRG
2 (bases 1 to 508)
Schaefer, H., Trauzold, A., Lettau, P., Kalthoff, H., Foelsch, U.R. an schmidt, W.E.
CDNA cloning and sequencing of a novel human early response gene and characterization of its expression in pancreatic carcinoma
                                                                                                                               Gastroenterology In press
3 (bases 1 to 1864)
Schaefer, H.

Direct Submission
Submitted (23-SEP-1997) H.Schaefer, Trauzold, Laboratory of Molecular Gastroenterology, 1st Dept.of Medicine, University of Kiel, Schittenhelmsrasse 12, Kiel, D-24105, FRG
4 (bases 1 to 1864)
Schafer, H., Diebel, J., Arlt, A., Trauzold, A. and Schmidt, W.E.
The promoter of human p22/PACAP response gene 1 (PRG1) contains functional binding sites for the p53 tumor suppressor and for
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Location/Qualifiers
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90.7%; Pred. No. 1.8e-215;
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/gene="PRG1"
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/gene="PRG1"
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="818-4"
1. .562
/gene="PRG1"
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FEBS Lett. 436 (2), 139-143 (1998)
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                                                   CCTGTGTCCCCCGTCCTCGAGCCCTTTAATCTGACTTCGGAGCCCTCGGACTACGCTCTG
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AFO71596 AFO71596 1693 bp DNA PRI 10-NOV-1998 LOCUS AFO71596 1693 bp DNA PRI 10-NOV-1998 DEFINITION Homo sapiens apoptosis inhibitor (IEX-1L) gene, complete cds. ACCESSION AF071596 1 GI:3851531 KEYWORDS SOURCE human.
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/translation="MCHSRSCHPTMT11,0APTPAPS") PGPRRGSGPELFTFDP1,PEP
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FCLPLVRRQLPVEEPNPAKRLLFLLLTIVFCQILMAEEGVPAPLPPEDAPNAASLAPT
PVSPVLEPFNLTSEPSDYALDLSTFLQQHPAAF"
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               Vertebrata;
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Wu,M.X. and Ao.Z.
Direct Submission
Submitted (10-JUN-1998) Tumor Immunology, Dana
Institute, 44 Hinney Street, Boston, MA 20115,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1048.6; DB 1
Pred. No. 2.6e-231;
0; Mismatches 4;
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/db_xref="taxon:9606"
359. .1693
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/gene="IEX-1L"
/note="immediate
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/gene="IEX-1L"
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/translation-"MCHSRSCHPTWILQAPTPAPSTIPGPRRGSGPEIFTEDPLPEP
AAAPAGRPSASRGHRKSRRVSLPSSGEYRRSGHSRCALPWSHWGTTRLOSLDLTCLL
FCLPLVRRQLPVEEPNPAKRLFKLLFLITIVFCQILMAFEGVPAPLPPEDAPNAASLAPT
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Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.
1 (bases 1 to 1309)
Wu,M.X., Ao,Z., Prasad,K.V.S., Wu,R. and Schlossman,S.F.
IEX-1L, an apoptosis inhibitor involved in NF-kappaH-mediated
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2 (bases 1 to 1309)
Ao,z. and Wu.M.X.
Direct Submission
Submitted (17-DEC-1997) Tumor Immunology, Dana f
                                PRI
(IEX-1L) mRNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85.4%; Score 1048.6; DB 10;
llarity 91.1%; Pred. No. 2.7e-231;
Conservative 0; Mismatches 4; In
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/codon_start=1
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                                                                                                                                                                                                                                                                                    , 44 Binney Street, Boston,
Location/Qualifiers
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                                                                                                                                                                                                     Science 281 (5379), 998-1001 (1998)
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/db_xref="taxon:9606"
1. 1309
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/protein_id-"AAC32558.1"
/db_xref-"GI:3449376"
                            1309 bp mkNA
anti-death protein
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/gene="IEX-1L"
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                                                                    GI:3449375
                                         Homo sapiens
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STS 101440. //OCE="Of PCR" / OF PCR /	STS 117236. Anotes STS Complem STS Complem / Standa	STS Complem // Ab. xre Complem // Ab. xre Complem // Ab. xre STS // Ab. xre STS // Ab. xre Complem // Ab. xr	STS (db) xre complem STS (note:) / note:) / note:) / strength / note:) / note: /	STS Complem STS Assured //standar //note="" //note="" //note=""	STS / ABS.XTS 188925. / ABS.XTS / AB	DASE COUNT 52458 a 48336	Ouery Match Best Local Similarity 91 Matches 1203; Conservative Oy 1 ATGGTCACTCTCGCAGG	Oy 61 CCCTCCACCATCCCGGGAC Db 97723 CCCTCCACCATCCCGGGAC Oy 121 CTCCCGGAGCCCGCAGCGG Oy 12783 CTCCCGGAGCCCGCAGCGG Oy 181 CGCAGCCGCAGGGTTCTCT IIIIIIIIIIIIIIIIIIIIIIIIIIIIII
61518 CTAATTAATATTATATGTATGTACGTCCTCCTAGGTGATGGACGTGTACGTAA 61577 789 TATTTATTTTAACTTATGTACGTGGAGGTGTCGAGGTGTCCCTCCTGCTGTAAATGCAGGTCTCT 848	61698 AGGAGAAGAATGGGGAGGACTCGGGTGGGGGAGGACGTCCGGCTGGGATGAAGTCTGG 61757 969 TGGTGCGTCGTAAGTTAAGAGGTGACTGCATCCTCCAGCTCCAACTCCGTCTTGTA 1028 11111111111111111111111111111111111	AACTCGCCTTTAGGGTGGCTGCGAGGTAGAGGGTTGGGGGTTGGTGGGCTGTCACGGAGC	APO00512 APO00512 LOCUS APO00512 APO00512 DEFINITION Homo sapiens genomic DNA, chromosome 6p21.3, HLA Class I region, section 11/20. ACCESSION APP00612	SOUNCE Homo sapiens DNA. SOUNCE Homo sapiens DNA. ORGANISM Homo sapiens ENkaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia: Eutheria: Primates: Cararrhin: Hominidae: Homo	REFERENCE 1 (sites) AUTHORS Shiina,S., Tamiya,G., Oka,A. and Inoko,H. TITLE Homo sapiens 2,229,817bp genomic DNA of 6p21.3 HLA class I region JOURNAL, Published Only in DataBase (1999) In press REFERENCE 2 (bases 1 to 20000) AUTHORS HILTAKAWA,M., Yamaguchi,H., Imai,K. and Shimada,J.	TITLE Direct Submission JOURNAL SUbmitted (21-26P-1999) to the DDBJ/FMBL/GenBank databases. Mika Hirakawa Japan Science and Technology Corporation (JST), Advanced Databases Department, 5-3, Yonbancho, Chiyoda-ku, Tokyo 102-0081, Japan (E-mail:mikatokyo.jst.go.jp.)	URL:http://www.talis.tokyo.jst.go.jp/, Tel:81-3-5214-8491, Fax:81-3-5214-8470) COMMENT This sequence is conducted by Tokai University as a JST sequencing Team. Principal Investigator: Hidetoshi Inoko Ph.D Phone:+81-463-93-1121, Fax:+81-463-94-8884, The sequence is submitted by Human Genome Sequencing in ALIS project of JST	Japan Science and Technology Corporation (JST) 5-3, Yonbancyo, Chiyoda-ku, Tokyo, 102-0081 Japan For further infomation about this sequences, please visit our sequence archive Web site (http://www-alis.tokyo.jst.go.jp/HGS/top. html) or send email to webmaster@www-alis.tokyo.jst.go.jp. FEATURES Location/Qualifiers source //organism="Homo sapiens" //db_xrefe=texon:9606" //map="6p21.3"

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:="sLSG4264;The location is between each flanking site;"staf="GDB:4566033"
:enent(114197...114328)
idard_name="D6S2115"
=="SHGC-13451;The location is between each flanking of PCR primers."
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ref-"GOB:735115"
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Shiina.T. and Taishima.N. Direct Submission Submission (29-JAN-1999) to the DDBJ/EMBL/GenBank databases. Takashi Shiina, Tokai University School of Medicine, Department of Molecular Life Science 2; Bohseidai, Isehara, Kanagawa 259-1193, Japan (E-mall:tshiina@is.icc.u-tokai.ac.jp, Tel:81-463-93-1121, Fax:81-463-94-88884)
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Shilaar., Tamiya,G., Oka,A., Takishima,N., Yamagata,T.,
Kikkawa,E., Iwata,K., Tomizawa,M., Okuaki,N., Kuwano,Y.,
Watanabe,K., Fukuzumi,Y., Itakura,S., Sugawara,C., Ono,A.,
Warazaki,M., Tashiro,H., Ando,A., Ikemura,T., Soeda,E., Kimura,M.,
Bahram,S. and Inoko,H.,
Molecular dynamics of MHC genesis unraveled by sequence analysis of
the 1,796,938-bp HLA class I region
Proc. Natl. Acad. Sci. U.S.A. 96 (23), 13282-13287 (1999)
                                                                                                                                               TATCCCCAACTGGGACTTCCGAGGCAACTTGAACTCAGAACACTACAGGGGAGACGCCAC 15320
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens genomic DNA, chromosome
clone:876L4, complete sequence.
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                                                                                                                   Score 1080.4; DB Pred. No. 1e-238; 0; Mismatches 1
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                       sapiens"
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Location/Qualifiers
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                     /organism="Homo s
/db_xref="taxon:9
/chromosome="6"
/clone="876L4"
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21396 c 21
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llarity 91.4%;
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/note="high quality variation versus 3' overlapping clone" 40509. .41109
//rpt_family="Alu" 42609. .4592
//rpt_family="Alu" 43240. .43370
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Best Local Similarity 91.4%; Pred. No. 1e-238;
Matches 1203; Conservative 0; Mismatches 1; Indels 112;
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/rpt_family"MIR"

43493. .4379. ...

/rpt_family"Alu"

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           complement(34547. .34595)
/rpt_family="MIR"
complement(36673. .36954)
/rpt_family="Alu"
complement(37002. .37230)
/rpt_family="Alu"
complement(40018. .40170)
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Fred Hutchinson Cancer Research Center
The Clinical Research Division
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Homo sapiens clone UWGC:y54c125 from 6p21, complete sequence.
AC006165
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Janer, M., Guillaudeux, T., Vu, Q., Kutyavin, T., Harter, H. and Geraghty, D.E.
                                                                                                                                                                                                                                                                                                                                                                                                                  ATCTITCHAGETCGCCTTTAGGGTGGCTGCGAGGTAGAGGGTTGGGGGTTGGTGGGCTTG
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                                                                                                    TATITGCTCCTAATTAATATTATATGTATTTATGTACGTCCTCCTAGGTGATGTGTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (08-DEC-1998) Human Genome Center, University Washington, Box 352145, Seattle, WA 98195, USA University of Washington Human Genome Center Box 352145, Seattle, WA 98195 Contact: Daniel E. Geraghty (geraghty@fhcrc.org)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1100 Fairview Ave. N., P.O. Box 19024 Seattle, WA 98109-1024 Classes 1 to 44118) Geraghty, D. E. and Olson, M.V.
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Sequence Validation:
This sequence has been validated by Multiple Complete Digest
Mapping. Comparison of the experimentally derived map digest
fragments with sequence-predicted fragments is given below
Small fragments below a variable cutoff (approximately 400-600bp)
are not mapped and hence do not appear in the table. There are no
significant remaining discrepancies between the experimental and
predicted values. Uniquely ordered fragment groups are separated
by dashed lines.
                                                                                                                        l error in 10,000 bp.
Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.
                                                                                          zero.
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                                     Sequence Quality Assessment:
This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality Quality levels above 40 are expected to have less than 1 error in 10,000 bp.
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/sub_clone="UWGC:y54c125"
/cell_line="CGM1"
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1. .44118
/organism="Homo sapiens"
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                                                                                                                                                                                               (DS) coverage:
                                                                                                                                                                                               Double stranded (DS) coverage:
DS or two chemistry coverage:
Single stranded regions:
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/rpt_family="MER3"
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2649. .2956
/rpt_family="Alu"
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/rpt_family="Alu"
1797. .2378
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/poor_ord_id="AaB36278.1"
/db_xref="G1:1488385"
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/db_xref="G1:1488385"
/db_xref="G1:1488385"
/db_xref="G1:1488386"
/db_xref="G1:14888
Identification and characterization of a radiation-inducible glycosylated human early-response gene cancer Res. 56 (7), 1498-1502 (1996) 96181295 GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 177109] from the original journal article. This sequence comes from Fig. 2A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCCTCCACCATCCCGGGACCCCGGCGGGGCTCCGGTCCTGAGATCTTCACCTTCGACCCT 120
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Pred. No. 3.7e-
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/db_xref="taxon:9606"
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/gene="IEX-1"
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/gene="IEX-1"
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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56: gb_htg3:*
57: gb_htg1:*
60: gb_htg2:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ž	Description	Y14551 Homo sapien	S81914 IEX-1-radia	AC006165 Homo sapi	AB023051 Homo sapi	AP000512 Homo sapi	AF039067 Homo sapi	AF071596 Homo sapi	X96438 H.saplens P	AF083421 Homo sapi	AJ227914 Homo sapi	X96437 R.norvegicu	AC074150 Mus muscu	X67644 M.musculus	AC022301 Mus muscu	A75448 Sequence 11	A78427 Sequence 11	G62116 1899 Human	AL355388 Homo sapi	A75468 Sequence 11	A78447 Sequence 11	AC026631 Homo sapi
	ID	HSDIF2	S81914	AC006165	AB023051	AP000512	AF039067	AF071596	HSPRG1	AF083421	HSA227914	RNPRG1	AC074150	MMG1.Y96	AC022301	A75448	A78427	G62116	AL355388	A75468	A78447	AC026631
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RNA-BINDING (RNP1) (BY SIMILARITY).
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 5
 Yan R., Rychlik W., Etchison D., Rhoads R.E.; "Amino acid sequence of the human protein synthesis initiation factor
 Mader S., Lee H., Pause A., Sonenberg N.;

"The translation initiation factor eIF-4E binds to a common motif
shared by the translation factor eIF-4 gamma and the translational
repressors 4E-binding proteins.";

Mol. Cell. Biol. 15:4990-4997(1995).

-! FUNCTION: COMPONENT OF THE PROPELEX EIF-4, WHICH IS
INVOLVED IN THE RECOGNITION OF THE MRNA CAP, ATP-DEPENDENT
UNAINDING OF 5'-TERMINAL SECONDARY STRUCTURE AND RECRUITMENT OF
MRNA TO THE RIBOSOME.

-!- PTH: PHOSPHORYLATED AT WULTIPLE SITES IN VIVO.

-! SIMILARITY: CONTAINS I RNA RECOGNITION MOTIF (RRM).

-! SIMILARITY: THE C-FERMINAL REGION IS SIMILAR TO THE N-TERMINAL
REGION OF WHEAT EUKARYOTIC INITIATION FACTOR (ISO)4F SUBUNIT P82.
 Gaps
 "Overlapping open reading frames revealed by complete nucleotide sequencing of turnip yellow mosaic virus genomic RNA."; Nucleic Acids Res. 16:6157-6173(1988).

-:- MISCELLANBOUS: THE 2006 KDA PROTEIN IS POTENTIALLY A POLYPROTEIN (BY HOMOLOGY TO THE LONGER PROTEIN OF THE SINDBIS VIRUS).
 01-FEB-1995 (Rel. 31, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
EUKARYOTIC TRANSLATION INITIATION FACTOR 4 GAMMA (EIF-4-GAMMA) (EIF-
4G) (EIF4G) (P220).
 2: RNA-directed RNA polymerase; Polyprotein; ATP-binding.
976 983 ATP (BY SIMILARITY).
1631 1665 POLYMERASE SITE (BY SIMILARITY).
1844 AA; 206640 MW; A016D758CB3D128C CRC64;
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 6
 83
 Length 1844;
 35 VPAPLPPEDAPNA----ASLAPTPVSPVLEPFNLTSEPSDYALDLSTFLQQHP
 Indels
 DB 1;
 Score 68.5; DB
Pred. No. 44;
6; Mismatches
 AA
 Biol. Chem. 267:23226-23231(1992).
 Haenni A.L.;
 MEROPS; C21.001,
INTERPRO; IPRO00606; -.
PFAM; PF01443; Viral_helicasel; 1.
Transferase; RNA-directed RNA poly
Transferase; RNA-directed RNA POLY
976 983 ATP (POLY)
 EMBL; X07441; CAA30322.1; ALT_SEQ.
 TISSUE-BRAIN;
MEDLINE-93054654; PubMed-1429670;
 SEQUENCE OF 408-525 FROM N.A.
MEDLINE-95379845; PubMed-7651417;
 ;
9
 15.5%;
35.2%;
 Conservative
 STANDARD;
Boyer J.C.,
 Homo sapiens (Human)
 S01956.
 Similarity
 SEQUENCE FROM N.A.
 PIR; S01956; S0
MEROPS; C21.001
 Query Match
Best Local Simi
Matches 19;
 gamma.
 IF4G_HUMAN
Q04637;
 SEQUENCE
 eIF-4
 IF4G_HUMAN
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 OF
 Q.F
 N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
H -> Y (IN DIFFUSE GASTRIC CANCER).
/FTId-VAR_001306.
T -> P (IN DIFFUSE GASTRIC CANCER).
D-> G (IN DIFFUSE GASTRIC CANCER).
 N -> S (IN LOBULAR BREAST CARCINOMA)
/FTId=VAR_001309.
 PFAM; PF00028; caunears...
PRINTS; PR00205; CADHERIN.
PROSITE; PS00232; CADHERIN.
Cell adhesion: Glycoprotein; Phosphorylation; Transmembrane;
Calcium-binding; Repeat; Signal; Disease mutation; Polymorphism.
POTENTIAL.
 MISSING (IN GASTRIC CARCINOMA; LOSS HETEROZYGOSITY).
 /FTIG-VAR_001318.

R -> Q (IN DIFFUSE GASTRIC CANCER).
/FTIG-VAR_001319.
A -> T (IN ENDOMETRIAL CANCER; LOSS
 MISSING (IN GASTRIC ADENOCARCINOMA).
/FTId-var_001308.
 /FTId=vAR_001312.
MISSING (IN GASTRIC CARCINOMA).
/FTId=vAR_001313.
FTId=vAR_001314.
/FTId=vAR_001314.
 D -> A (IN DIFFUSE GASTRIC CANCER). /FIId-vAR_001311.
 T -> L (IN DIFFUSE GASTRIC CANCER)
/FIId=VAR_001316.
V -> N (IN DIFFUSE GASTRIC CANCER)
 /FTId=VAR_001317.
V -> A (IN DIFFUSE GASTRIC
 /FIId=VAR_008713.
A -> T (IN THYROID CANCER)
 EXTRACELLULAR (POTENTIAL).
 POTENTIAL.
CYTOPLASMIC (POTENTIAL).
 EPITHELIAL - CADHERIN.
 E -> D.
/FTId=VAR_001310.
 D -> G (IN DIFFUS
 /FTId=VAR_001315
 HETEROZYGOSITY
 CADHERIN 1. CADHERIN 2. CADHERIN 3. CADHERIN 4. CADHERIN 4.
 SER-RICH.
 PFAM; PF01049; Cadherin_C_term; 1. PFAM; PF00028; cadherin; 5.
 ^
 EMBL, 213009; CAA78353.1; -. EMBL, 218923; CAA79356.1; -. EMBL, X12790; CAA31279.1; -. EMBL; L34545; AAA21764.1; -.
 INTERPRO; IPR000233; -.
 27
8882
707
707
731
3375
882
882
893
893
851
 558
637
123
 193
 244
 315
 370
 400
 423
 463
 470
 470
 473
 592
 598
 487
 617
 PIR, S25141; IJHUCE.
PIR, S37654; S37654.
HSSP; P09803; 1SUH.
MIM; 192090; -.
 838
558
637
123
 315
 193
 244
 370
 400
 418
 463
 470
 470
 473
 487
 592
 598
 CARBOHYD
 TRANSMEM
 SIGNAL
PROPEP
CHAIN
 VARIANT
 VARIANT
 VARIANT
 DOMAIN
REPEAT
 REPEAT
REPEAT
 REPEAT
REPEAT
 VARIANT
 VARIANT
 VARIANT
 VARIANT
 VARIANT
 VARIANT
 DOMAIN
 /ARIANT
 VARIANT
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 /ARIANT
 VARIANT
 DOMAIN
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/FTId-VAR\_001320

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 SEQUENCE FROM N.A.
MEDLINE=95024004; Pubmed=7937872;
MEDLINE=95024004; Pubmed=7937872;
MEDFESSION A., Farang Q., Tonks N.K.;
"Expression of DEP-1, a receptor-like protein-tyrosine-phosphatase, is enhanced with increasing cell density.";
Proc. Natl. Acad. Sci. U.S.A. 91:9680-9684(1994).
-!- FUNCTION: MAY CONTRIBUTE TO THE MECHANISM OF CONTACT INHIBITION OF CELL GROWTH.
 588 VNDNAPIPEPR-----TIFFCERNPKPQVINI---IDADLPPNTSPFTAELTHGA 634
 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
115-DEC-1998 (Rel. 37, Last annotation update)
PROTEIN-TYROSINE PHOSPHATASE ETA PRECURSOR (EC 3.1.3.48) (R-PTP-ETA)
PUPPRJ OR DEP1.
 Gaps
 1 VRRQLPVEEPNPAKRLLFLLTIVFC-----GILMAEEGVPAPLPPEDAPNAASLA--- 51
 -!- CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)0 -
PROTEIN TYROSINE + ORTHOPHOSPHATE.
-!- SUBCELLUAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- FTM: N- AND O-GLYCOSYLATED.
-!- SIMILARITY: CONTAINS 1 PROTEIN-TYROSINE PHOSPHATASE DOMAIN.
-!- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.
-!- DATABASE: NAME-PROW; NOTE-CD guide CD148 entry.
-!- WMMA-"http://www.ncbi.nlm.nih.gov/prow/cd/cd148.htm".
 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 /FTId=vAR_001321.
S -> G (IN OVARIAN CANCER; LOSS OF HETEROZYGOSITY).
/FTId=vAR_001322.
 33;
 POTENTIAL.
PROTEIN-TYROSINE PHOSPHATASE ETA.
 -> V (IN ENDOMETRIAL CANCER).
 Length 882;
 INTERPRO; IPRO00242; ...
INTERPRO; IPRO00387; ...
INTERPRO; IPRO01867; ...
INTERPRO; IPRO0187; ...
PFAM; PF00102; V_phosphatase; 1.
PFAM; PF00041; fn3; 5.
PRINTS; PR00700; PRTYPHPHTASE.
PROSITE; PS00038; TYR_PHOSPHATASE_1; 1.
PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.
PROSITE; PS00055; TYR_PHOSPHATASE_2; 1.
PROSITE; PS00055; TYR_PHOSPHATASE_2; 1.
SIGNAL 35
PROTEIN-TYROSINE PHOSPHATASE GOTENTIAL.
CHAIN 36 1337
PROTEIN-TYROSINE PHOSPHATASE E
 31; Indels
 SANWTIQYNDPTQESIILKP-KMALEVGDYKINLKLMDNQN 674
 52 ------PIPVSPVLEPFNLTSEPSDYALDLSTFLQQH 82
 DB 1;
 AA.
 11; Mismatches
 Score 68.5; 1
Pred. No. 20;
 1337
 or send an email to license@isb-sib.ch).
 15.5%;
25.7%;
 EMBL; U10886; AAB36687.1; -.
 26, Conservative
 STANDARD;
711
 838
 Similarity
711
 838
 HSSP; P18052;
 MIM; 600925
 PTPJ_HUMAN
 Query Match
Best Local 3
VARIANT
 VARIANT
 012913
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modified and this statement is not removed. Usage by and for commercial cutifies requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
 1;
 EMBL outstation
between the Swiss institute of Bioinformatics and the EMBL outstatio
the European Bioinformatics institute. There are no restrictions on
use by non-profit institutions as long as its content is in no
 CADI_HUMAN STANDARD; PRT; 882 AA.
P12870: 014216;
01-0CT-1989 (kel. 12, Created)
01-0UL-1993 (Rel. 26, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
EPITHELIAL-CADHERIN PRECURSOR (E-CADHERIN) (UVOMORULIN) (CAM 120/80).
 Gaps
 MEDLINE-94380041; PubMed-8093045;
Bussemakers M.J., Giroldi L.A., van Bokhoven A., Schalken J.A.;
"Transcriptional regulation of the human B-cadherin gene in human
prostate cancer cell lines: characterization of the human E-cadherin gene promoter.";
 Birchmeier W.;
 Mansouri A., Spurr N., Goodfellow P.N., Kemler R.;
Characterization and chromosomal localization of the gene encoding
the human cell adhesion molecule uvomorulin.";
Differentiation 38:67-71(1988).
 Bussemakers M.J.G., Mees S.G.M., van Bokhoven A., Debruyne F.M.J.,
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
 Schalken J.A.; "Molecular cloning and characterization of the human E-cadherin
 ;
 MEDLINE-94306394; Pubmed-8033105;
Becker K.-F., Atkinson M.J., Reich U., Becker I., Nekarda H.,
Siewert J.R., Hoefler H.;
 Length 181;
 Indels
 Kelker W., Warda A., Oda T., Hirohashi S., Kemler R., Bi
Submitted (XXX-1992) to the EMBL/GenBank/DDBJ databases.
 9F4831DCEB7DFF2A CRC64;
 Biochem. Biophys. Res. Commun. 203:1284-1290(1994)
 van Roy F.;
(CDH1) gene.";
 Query Match 15.5%; Score 68.5; DB 1; Best Local Similarity 45.9%; Pred. No. 3.5; Matches 17; Conservative 5; Mismatches 14;
 33 EGVPAPLPPEDAPNA-ASLAPTPVSPVLEPFNLTSEP 68
 MEDLINE-98415721; Pubmed-9744472;
Berx G., Becker K.-F., Hoefler H.,
"Mutations of the human E-cadherin
 MEDLINE-93211394; PubMed-8459805;
 MEDLINE-89031725; PubMed=3263290;
 Mol. Biol. Rep. 17:123-128(1993)
 EMBL; AL050173; CAB43307.1; -.
 181 AA; 19799 MW;
 SEQUENCE OF 172-311 FROM N.A.
 dum. Mutat. 12:226-237(1998).
 VARIANTS ALA-370 AND ASN-473
 SEQUENCE OF 1-16 FROM N.A.
 Hypothetical protein
 (Human)
 CDH1 OR UVO OR CDHE.
Homo sapiens (Human)
 REVIEW ON VARIANTS.
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 gene promoter.
 TISSUE-LIVER;
 NON_TER
SEQUENCE
 CAD1_HUMAN
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 VARIANTS GASTRIC CARCINOMA ASP-400 DEL AND ASP-418--PHE-423 DEL.
MBDLLIRB-91197648; PUDMed-9045944;
Tamura G., Sakata K., Nishizuka S., Maesawa C., Suzuki Y., Iwaya T.,
Terashima M., Saito K., Satodate R.;
"Inactivation of the E-cadherin gene in primary gastric carcinomas and
gastric carcinoma cell lines.";
"Upp. J. Cancer Res. 87:1153-1159(1996).
 -!- SUBUNIT: HOMODIMER.
-!- SUBUNIT: HOMODIMER.
-!- SUBUNIT: HOMODIMER.
-!- SUBUNIT: HOMODIMER.
-!- SUBUNIT: NON-NEURAL EPITHELIAL TISSUES.
-!- DISEASE: DEFECTS OF CHI IS REGARDED AS ONE OF THE MAIN MOLECULAR EVENTS INVOLVED IN DYSFUNCTION OF THE CELL-CELL ADHESION SYSTEM, TRIGGERIAC CANCER INVASION (GASTRIC, BREAST, OVARY, ENDOMETRIUM AND THYROLD) AND METASTASIS.
-!- SIMILARITY: BELONGS TO THE CADHERIN FAMILY.
 Shimoyama Y., Birchmeier W.,
 Hirohashi S.;
in invasive lobular carcinoma
 cancer patients.";
J. Hun. Genet. 44:177-180(1999).
-1. FUNCTION: CADHERINS ARE CALCIUM DEPENDENT CELL ADHESION PROTEINS.
THEY PREFERENTIALLY INTERACT WITH THEMSELVES IN A HOMOPHILIC MANNER IN CONNECTING CELLS; CADHERINS MAY THUS CONTRIBUTE TO THE SORTING OF HETEROGENEDIS CELL TYPES. E-CADHERIN INS A POTENT INVASIVE SUPPRESSOR ROLE.
 "E-cadherin gene mutations in human gastric carcinoma cell lines."; Proc. Natl. Acad. Sci. U.S.A. 91:1858-1862(1994).
 s:
 MEDLINE-94355985; PubMed-8075649; Kisinger J.I., Berchuck A., Kohler M.F., Boyd J.; Mutations of the E-cadherin gene in human gynecologic cancers."; Nat. Genet. 7:99-102(1994).
 VARIANTS GASTRIC CARCINOMA GLY-244 AND ALA-487.
MEDLINE-99253140; PubMed-10319582;
Yoon K.-A., Ku J.-L., Yang H.-K., Kim W.H., Park S.Y., Park J.-G.;
"Germline mutations of E-cadherin gene in Korean familial gastric
 tumors.";
"E-cadherin gene mutations provide clues to diffuse type gastric
 Muta H., Noguchi M., Kanai Y., Ochiai A., Nawata H., Hirohashi
"E-cadherin gene mutations in signet ring cell carcinoma of the
 MEDLINE-98196671; PubMed-9537325; Guilford P., Hopkins J., Harraway J., McLeod M., McLeod N., Harawira P., Taite H., Scoular R., Miller A., Reeve A.E.; "E-cadherin germine mutations in familial gastric capicer."; Nature 392:402-405(1998).
 GYNECOLOGIC CANCERS THR-617; VAL-711 AND GLY-838
 MEDLINE-97138061; PubMed-89955087;
Soares P., Berx G., van Roy F., Sobrinho-Simoes M.;
"E-cadharin gene alterations are rare events in thyroid
Int. J. Cancer 70:32-38(1997).
 VARIANT GASTRIC ADENOCARCINOMA GLY-274--PRO-277 DEL
 SER-315
 MEDLINE-94173928; PubMed-8127895;
Oda T., Kanai Y., Oyama T., Yoshiura K.,
Sugimura T., Hirohashi S.;
 Jpn. J. Cancer Res. 85:1035-1039(1994).
[8]
 MEDLINE-55049851; Pubmed-7961105;
Kanai Y., Oda T., Tsuda H., Ochiai A.,
"Point mutation of the E-cadherin gene
 J. Cancer Res. 87:843-848(1996).
 VARIANT GASTRIC CARCINOMA PRO-193.
 VARIANT LOBULAR BREAST CARCINOMA
 MEDLINE-96390918; PubMed-8797891;
 Cancer Res. 54:3845-3852(1994).
 VARIANT THYROID TUMOR THR-592
 VARIANTS ASP-336 AND ILE-470
 breast.
 VARIANTS
 stomach.
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EMBL; J052.

DR PIR; A31107; A311.

DR PGD; S0006152; FAS2.

DR NITERPRO; IPR000255; --

DR INTERPRO; IPR000255; --

DR NTERPRO; IPR000258; --

DR NOSITE; PS00012; PHOSPHOPANTETHEINE; 1.

DR PROSITE; PS00606; B_KETOACYL_SYNTHASE; 1.

KW Transferase; NaDP; Phosphopantetheine; 0xidoreductase;

KW Transferase; NaDP; Phosphopantetheine; 1.

P ACYL CARRIER.

FT DOMAIN 682 881 BETA-KETOACYL REDUCTASE.

FT DOMAIN 7 1894 BETA-KETOACYL SYNTHASE.

DOMAIN 180 PHOSPHOPANTETHEINE; 1.

RETA-KETOACYL SYNTHASE.

1312 BETA-KETOACYL SYNTHASE.

1312 BETA-KETOACYL SYNTHASE.

1312 BETA-KETOACYL SYNTHASE.

1313 ARCOBESSI3 CRC64;

1.ength 1894;

G->S: CERULENIN-RESISTANCE.

1.ength 1894;
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LONG-CHAIN FATTY ACIDS FROM ACETYL-COA, MALONYL-COA AND NADPH.

THE ALPHA SUBBUIT CONTAINS DOMAINS FOR: ACYL CARRIER PROTEIN,
3-OXOACYL-IACYL-CARRIER PROTEIN) REDUCTARE, AND 3-OXOACYL-IACYL-CARRIER PROTEIN) SYMTHASE. THIS SUBBUIT COMPLIATES THE BINDING
OF THE SIX BETA SUBBUNITS. TO THE ENZYME COMPLEX.

-!-CATALYTIC ACTIVITY: ACETYL-COA + N MALONYL-COA + ZN NADPH =
LONG-CHAIN FATTY ACID + (N+1) COA + N CO(2) + 2N NADPH -)
-!-CATALYTIC ACTIVITY: ACYL-CARRIER PROTEIN] + MALONYL-(ACYL-CARRIER PROTEIN] + CO(2) +
-!-CARRIER PROTEIN] = 3-OXOACYL-(ACYL-CARRIER PROTEIN] + CO(2) +
-!-CATALYTIC ACTIVITY: (3R)-3-HYDROXYACYL-(ACYL-CARRIER PROTEIN) +
-!-SUBUNIT: FATTY ACID SYNHHETASE ARE [ALCHA(6)] HEXAMERS OF
TWO MULTIFUNCTIONAL SUBUNITS (ALPHA 6 BETA)
-!-SIMILARITY: TO THE FATTY ACID SYNTHETASE, SUBUNIT ALPHA FROM
OTHER FUNGI.
 01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-JUL-1999 (Rel. 38, Last annocation update)
EUKARYOTIC TRANSLATION INITIATION FACTOR 4 GAMMA (EIF-4-GAMMA) (EIF-
 Euteleostomi;
 Lamphear B.J., Yan R., Yang F., Waters D., Liebig H.-D.
Klump H., Kuechler E., Skern T., Rhoads R.E.;
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eu
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus
 DIF4G.
Oryctolagus cuniculus (Rabbit).
Oryctolagus cuniculus (Rabbit).
 68
 31 AEEGVPAPLPPEDAPNAASLAPTPV---SPVLEPFNLTSEP
 PRT; 1402 AA.
 SEQUENCE FROM N.A., AND SEQUENCE OF 479-500.
STRAIN-NEW ZEALAND WHITE; TISSUE-BRAIN;
MEDLINE-93374895; PubMed-8396129;
 STANDARD;
 IF4G_RABIT
 IF4G_RABIT
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 PARTIAL SEQUENCE.
MEDLINE-33054654; PubMed-1429670;
Yan R., Rychlik W., Etchison D., Rhoads R.E.;
"Anino acid sequence of the human protein synthesis initiation factor
 SIMILARITY: CONTAINS I RNA RECOGNITION MOTIF (RRM).
SIMILARITY: THE C-TERMINAL REGION IS SIMILAR TO THE N-TERMINAL
REGION OF WHEAT EUKARYOTIC INITIATION FACTOR (ISO)4F SUBUNIT P82.
 Gaps
 J. Biol. Chem. 267:23226-23231(1992).
-!- FUNCTION: COMPONENT OF THE PROTEIN COMPLEX EIF-4, WHICH IS INVOLVED IN THE RECOGNITION OF THE MRNA CAP, ATP-DEPENDENT UNAINDING OF 5'-TERMINAL SECONDARY STRUCTURE AND RECRUITMENT OF
 QLPVEEPNPAKRLLFLLLTIVFCQILMAEEGVPAPLPPEDAPNAASLAPTPVS-PVLEPF 62
"Mapping the cleavage site in protein synthesis initiation factor eIF-4 gamma of the 2A proteases from human Coxsackievirus and
 Euteleostomi;
 POLY-GLU.
RNA-BINDING (RNP2) (BY SIMILARITY).
RNA-BINDING (RNP1) (BY SIMILARITY).
 32;
 Koehrer K., Beyer A., Mewes H.-W., Gassenhuber J., Wiemann S.;
Submitted (MAY-1999) to the EMBL/GenBank/DibJ databases.
 DB 1; Length 1402;
 Craniata, Vertebrata; Eutele
Catarrhini, Hominidae; Homo.
 PFAM, PF02020; IF5_e1F4_e1F2; 1.
PROSITE; PS00030; RRM_RNP_1; FALSE_NEG.
Initiation factor; Protein biosynthesis; Phosphorylation;
 Indels
 POLY-GLU.
AW: 7FD85D7E30519230 CRC64;
 Š
 21;
 30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
31-CTT-2000 (Rel. 40, Last annotation update)
PROTEIN C210RF25 (FRAGMINT).
 AA.
 15.6%; Score 69; DB
30.2%; Pred. No. 29;
Live 7; Mismatches
 181
 268:19200-19203(1993)
 135 VTLSKPVPVSEFSSSPIQVLTPLASH 160
 63 NLTSEP-----SDYALDLSTFLQQH
 154050 MW;
 Chordata;
 Mammalia; Eutheria; Primates;
 EMBL; L22090; AAA31242.1; -
 MRNA TO THE RIBOSOME
 Conservative
 STANDARD;
 602 60
698 70
1393 139
1402 AA;
 IPR000504;
 Homo sapiens (Human).
 Eukaryota; Metazoa;
 Similarity
 SEQUENCE FROM N.A.
 Biol. Chem.
 TISSUE-UTERUS;
 RNA-binding
 rhinovirus
 C210_HUMAN
 Query Match
Best Local S
 INTERPRO
 SEQUENCE
 C210RF25.
 DOMAIN
DOMAIN
 DOMAIN
 DOMAIN
 RESULT 11
C210_HUMAN
 Matches
ID
AC
DT
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 SEQUENCE OF 111-2715 FROM N.A. (LONG ISOFORM).
TISSUE=TESTIS, AND LEUKOCYTE;
MEDLINE=20105772; Pubmed=10637508;
Huntsman D.G., Chin S.-F., Muleris M., Batley S.J., Collins V.P.,
Wiedemann L.M., Aparicio S., Caldas C.;
Wiedemann L.M., Aparicio S., Caldas C.;
Collins V.P.,
MLS., The second human homolog of the Drosophila trithorax gene, maps
to 19413.1 and is amplified in solid tumor cell lines.";
 - SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY)
- ALTERNATIVE PRODUCTS: 2 ISOFORMS: A LONG FORM (SHOWN HERE) AND A THUNCATED FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
- I ISSUE SPECIFICITY: WIDELY EXPRESSED HIGHEST LEVELS IN TESTIS.
ALSO FOUND IN BRAIN, BONE MARROW, HEART, MUSCLE, KIDNEY, PANCREAS, SPLEEN, TYWMOS, PROSTATE, OVARY, INTESTINE, COLON, PERIPHERAL BLOOD LYMPHOCYTES, AND PLACENTA.
- I DISEASE: OFFUR MAPLIFIED IN PANCREATIC CARCINOMAS.
- SIMILARITY: BELONGS TO THE TRITHORAX FAMILY OF TRANSCRIPTION
 Nagase T., Ishikawa K.-I., Nakajima D., Ohira M., Seki N., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; "Prediction of the coding sequences of unidentified human genes. VII. The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro."; DNA Res. 4:141-150(1997).
 PARTIAL SEQUENCE FROM N.A. (LONG AND TRUNCATED ISOFORMS).

TISSUE-PLACENTA, AND BONE MARROW;

MEDLINE-99339983; PubMed-10409430;

FitzGerald K.T., Diaz M.O.;

"MLL2: A new mammalian member of the trx/MLL family of genes.";

Genomics 59:187-192(1999).

-:- FUNCTION: POSSIBLY ACTS AS A TRANSCRIPTIONAL REGULATORY FACTOR.
 SEQUENCE FROM N.A. (LONG ISOFORM).
Lamerdin J.E., McCready P.M., Adamson A.W., Burkhart-Schultz K.,
Garcia E., Kyle A., Ramirez M., Stilwagen S., Garnes J., Danganan
Bruce R., Quan G., Montgomery M., Ow D., Kobayashi A., Olsen A.O.,
Carrano A.V.;
Angrand P.O., Valvatne H., Jeanmougin F., Adamson A., van der Hoeven F., Olsen L., Tekotte H., Huang N., Poch O., Lamerdin J., Chambon P., Losson R., Stewart A., Aasland R.; Mammallan trithorax- and ASHI-like proteins: putative chromatin regulators which contain PHD fingers and SET domains.": Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
 "Sequence analysis of a 1 Mb region in human 19q13.1."; Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
 -:- SIMILARITY: CONTAINS 1 BROWODOMAIN.
-:- SIMILARITY: CONTAINS 1 'SET' DOMAIN.
-:- SIMILARITY: CONTAINS 3 PHD-FINGER DOMAINS.
 SEQUENCE OF 816-2715 FROM*N.A. (LONG ISOFORM).
 -; NOT_ANNOTATED_CDS.
 MEDLINE=97349984; PubMed=9205841;
 AAD56420.1; -.
 EMBL; AF104918; AAD17932.1; -.
 EMBL; AJ007041; CAB45385.1; -
 ; AAD26113.1; -
 AD000671; -; NOT_A
AB002302; BAA20763
 INTERPRO; IPR002857;
 TISSUE-BRAIN;
 INTERPRO;
 INTERPRO;
 EMBL;
 EMBL;
 EMBL;
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VSARSSRVIKTPRREMDEDPPKPPKVEVSPVLRPPITTSPP
VPQEPAPVPS -> PLSQSLLLPMTLQLSLSLGQWAAPTTS
ACLDSPLWSPLLLRPRCPLTGLQL (IN ISOFORM
 Zinc-finger; Metal-binding;
 Gaps
 of
 Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
Saccharomycetaceae; Saccharomyces.
 SEQUENCE FROM N.A.
MEDLINE-88315020; PubMed-2900835;
Mohamed A.H., Chirala S.S., Mody N.H., Huang W.Y., Wakil S.J.;
Mohamed A.H., Chirala S.S., Mody N.H., Huang W.Y., Wakil S.J.;
Mohamed A.H., Cofirala S.S., Mody N.H., Huang W.Y., Wakil S.J.;
Primary structure of the multifunctional alpha subunit protein-
yeast fatty acid synthase derived from FAS2 gene sequence.";
J. Biol. Chem. 263:12315-12325(1988).
 MEDLINE-94316198; PubMed-8041367;
Inokoshi J., Tomoda H., Hashimoto H., Watanabe A., Takeshima H.,
 'Cerulenin-resistant mutants of Saccharomyces cerevisiae with an
 1;
 8 EEPNPAKRLLFLLLTIVFCQILMAEEGVPAPLPPEDAPNAASLAPT-PVSPVLEP 61
 altered fatty acid synthase gene.";
Mol. Gen. Genet. 244:90-96(1994).
-!- FUNCTION: FATTY ACID SYNTHETASE CATALYZES THE FORMATION OF
 MISSING (IN ISOFORM TRUNCATED).
K -> E (IN REF. 5).
E -> Q (IN REF. 5).
H -> Y (IN REF. 5).
D -> N (IN REF. 5).
D -> N (IN REF. 5).
Mw, CO61589918BEB79F CRC64;
 Length 2715;
 01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)

**TYT ACID SYNTHASE, SUBUNIT ALPHA (EC 2.3.1.86) [INCLUDES: EC 1.1.100; EC 2.3.1.41].
 27; Indels
 SIMILARITY).
SIMILARITY).
SIMILARITY).
 BROMODOMAIN (DIVERGENT)
 POLY-PRO.
ASP/GLU-RICH (ACIDIC)
 ;;
 Alternative splicing
A T HOOK (BY SIMI)
 В
 PRT; 1894 AA
 Mismatches
 43;
 (BY
(BY
(BY
 Score 70.5;
Pred. No. 43
 DOMAIN.
 TRUNCATED)
 A.T HOOK (
A.T HOOK (
PHD 1.
PHD 2.
 PRO-RICH
 POLY-GLN
 POLY - PRO
 POLY - PRO
 7 1317 E -> 2 1362 H -> 3 1438 D -> 2 2622 D -> 3 AA; 293511 MW;
 SET
 8;
 th 16.0%; Similarity 34.5%; 19; Conservative
 PFAM; PF02008; zf-CXXC; 1.
DNA-binding; Bromodomain; 1
Transcription regulation; 1
DNA_BIND 37
 STANDARD;
 941
1317
1362
1438
2622
 MUTAGENESIS OF GLY-1257
 Best Local Similarity
 583
834
941
1317
1362
1438
2622
2715
 STRAIN-S288C;
 FAS2_YEAST
P19097;
 Omura S.;
 DOMAIN
VARSPLIC
 VARSPLIC
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
 DNA_BIND
 Query Match
 DOMAIN
 Matches
 FAS2_YEAST
 2182
 QQ
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 Platelet; Transmembrane; Glycoprotein; Hemostasis; Blood coagulation; Repeat; Icucine-repeat; Signal; Cell adhesion; Disease mutation; bolymorphism; von Willebrand disease; Bernard Soulier syndrome. SIGNAL
 THROMBIN (THE LATTER SITE WITH UNKNOWN FUNCTION) ARE IN THE AMINO-TERMINAL PART OF THE MOLECULE.
SIMILARITY: THE REPEATED LEUCINE-RICH (LRR) SEGMENT IS FOUND IN MANY PROTEINS. NUMBER IN THIS PROTEIN: 8.
 PLATELET GLYCOPROTEIN IB ALPHA CHAIN
 MISCELLANEOUS: BINDING SITES FOR VON WILLEBRAND FACTOR AND
 /FTId=VAR_005256.
T -> M (IN ALLOANTIGEN SIBA(+)).
/FTId=VAR_005257.
 GLYCOCALICIN.
EXTRACELLULAR (POTENTIAL)
 19514119B45DF573 CRC64;
 CYTOPLASMIC (POTENTIAL).
LEUCINE-RICH REPEATS.
 /FTId-VAR_005260.
3 -> V (IN PSEUDO-VWD).
/FTId-VAR_005261.
 -> V (IN PSEUDO-VWD).
 N-LINKED (GLCNAC.
 MISSING (IN BSS).
/FTId=VAR_005259.
 A -> V (IN BSS).
/FTId=VAR_005258.
 -> S (IN BSS)
 LER 1.
LER 2.
LER 3.
LER 4.
LER 6.
LER 6.
LER 6.
LER 8.
THR/PRO-RICH.
 THR/PRO-RICH
THR/PRO-RICH
 THR/PRO-RICH
 THR/PRO-RICH
 EMBL; J02940; AAA52595.1;
 X.
 , M22403; AAA52596.1; -, A27075; NBHUIA.
 INTERPRO, IPRODIGII; -.
PFAM: PFO0560: LRR: 6.
PFAM: PF01463: LRRCT; 1.
PFAM: PF01463: LRRNT; 1.
PRINTS; PROD019: LEURICHRPT.
 68955
ACTIN-BINDING PROTEIN.
 INTERPRO; IPR000372; -.
 255
 195
 249
 161
 172
 626 AA;
 255
 249
 195
 225
 205
3379
387
400
400
422
202
205
 161
 MIM; 231200;
 177820;
 DOMAIN
TRANSMEM
DOMAIN
 CARBOHYD
CARBOHYD
CARBOHYD
 DISULFID
 SEQUENCE
 DISULFID
 VARIANT
 VARIANT
 VARIANT
 VARIANT
 VARIANT
 VARIANT
 VARIANT
 REPEAT
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 CHAIN
 DOMAIN
 REPEAT
 REPEAT
 REPEAT
 REPEAT
 REPEAT
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DB 1; Length 626;

Score 71.5;

16.2%;

Query Match

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 5
 Baer R., Bankler A.T., Biggin M.D., Deininger P.L., Farrell P.J., Gibson T.J., Haftull G., Hudson G.S., Satchwell S.C., Seguin C., Tuffnell P.S., Barrell B.G., "DNA sequence and expression of the B95-8 Epstein-Barr virus genome."; "DNA sequence and expression of the B95-8 Epstein-Barr virus genome."; "Lona sequence and expression of the B95-8 Epstein-Barr virus genome."; "Lunctron: TRANSCRIPTION ACTIVATION.
-: - RUNCTLON: TRANSCRIPTION ACTIVATION.
-: - MISCELLANEOUS: BRLF1 PROTEIN IS AN EARLY OR IMMEDIATE EARLY
 Gaps
 Gaps
 TRX2_HUMAN STANDARD; PRT; 2715 AA.
09UMN6; Q9UK25; 095836; 09Y669; Q9Y668; 015022;
01-OCT-2000 (Rel. 40, Created)
01-OCT-2000 (Rel. 40, Last annotation update)
01-OCT-2000 (Rel. 40, Last annotation update)
TRITHORAX HOMOLOG 2 (MIXED LINEAGE LEUKEMIA GENE HOMOLOG 2 PROTEIN)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Transcription regulation; Activator; DNA-binding; Early protein.
SEQUENCE 605 AA; 66594 MW; BSB7DF0593FADB08 CRC64;
 :
 ..
 16.0%; Score 70.5; DB 1; LeAgth 605; 47.5%; Pred. No. 8.2; Live 2; Mismatches 18; Indels
 Indels
 Epstein-barr virus (strain B95-8) (Human herpesvirus 4).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Lymphocryptovirus.
 453 PPGSPWANRPLPASLAPTPTGPVHEPVGSLTPAPVPQPLD 492
 11;
 36 PAPLPPEDAPNAASLAPTPVSPVLEPF-NLTSEPSDYALD 74
 36 PAPLP-----PEDAPNAASLAPTPVSPVLEPFNLTSEPS 69
 Last sequence update)
Last annotation update)
 Mismatches
 PROTEIN.
-:- SIMILARITY: TO HVS-1 EDRF1 (GENE 50).
 Pred. No.
 SEQUENCE FROM N.A. (LONG ISOFORM)
 SEQUENCE FROM N.A.
MEDLINE-84270667; Pubmed-6087149;
 01, Created)
 TRANSCRIPTION ACTIVATOR BRLF1
 EMBL; V01555; CAA24814.1;
45.0%;
 Conservative
 19; Conservative
 STANDARD;
 TRX2 OR HRX2 OR MLL2.
 Homo sapiens (Human).
 PIR; A03771; QQBE29.
PIR; S33019; S33019.
 Best Local Similarity
 Best Local Similarity
Matches 18; Conserv
 21-JUL-1986 (Rel.
21-JUL-1986 (Rel.
01-APR-1993 (Rel.
 TRANSFAC; T00710;
 (KIAA0340)
 Query Match
 BRL1_EBV
 TRX2_HUMAN
 Matches
 Q
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 g
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autosomal dominant variant of Bernard-Soulier disease.";

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4
 MEDLINE-89025874; PubMed-2845978; Wenger R.J.; Wenger R.H., Kieffer N., Wicki A.N., Clemetson K.J.; "Structure of the human blood platelet membrane glycoprotein Ib alpha
 dimorphism
 9
 58
 MEDLINE-92110577; PubMed-1730088;
Miller J.L., Lyle V.A., Cundingham D.;
"Mutation of Luctine-57 to phenylalanine in a platelet glycoprotein
Ib alpha leucine tandem repeat occurring in patients with an
 Gaps
 (GP-IB ALPHA) (GPIBA)
 .
E
 MEDLINE-87289654; PubMed-3497398; Titani K., Takio K., Handa M., Ruggeri Z.M.; Amino acid sequence of the von Willebrand factor-binding domain of platelet membrane glycoprotein Ib."; Proc. Natl. Acad. Sci. U.S.A. 84:5610-5614(1987).
 5 KLPPLSPSVIRRILFYLLMLLFCQQLAMIFWRIGL----PDNAP-VSSVQITPPAQARQQ
 OLPVEEPNPAKRLLFLLTIVFCQ---ILMAEEGVPAPLPPEDAPNAASLAPTPVSPVLE
 Euteleostomi;
 Lopez J.A., Chung D.W., Fujikawa K., Hagen F.S., Papayannopoulou
 13;
 "Cloning of the alpha chain of human platelet glycoprotein Ib: transmembrane protein with homology to leucine-rich alpha 2
 272;
 acid
 "Génetic and structural characterization of an amino acid
in glycoprotein Ib alpha involved in platelet transfusion
refractoriness.";
 Hess D., Schaller J., Rickli E.E., Clemetson K.J.; "Identification of the disulphide bonds in human platelet
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelo
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
 Murata M., Furihata K., Ishida F., Russell S.R., Ware J.,
 Indels
 Length
 22;
 DB 1;
 Natl. Acad. Sci. U.S.A. 84:5615-5619(1987)
 Commun. 156:389-395(1988)
 01-APR-1988 (Rel. 07, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Lengal 28, Last annotation)
 626 AA
 ; Score 72.5; Di
; Pred. No. 2.2;
16; Mismatches
 SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE-87289655; Pubmed-3303030;
 PRT;
 Eur. J. Biochem. 199:389-393(1991)
 MEDLINE #91301149; PubMed # 2070794;
 MEDLINE=92265982; PubMed=1586750;
 Created)
 Blood 79:3086-3090(1992).
 Conservative
 STANDARD;
 Biochem. Biophys. Res.
 07,
 61 PFNLTSEPSDYAL 73
 59 PVTL----NDFTL 67
 Homo sapiens (Human)
SEQUENCE OF 17-315.
 VARIANT BSS PHE-73.
 SECUENCE FROM N.A.
 01-APR-1988 (Rel.
01-APR-1988 (Rel.
15-JUL-1999 (Rel.
 MEDLINE=87289655;
 DISULFIDE BONDS
 glycoprotein.
 glycocalicin.
 SIBA
 GPBA_HUMAN
 Roth G.J
 VARIANT
 Ruggeri
 GPBA_HUMAN
 GP1BA
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A GENERAL PROPERTY OF ALTHOUGH TO THE PROPERTY OF HEAD OF THE CONDUCTOR OF THE THE CONDUCTOR OF THE SUBGREATE OF THE CONDUCTOR OF THE THE CONDUCTOR OF THE SUBENDOTHELIUM.

TO THE CONDUCTOR OF THE FORMATION OF PLATELET PLUGS BY BINDING TO VON WILLERSAND FACTOR, WHICH IS ALREADY BOUND TO THE SUBENDOTHELIUM.

TO SUBGRELIULAR LOCATION: TYPE I MEMBRANE PROTEIN.

TO SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

TO THE GLYCOCALICIN, WHICH IS APPROXIMATELY CONTINUENT LINKAGE.

TO THE CONDUCTOR OF THE WOLECULE, IS CLEAVED OFF BY CALPAIN.

DURING PLATELET LYSIS.
 MEDIINE-93253059; PubMed-8486780;
Murata M., Russell S.R., Ruggeri Z.M., Ware J.;
"Expression of the phenotypic abnormality of platelet-type yon
Willebrand disease in a recombinant glycoprotein Ib alpha fragment.";
J. Clin. Invest. 91:2133-2137(1993).
 MISCELLANEOUS: PLATELET ACTIVATION APPARENTLY INVOLVES DISRUPTION
 DOLYMORPHISM: POSTITION 161 IS ASSOCIATED WITH PLATELET-SPECIFIC ALLOANTIGEN SIBA. SIBA(+) HAS THR-161 AND SINA(+) HAS MET-161.

SIBA IS INVOLVED IN NEONATAL ALLOIMMUNE THROMBOCYTOPENIA (NATP). DISEASE: DEFECTS IN GPIBA ARE ONE THE CAUSES OF BERNARD-SOULIER SYNDROWE (BSS). BSS PATIENTS HAVE UNUSUALLY LARGE PLATELETS AND HAVE A CLINICAL BLEEDING TENDENCY.

DISEASE: DEFECTS IN GPIBA ARE ONE THE CAUSES OF OVIN WILLEBRAND DISEASE: (WUD) KNOWN AS PLATELET-TYPE VON WILLEBRAND DISEASE. OF PSEUDO-VON WILLEBRAND DISEASE. THIS AUTOSOMAL DOMINANT BLEEDING DISORDER IS CAUSED BY AN INCREASED AFFINITY OF GP-1B FOR SOLUBLE OF THE DEPOLITION IN MAPRIRED HEMOSTATIC FUNCTION DUE TO THE REMOVAL
 q
 VARIANT BSS SER-225.
MEDLINE=95118882; PubMed=7819107;
Simsek S., Noris P., Lozano M., Pico M., von Dem Borne A.E.G.K.,
Ribera A., Gallardo D.;
Ribera A., Gallardo D.;
Cys209 Ser mutation in the platelet membrane glycoprotein Ib alpha
gene is associated with Bernard-Soulier syndrome.";
 platelet glycoprotein
 Russell S.D., Roth G.J.; "Pseudo-von Willebrand disease: a mutation in the platelet glycoprotein Ib alpha gene associated with a hyperactive surface
 OF THE MACROMOLECULAR COMPLEX OF GP-IB WITH THE PLATELET GLYCOPROTEIN 1X (GP-IX) AND DISSOCIATION OF GP-IB FROM THE
 Σ
 MEDLINE-91271273; PubMed-2052556; Miller J.L., Cunningham D., Lyle V.A., Finch C.N.; Mutation in the gene encoding the alpha chain of platelet glycoprotein Ib in platelet-type von Willebrand disease."; Proc. Natl. Acad. Sci. U.S.A. 88:4761-4765(1991).
 "Point mutation in a leucine-rich repeat of plate alpha resulting in the Bernard-Soulier syndrome." J. Clin. Invest. 92:1213-1220(1993).
 MEDLINE-93388851; PubMed=7690774;
Ware J., Russell S.R., Marchese P., Murata M.,
de Marco L., Ruggeri Z.M.;
 Br. J. Haematol. 88:839-844(1994).
 VARIANT BSS LEU-195 DEL.
MEDLINE-95178321; Pubmed-7873390;
 VARIANT PSEUDO-VWD VAL-255.
MEDLINE=93214031; PubMed=8384898;
 FROM THE CIRCULATION
 VARIANT PSEUDO-VWD VAL-249
 VARIANT PSEUDO-VWD VAL-249
 receptor.";
Blood 81:1787-1791(1993).
 Blood 79:439-446(1992).
 VAL-172
 VARIANT

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 ;
9
 01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-NVV-1995 (Rel. 32, Last annotation update)
GENERAL SECRETION PATHWAY PROTEIN C (PECTIC ENZYMES SECRETION PROTEIN
 Lindeberg M., Collmer A.; "Analysis of eight out genes in a cluster required for pectic enzyme secretion by Erwinia chrysanthemi: sequence comparison with secretion
 25; Gaps
 1 VRRQLPVE-----EPNPAKRLLFILLTIVFCQILMAEEGVPAPLPPEDAPNAASLAPT 53
 genes from other gram-negative bacteria.";
J. Bacteriol. 174:7385-7397(1992).
-!- FUNCTION: INVOLVED IN A GENERAL SECRETION PATHWAY (GSP) FOR THE EXPORT OF PROTEINS. REQUIRED FOR THE TRANSLOCATION OF THE
 Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Pectobacterium.
 DB 1; Length 1595;
 TSCPVPCHFPRS -> HILPSPLSLPAQR
 37; Indels
 -> P (IN REF. 2).
33AE31F0767A219F CRC64;
 54 --PVSPVLEPF--NLTSEP----SDYALDLSTFLQQ----HPAAF 86
 MULTIPLE PECTIC ENZYMES.
-!- SUBCELLULAR LOCATION: INNER MEMBRANE (PROBABLE).
-!- SIMILARITY: BELONGS TO THE EXEC/PULC/OUTC FAMILY.
 factor; Neurogenesis
 ; Score 78.5; DE; Pred. No. 3.9; 14; Mismatches
 GLY-RICH.
DH.
 PH.
GLN-RICH.
HIS-RICH.
 (IN REF.
 PRT;
 MEDLINE-93054355; PubMed-1429461;
 17.8%;
 PFAM; PF00621; RhoGEF; 1.
PROSITE; PS00720; GDS_CDC25;
PROSITE; PS50003; PH_DOMAIN;
 Guanine-nucleotide releasing
 EMBL; L02214; AAA24830.1; -.
 1462 1462
1595 AA; 177837
 INTERPRO; IPR000651; -.
INTERPRO; IPR001849; -.
INTERPRO; IPR001895; -.
PFAM; PF00169; PH; I.
PFAM; PF00618; RasGEF; 1.
 Query Match
Best Local Similarity 28.3%.
 FLYBASE; FBgn0001965; Sos
 STANDARD;
 Erwinia chrysanthemi
 SEQUENCE FROM N.A. STRAIN=EC16;
 GSPC_ERWCH
P31698;
 CONFLICT
 DOMAIN
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 'n
 GSQC_ERWCH STANDARD; PRT; 272 AA.
001564;
01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-JUN-1995 (Rel. 32, Last annotation update)
GENERAL SECRETION PATHWAY PROTEIN C (PECTIC ENZYMES SECRETION PROTEIN
 Gaps
 4 OLPVEEPNPAKRLLFLLTIVFCQ----ILMAEEGVPAPLPPEDAPNAASLAPTPVSPVLE 60
 Condemine 5. Dorse Condemine G., Dorse Condemine G., Dorse I C., Hugouvieux-Cotte-Pattat N., Robert-Baudouy J "Some of the out genes involved in the secretion of pectate lyases i Erwinia chrysanthemi are regulated by kdgr.";

Minia chrysanthemi are regulated by kdgr.";

Minia chrysanthemi are regulated by kdgr.";

1. FUNCTION: INVOLVED IN A GENERAL SECRETION PATHWAY (GSP) FOR THE EXPORT OF PROFINS. REQUIRED FOR THE TRANSLOCATION OF THE MULTIPLE PECTIC ENZYMES.

1. SUBCELLULAR LOCATION: INNER MEMBRANE (PROBABLE).

1. SIMILARITY: BELONGS TO THE EXEC/PULC/OUTC FAMILY.
 Proteobacteria; gamma subdivision; Enterobacteriaceae;
 13;
 16.6%; Score 73.5; DB 1; Length 272; 30.1%; Pred. No. 1.7;
 25; Indels
PIR; A47021; A47021.
INTERPRO; IPR001478; -.
INTERPRO; IPR001639; -.
PRAM; PF00595; PD2; 1.
PRINTS; PR00810; BCTERIALGSPC.
PROSITE; PS01141; T2SP_C; 1.
Transport; Transmembrane; Inner membrane.
16 CYTOPLASMIC (POTENTIAL).
 CYTOPLASMIC (POTENTIAL).
POTENTIAL.
PERIPLASMIC (POTENTIAL).
0E2C1A952B426D5A CRC64;
 POTENTIAL.
PERIPLASMIC (POTENTIAL).
1064C7311F9714405 CRC64;
 22; Conservative 13; Mismatches
 PFAM; PF00595; PDZ; 1.PRIALGSPC.
PRINTS; PR00810; BCTPRIALGSPC.
PROSITE; PS00141; T2S_C; 1.
Transport; Transmembrane; Inner membrane.
 or send an email to license@isb-sib.ch)
 MEDLINE-93086427; Pubmed-1453958;
 30162 MW;
 30301 MW;
 EMBL; X65265; CAA46369.1; -.
 INTERPRO; IPR001478; -.
 61 PFNLTSEPSDYAL 73
 | | :|: |
PVTL----NDFTL 67
 Erwinia chrysanthemi.
 IPR001639;
 272 AA;
 272 AA;
 Query Match
Best Local Similarity
Matches 22; Conserv
 SEQUENCE FROM N.A.
 Pectobacterium
 Bacteria;
 DOMAIN
SEQUENCE
 RANSMEM
 TRANSMEM
 INTERPRO
 SEQUENCE
 GSOC_ERWCH
 DOMAIN
 DOMAIN
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
 ;
0
 CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
 11 VRRQLPVEEPNPAKRLFLLLTIVFCQILMAEEGVPAPLPPEDAPNAASLAPTPVSPVLE 130
 Gaps
 1 VRRQLPVEEPNPAKRLLFLLLTIVFCQILMAEEGVPAPLPPEDAPNAASLAPTPVSPVLE 60
 -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (POTENTIAL).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
 EXTRACELLULAR (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
A -> G (IN REF. 1).
P -> R (IN REF. 1).
83C06116C80B9240 CRC64;
 01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
RADIATION-INDUCIBLE IMMEDIATE-EARLY GENE IEX-1 (IMMEDIATE EARLY
PROTEIN GLY96) (IMMEDIATE EARLY RESPONSE 3 PROTEIN)
MLS MUSCULUS (MOUSE)
 .
0
 100.0%; Score 442; DB 1; Length 156; 100.0%; Pred. No. 3.6e-37;
 0; Indels
 -1- INDUCTION: BY SERUM GROWTH FACTORS AND TPA.
 153 AA.
 Signal-anchor.
 0; Mismatches
 -!- SIMILARITY: STRONG, TO HUMAN ORTHOLOG.
 131 PFNLTSEPSDYALDLSTFLQQHPAAF 156
 EMBL; S81914; AAB36278.1; -.
EMBL; X96438; CAA65304.1; -.
EMBL; X14551; CAA74886.1; -.
EMBL; T49531; -; NOT_ANNOTATED_CDS.
MIM; 602996; -.
 PRT;
 61 PFNLTSEPSDYALDLSTFLQQHPAAF 86
 16928 MW;
 Transmembrane;
 Conservative
 STANDARD;
 82
93
 100
133
54
106
156 AA;
 AND THE UTERUS
 Similarity
 SEQUENCE FROM N.A.
 83
 CELL CYCLE.
 Glycoprotein;
 IEX1_MOUSE
P46694;
 CONFLICT
 FRANSMEM
 Query Match
 CARBOHYD
 Best Local
Matches 8
 DOMAIN
 IEX1_MOUSE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
 3
 Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda, Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
 Signal-anchor.
CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 Gaps
 1 VRRQLPVEEPNPAKRLLFLLLTIVFCQILMAEEGVPAPLPPEDAPNAASLAPTPVS---- 56
 MEDLINE-92034991; PubMed-1934068; Simon M.A., Bowtell D.L., Dodson G.S., Laverty T.R., Rubin G.M.; Rabin M.A., Bowtell D.D.L., Dodson G.S., Laverty T.R., Rubin G.M.; Rasal and a putative guanine nucleotide exchange factor perform crucial steps in signaling by the sevenless protein tyrosine kinase."; Tateps in signaling by the sevenless protein tyrosine for 16 7701-716 (1991).

-I- FUNCTION: PROMOTES THE EXCHANGE OF RAS-BOUND GDP BY GTP. SOS IS IMPLICATED IN NEURONAL DEVELOPMENT.

-I- SIMULARITY: CONTAINS 1 DBL-HOMOLOGY DOMAIN (DH).

-I- SIMILARITY: CONTAINS 1 PH DOMAIN.

-I- SIMILARITY: CONTAINS 1 RASGEF DOMAIN.
 Bonfini L., Karlovich C.A., Dasgupta C., Banerjee U., "The Son of sevenless gene product: a putative activator of Ras."; Science 255:603-606(1992).
 œ
 Query Match 61.8%; Score 273; DB 1; Length 153; Best Local Similarity 68.2%; Pred. No. 1.8e-20; Matches 58; Conservative 5; Mismatches 14; Indels
 EXTRACELLULAR (POTENTIAL)
 N-LINKED (GLCNAC. . .) (Property CA 4 2 9 E 3 B 0 1 2 0 D E 1 1 CRC 6 4;
 01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
115-JUL-1999 (Rel. 38, Last annotation update)
SON OF SEVENLESS PROTEIN.
 PRT; 1595 AA
 (POTENTIAL)
 or send an email to license@isb-sib.ch).
 EMBL; X67644; -; NOT_ANNOTATED_CDS.
PIR; S33363; S33363.
MGD; MGI:104814; IER3.
 129 APPVLEPLNLTSESSDYALDLKAFL 153
 57 -- PVLEPFNLTSEPSDYALDLSTFL 79
 STRAIN-OREGON-R;
MEDLINE-92141820; Pubmed-1736363;
 .
X
 EMBL; M83931; AAB04680.1; -. EMBL; M77501; AAA28904.1; -.
 Glycoprotein; Transmembrane;
DOMAIN 1 85
 16875
 STANDARD;
 85
102
 153
 PIR; A41216; A41216.
 103
137
153 AA;
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 HSSP; P04002; 1WFA
 98
 SOS_DROME
P26675;
 TRANSMEM
 CARBOHYD
 SEQUENCE
 DOMAIN
 SOS_DROME
 RESULT
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14
64
34
 January 30, 2001, 23:12:24 ; Search time 43.61 Seconds (without alignments) 63.685 Million cell updates/sec
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 US-08-799-910-10_COPY_71_156
442
1 VRRQLPVEEPNPAKRLLFLL......EPSDYALDLSTFLQQHPAAF 86
 GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
 Total number of hits satisfying chosen parameters:
 88757 seqs, 32294092 residues
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 OM protein - protein search, using sw model
 BLOSUM62 Gapoxt 0.5
 Minimum DB seq length: 0
Maximum DB seq length: 200000000
 SwissProt_39:*
 Title:
Perfect score:
Sequence:
 Scoring table:
 Database :
 Searched:
 Run on:
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| Description         | P46695<br>P46694<br>P26675<br>P26675<br>P001564<br>P007359<br>P00907<br>P19097<br>P19097<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P129130<br>P1291 | 081973<br>Q01101           |
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| SUMMARIES           | IEXI_HUMAN IEXI_MOUSE GSPC_ERWCH GSQC_ERWCH GSQC_ERWCH GSQC_ERWCH GSQC_ERWCH FAZZ_HUMAN FAZZ_YEAST TRX2_HUMAN PPDJ_HUMAN PPDJ_HUMAN POLR_TYMV IF4G_RABIT C210_HUMAN POLR_TYMV ILV4G_RABIT LIVB_RYCAV MODD_MYCHO ESNB_ESEU ESNB_ESU MODD_MYCH MAN MYSB_CHICK MYSB_ESU                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | C933_SOYBN<br>IA1_HUMAN    |
| DB                  |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                            |
| Length              | 156<br>1595<br>272<br>272<br>626<br>626<br>626<br>1402<br>1814<br>1814<br>1335<br>586<br>412<br>1395<br>588<br>312<br>588<br>312<br>588<br>312<br>588<br>412<br>1093<br>312<br>312<br>312<br>312<br>312<br>312<br>312<br>312<br>312<br>31                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | 510                        |
| %<br>Query<br>Match | 0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.0000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.0000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.0000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.0000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.0000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.0000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.0000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.000<br>0.0000<br>0.000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.0000<br>0.00                                                                                                                                                                                                                         |                            |
| Score               | 44 8 8 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 64                         |
| Result<br>No.       | 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | 3 E                        |

| P54839 P54839 P54830 P34830 P3636 | 14. 14. 15. 347 1 FYNL-MUNAN P548139  56. 64 14.5 590 1 FYNL-MUNA P548139  56. 51. 14. 4 44.1 1 WALL-MUNAN P548139  56. 51. 14. 4 44.1 1 WALL-MUNAN P548139  56. 51. 14. 4 10. 1 WALL-MUNAN P548139  56. 51. 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 14. 1 |         |                                         | ;        |                                          |                  | ,      | •          |                     |                 |
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| 59 6 4 14.5 540 1 F72LHHURE P938139 6 6 14.5 560 1 F72LHHURE P938139 6 5 5 14.4 5 960 1 F72LHHURE P938139 6 5 5 14.4 5 960 1 F72LHHURE P938139 6 5 5 14.4 5 960 1 F72LHHURE P938139 6 5 5 14.4 540 1 WUSA_WTCPN P201734 6 5 5 14.4 5 10 ANIE, MUSCA_WTCPN P20175 6 5 14.4 176 1 POLE_TYMCT P20175 6 1 14.3 14.4 1 POLE_TYMCT P20175 6 1 14 | 35 6 4 14.5 540 1 F72_HRIDE  36 6.4 14.5 540 1 F72_HRIDE  38 6.5 14.4 35 96 1 F72_HRIDE  38 6.5 14.4 36 1 MSA_HURAN  40 55.5 14.4 340 1 MSA_HURAN  41 55.5 14.4 340 1 MSA_HURAN  42 55.5 14.4 340 1 MSA_HURAN  43 55.5 14.4 340 1 MSA_HURAN  44 5.5 14.4 370 1 MSA_HURAN  45 6.3 14.3 13.3 14.4 176.1 POLE_THACK  45 6.3 14.3 13.3 14.4 176.1 POLE_THACK  45 6.3 14.3 13.3 14.4 176.1 POLE_THACK  46 6.3 14.3 14.4 176.1 POLE_THACK  47 10.1 MSA_HURAN  48 6.3 14.3 14.4 176.1 POLE_THACK  48 6.3 14.3 14.4 176.1 POLE_THACK  48 6.3 14.3 14.4 176.1 POLE_THACK  49 10.1 MSA_HURAN  48 6.3 14.3 14.4 176.1 POLE_THACK  49 10.1 MSA_HURAN  48 6.3 14.3 14.4 176.1 POLE_THACK  49 10.1 MSA_HURAN  49 10.1 MSA_HURAN  49 10.1 MSA_HURAN  49 10.1 MSA_HURAN  40 1 MSA_HURAN  40 MSA_HURAN  40 MSA_HURAN  40 MSA_HU |         | 34                                      | 64       | 14.5                                     | 537              | ٦,     | PTN5_HUM   | z                   | hom             |
| 36                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | 36 64 14.5 590 1 FT21.HHTEP  38 63.5 14.4 443 1 HAX3_HUMAN  38 63.5 14.4 443 1 HAX3_HUMAN  40 63.5 14.4 443 1 HAX3_HUMAN  40 63.5 14.4 470 1 NUSA_MYCRP  41 63.5 14.4 176 1 POLE_OTWY  42 63.5 14.4 176 1 POLE_OTWY  43 63 14.3 420 1 EFTA_HALAA  44 63 14.3 420 1 EFTA_HALAA  45 63 14.3 420 1 EFTA_HUMAN  P201275  ALIGNMENTS  SULT 1  XHUMAN  STANDARD, PRT, 156 AA.  P46655, 093044, 092691,  D-00-1996, Rel. 36, Last sequence update)  10-100-1996, Rel. 36, Last sequence update  10-100   |         | 32                                      | 64       | 14.5                                     | 541              | -      | PTN5_MOU   | ω                   | 5110            |
| 37 66 14.5 966 18.586. PRAYTON 0413629 163.5 14.4 43.0 1 NUSANYTON 041363 163.5 14.4 43.0 1 NUSANYTON 041363 163.5 14.4 43.0 1 NUSANYTON 041363 163.5 14.4 176 10 ADE NUCKA WTCH 063.5 14.4 176 10 ADE NUCKA WTCH 07159 1759 1769 1769 1769 1769 1769 1769 1769 176                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 37 66 14.5 966 18.586. PRATE   0415639   0415639   041563   041563   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156   04156     |         | 36                                      | 64       | 14.5                                     | 290              | -      | FTZ1 RHI   | 60                  | 4               |
| 38 63.5 14.4 443 1 NAX HINNA 04335   40 63.5 14.4 443 1 NUSA_WYCPN   63.5 14.4 14.1 10 NUSA_WYCPN   63.5 14.4 17.1 1 POLE_CYNY   63.1 14.3 14.4 1 POLE_CYNY   72.2 1 POLE_CYNY   63.1 14.3 14.4 1 POLE_CYNY   72.2 1 POLE_CYNY   | 38 63.5 14.4 443 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |         | 37                                      | 64       | 14.5                                     | 996              | _      | SSN6 YEA   |                     |                 |
| SULT 1  ALIGNMENTS   39 655 14.4 950 10.5 MINSALWEEN DATA DATA DATA DATA DATA DATA DATA DAT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |         | . ac                                    | ç        |                                          | 7 7              | -      | UVA 2 LINE |                     |                 |
| SULT 1  XHUMAN STANDARD; PRT; 156 AA. P10581  ALIGNMENTS  PROSESS: 033044; 032631;  DI-WOV-1995 (Rel. 32 created) DI-WOV-1996 (Rel. 32 crelated) DI-WOV-1996 (Rel. 32 created) DI-WOV-1996 (Rel. 32 create   | SULT 1  X_180ABN  ALIGNMENTS  43 63 14.4 1976   DOLE_COWN  44 63 14.3 598   1 NR41_HUMAN  ALIGNMENTS   |         |                                         | ) (      | * * * *                                  | יי<br>דע         | - ۱    | EDH CAVE   |                     | рошоц           |
| SULT 1  SOLIC TO SOLID THE STANDARD POLE CONNU POLICY POLICY POLICY PART 6 5 1 4 4 1 1776 1 POLE CONNU POLICY POLICY POLICY PART 6 5 1 4 4 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | SULT 1  ALGUMAN STANDARD; PRT; 156 AA. P7278 1 90LR ONNY  A 63 14.3 1844 1 90LR CNNY  A 720 1 EFIALMAN P22758  ALIGNMENTS  SULT 1  X_LHUNAN STANDARD; PRT; 156 AA. P4655; 030444; 030561;  10.70V.1995 (Rel. 32, Created)  10.70V.1995 (Rel. 32, Created)  10.70V.1996 (Re |         | ١.                                      | 7 (      | * <                                      | 7 6              | ٦.     | NOSA_MIC   |                     |                 |
| SULT 1  XHUMAN STANDARD; PRT; 156 AA. P5281736  43 63 14.3 598 1 NR41_HUMAN P5281736  ALIGNMENTS  AL   | ALIGNMENTS  SULT 1  ALIGNMENTS  ALIGNMENTS  STANDARD; PRT; 156 AA.  PREALHUMAN STANDARD; PRT; 156 AA.  PREALHUMAN STANDARD; PRT; 156 AA.  PREALHUMAN STANDARD; PRT; 156 AA.  PROPERN CLY95) (IMMEDIATE ENGLY RESPONSE IEXT (IMMEDIATE ENGLY)  10-WAY-2000 (Rel. 30, Last sequence update)  10-WAY-2000 (Rel. 30, Last sentotation update)  10-WAY-2000 (Rel. 30, Last sequence update)  10-WAY-2000 (Rel. 30, Last sequence update)  10-WAY-2000 (Rel. 30, Last sentotation update)  10-WAY-2000 (Rel. 30, Last sentotation update)  10-WAY-2000 (Rel. 30, Last sentotation update)  RADIATION INDUCIBLE INMEDIATE ENLY RESPONSE IEXT (IMMEDIATE ENCLY RESPONSE IEXT)  RESPONSE IN FORCE IN (IMMEDIATE ENLY RESPONSE IEXT)  RESPONSE IN (IMMEDIATE ENLY RESPONSE IEXT)  RESPONSE IN (IMMEDIATE ENLY RESPONSE IEXT)  RODIATION SEPTION N. A.  TISSUE-PLACENTA;  WEDLINE-96121139; Pubmed-8603392;  TOTAL AND                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |         | , _                                     | . ~      |                                          | 1776             | ٠,     | DOI B OWN  |                     | neurosp         |
| ALGONMENTS  SULT 1  TEXL-HUMAN STANDARD; PRT; 156 AA. P56919  ALGONMENTS  SULT 1  TEXL-HUMAN STANDARD; PRT; 156 AA. P4695; 03044; 030569; 1  10-VU-1998 (Rel. 32, Created) 10-VU-1998 (Rel | ALIGNMENTS  SULT  ALIGNMENTS  ALIGNMENTS  SULT  ALIGNMENTS  SULT  ALIGNMENTS  ALIGNMENTS  ALIGNMENTS  SULT  TEXT_HUMAN  STANDARD; PRT; 156 AA.  #6655; 03044; 0305461;  15-UGL-1998 (Rel. 32, Created)  15-UGL-1998 (Rel. 32, Created)  15-UGL-1998 (Rel. 32, Last annotation update)  30-NAY-2000 (Rel. 34, Last annotation update)  30-NAY-2000 (Rel. 34, Last annotation update)  30-NAY-2000 (Rel. 35, Last annotation update)  30-NAY-2000 (Rel. 36, Last annotation update)  BADIATION INDUCIBLE INEDIATE EARLY RESPONSE 3 PROTEIN)  (DIF-2 PROTEIN) (PRGI PROTEIN) (DIFFERENTIATION-DEPENDENT GE  FROME 1 PROTEIN) (PRGI PROTEIN) (DIFFERENTIATION-DEPENDENT GE  REAL RELACENTA,  HORD SAPLAR REALDS (RESPONSE 3 PROTEIN)  SEQUENCE FROW N.A.  ***SULTANCE FROW N.A.**  ***SULTANCE FROW N.A.**  ***SULTANCE FROM N.A.**  ***SULTANC |         | ~                                       | ~        | 14 4                                     | 1844             |        | MAE GIOG   |                     | STUDIES         |
| ALIGNMENTS  SULT 1  XHUMAN  TEXL_HUMAN  TO 1.40295 (Rel. 36. Last sequence update)  15UL-1998 (Rel. 36. Last sequence update)  15UL-1998 (Rel. 36. Last sequence update)  TEXL_HUMAN       | ALIGNMENTS  SULT 1  ALLINDAN  ALIGNMENTS  STANDARD; PRT; 156 AA.  PAGGS1: G193044: 092691.  TEXL_HUMAN  PAGGS1: G93044: 092691.  TEXL_HUMAN  PAGGS1: G93044: 092691.  TEXL_HUMAN  PAGGS1: G93044: 092691.  TEXL_HUMAN  PAGGS1: G193044: 092691.  TEXL_HUMAN  PAGGS1: G193044: 092691.  SPANDARTON INDUCIBLE INMEDIATE PARLY RESPONSE 1 PROTEIN (PAGAPE PAGENET INMEDIATE PAGENET CARE ITEX.1 (IMMEDIATE CARE ITEX.1 (I |         | . ~                                     | 1        |                                          | 200              | ٦,     | 777        |                     | turnip          |
| ALIGNMENTS  SULT 1  X_HUMAN  STANDARD:  PRT; 156 AA.  PRT; 156 AA.  PRGESS: 093044: 092691.  15-JUL 1998 (Rel: 36, Last Sequence update)  REDING SPORTING (Rel: MEDIATE-EARLY RESPONSE 3 PROTEIN) (PACAP-REDING TO THE SPORTING (Rel: MEDIATE-EARLY RESPONSE 3 PROTEIN) (PACAP-REDING TO THE SPORTING (Rel: MEDIATE-EARLY RESPONSE 3 PROTEIN)  ENGREY (REL: MEDIATE-EARLY RESPONSE 3 PROTEIN)  TISSUE-ELAGEBRA;  MEDIATE-GÓTELDES; PUDMEG-8603392;  TIGGATEL (CALCENTA);  MEDIATE-GÓTELDES; PUDMEG-8603392;  TO CANCER FROM N.A.  SEQUENCE FROM N.A.  MEDIATE-97139426; Pubmed-863710;  TIGGATEL H. TRUZOLD A. SIGGATE C., FOLSCH U.R., Schmict (PRE) (Rel: MEDIATE)  TIGGATEL AND CONTRACT (CALCENTAL OF A DATE (CALCE | ALIGNMENTS  SULT 1  LALL HUMAN STANDARD; PRT; 156 AA. 14.3 598 1 NR41_HUMAN PROJUCE  P46551.03044; 0.025451; PRT; 156 AA. 10.0487-2006 (Rel. 35, Leat sequence update)  10.0487-2006 (Rel. 36, Leat sequence update)  10.0497-2006 (Rel. 36, Leat sequence update)  10.0407-2006 (Rel. 2006)  10.0407-20 |         |                                         | 3 (      | , ,                                      | 7 6              | ٠,     | FE 2 / MOO |                     |                 |
| ALIGNMENTS  ALIGNMENTS  ALIGNMENTS  TEXT_HUMAN  PAGESS, 093044; 092691;  10NOV-1999 (Rel. 35, Last sequence update)  15-ULU-1998 (Rel. 35, Last sequence update)  15-ULU-1998 (Rel. 35, Last sequence update)  15-ULU-1999 (Rel. 36, Last sequence update)  RADIATION-INDICIBLE INMEDIATE ENRIL GREE IEXT. (IMMEDIATE ENRIL GREE IEXT.)  RADIATION-INDICIBLE INMEDIATE ENRIL GREE IEXT. (IMMEDIATE ENRICHER)  RADIATION-INDICIBLE INMEDIATE ENRIL GREE IEXT. (IMMEDIATE ENRICHER)  REMORTS OR PROTEIN) (PROTEIN) (DIFFERENTIATION-DEPENDENT GE  ENGRE! PROTEIN) (PROT PROTEIN) (DIFFERENTIATION-DEPENDENT GE  ENGRE! PROTEIN) (PROT PROTEIN) (DIFFERENTIATION-DEPENDENT GE  ENGRE! PROTEIN) (DIF-2 PROTEIN)  MARMADIALS GREECH AND                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | ALIGNMENTS  SULT 1  NHUMAN  PAGES, 093043; 092691,  10NOV-1995 (Rel. 32, Last sequence update)  10NOV-1996 (Rel. 32, Last sequence update)  10NOV-1996 (Rel. 32, Last annotation update)  10NOV-1996 (Rel. 32, Rel. 32, R                                                |         | , r                                     | 2 0      | 7.7                                      | 4 10             | ٠,     | EFIA_HAL   |                     | haloarcul       |
| ALIGNMENTS  SULT 1  XHUWAN  STANDARD; PRT; 156 AA.  946655, 09044; 092591  10-1099 (Rel. 32, Created)  10-10-1999 (Rel. 36, Last sequence update)  RADIATION-INDUCIBLE IMMEDIATE_ERALY GENE IEX-1 (IMMEDIATE ERALY RESPONSE 3 PROTEIN) (PACAP-R GENE I PROTEIN) (PROJECTION)  10-10-1999 (Rel. 36, Last sequence update)  RADIATION-INDUCIBLE IMMEDIATE_ERALY RESPONSE 3 PROTEIN) (PACAP-R GENE I PROTEIN) (INFO PROTEIN)  10-10-1999 (Rel. 36) (IMMEDIATE_ERALY RESPONSE 3 PROTEIN) (PROJECTION)  ELKAT-YOOKO (Rel. 39) (IMMEDIATE_ERALY RESPONSE 3 PROTEIN)  ELKAT-YOCK (Human)  TISSUE-LOCKERTA  TISSUE-LOCKERTA  TISSUE-LOCKERTA  TISSUE-LOCKERTA  TISSUE-LOCKERTA  TOTAL TRANSIAL OF THE ALIAN TO THE ADMINISTICATION OF A RADIATION-INDUCED OF A RADIATION OF A RADIATION-INDUCED OF A RADIATION OF A R   | ALIGNMENTS  SULT 1  XHUNAN STANDARD; PRT; 156 AA. 44665; 03044; 02261  01-NOV-1996 (Rel. 36, Last sequence update)  30-MX-2000 (Rel. 39, Last sequence update)  30-MX-2000 (Rel. 36, Last sequence update)  30-MX-2000 (Rel. 39, Last sequence update)  50-MX-2000 (Rel. 39, Last sequence update)  REDIATION-INDICIBLE IMMEDIATE EARLY RESPONSE 3 PROWEIN) (PACAP-RESPONSE 3 PROWEIN) (PACAP-RESPONSE 3 PROWEIN) (PACAP-RESPONSE 3 PROWEIN) (PACAP-RESPONSE)  ENEMTATION-INDICIBLE IMMEDIATE EARLY RESPONSE 3 PROWEING GENE 1 RR3 OR PROJECT PROMEIN)  ELKATYCK: MEKAZOR3 (CHURAD)  SEQUENCE FROM N.A.  TISSUED-LACKERNA;  MONDIARS-96231139; PURMED-8663332;  KONDIARS-96231139; PURMED-8653710;  CACCET RES. 56:1498-1502(1999).  SEQUENCE FROM N.A.  PROJI. A NOVEL GATILY-RESPONSE GENE TRANSCRIPTION-1INDICIBL IN APPLIANT AGENIAL CYCLASE ACTIVATION Of a ROVEL MACAP-RESPONSE SOLITING.  SCHEEFER H., TRANZOLI A., SLEGAL C., FOLSCH U.R., SCHMIGE WELLINGS CONTROL OF AN APPLIANT AGENIAL CYCLASE ACTIVATION OF AN APPLIANT AND APPLIANT AGENIAL CYCLASE ACTIVATION OF AN APPLIANT AND AND APPLIANT AND A   |         | 7                                       | 0        | ٠. ۴                                     | n<br>n           | 4      | NK4 I_HUM  |                     | homo sapi       |
| ALIGNMENTS  SULT 1  X1_HUMAN  P4655; 093044; 092691;  10-NOV-1995 (Rel. 35, Last annotation update)  10-NOV-1995 (Rel. 36, Last annotation update)  10-NOV-1996 (Rel. 36, Last annotation update)  10-NOV-1996 (Rel. 36, Last annotation update)  BADIATON-INDICIBLE IMMEDIATE EARLY RESPONSE 3 PROPEIN) (PAGAP R GENE 1 PROTEIN) (PRIC 10 PROTEIN) (PRIC 10 PROTEIN) (DIFPERENTIATION-DEPENDENT GENE LERA OR PROTEIN OR DIFPERENTIATION-DEPENDENT GENE LERA OR PROTEIN OR DIFPERENT GENE LERA OR DIFPERENT GENE LERA OR DIFPERENT GENE LERA OR LEAR OR DIFPERENT GENE LERA OR DIFPERENT GENE LEAR OR DIFPERENT GENE GENE GENE GENE GENE GENE GENE G                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | ALIGNMENTS  SILT 1  X1_HUMAN STANDARD; PRT; 156 AA, P6659; 093044; 092691; 016.0044; 092691; 016.0044; 092691; 016.0044; 092691; 016.0044; 092691; 016.0044; 092691; 016.0044; 092691; 016.0044; 092691; 016.0044; 092691; 016.0044; 092691; 016.0044; 092691; 016.0044; 092691; 016.0044; 092691; 016.0044; 092691; 016.0044; 092691; 016.0044; 092691; 016.0044; 092691; 016.0044; 092691; 016.0044; 092691; 016.0044; 092691; 016.0044; 092691; 016.0044; 092691; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016.0044; 016 |         |                                         |          |                                          |                  |        |            |                     |                 |
| PRT; 156 AA.  PERZI,HUMAN STANDARD; PRT; 156 AA.  P46655; 093044; 092691; 10-NOV-1995 (Rel. 32, Created) 10-NOV-1995 (Rel. 32, Created) 10-NOV-1995 (Rel. 32, Last sequence update) 10-NAY-2000 (Rel. 33, Last annotation update) 10-MAY-2000 (Rel. 33, Last annotation update) 10-MAY-2000 (Rel. 34, Last annotation update) 10-MAY-2000 (Rel. 36, Last sequence update) 10-MAM-2000 (Rel. 36, MATHAT SHOWN UP TO REMBLIGAR LAST SHOWN TO MOUSE ORTHOLOG (REMBERS) 10-MAM-2000 (Rel. 26, Last SEQUENCE DERFORE PROM THAT SHOWN TO PROMENTED TO REMBERS IN SECONDARY (Rel. 26, MATHAT SHOWN TO MEMBERS IN SECONDARY (Rel. 26, MATHAT SHOWN TO MOUSE ORTHOLOG (Rel. 26, MATHAT SHOWN TO MEMBERS IN SECONDARY (Rel. 26, MATHAT SHOWN TO MEMBERS IN SECONDARY (Rel. 26, MATHAT SHOWN TO M | PRT; 156 AA.  PIEXL; HUMAN  STANDARD; PRT; 156 AA.  P46655; 093044; 092691;  10-NOV-1995 (Rel. 32, Created)  10-NOV-1995 (Rel. 39, Last annotation update)  RADIATION-PHOCINEL EMELY RESONSE 3 PROPEIN)  PROPEIN GLY69 (IMMEDIATE EMELY RESONSE 3 PROPEIN)  PROPEIN (GLY6) (IMMEDIATE EMELY RESONSE 3 PROPEIN)  PROPEIN (GLY6) (IMMEDIATE EMELY RESONSE 3 PROPEIN)  PROPEIN (HUMAN)  ENGAGE (HUMAN)  PROPEIN (HUMAN)  FROUGH (HUM |         | •                                       |          |                                          |                  |        | ALIGN      |                     |                 |
| NULT 1  X1_ENLANA  STANDARD;  PRT; 156 AA.  PG655; 09304, 09261,  10-NOV-1995 (Rel. 32, Created)  10-NOV-1995 (Rel. 32, Last annotation update)  10-NOV-1996 (Rel. 32, Last annotation update)  10-NOV-1996 (Rel. 32, Last annotation update)  10-NOV-1996 (Rel. 34, Last annotation update)  10-NOV-1996 (Rel. 36, Last annotation update)  10-NOV-1996 (Rel. 36, Last annotation update)  10-NOV-1996 (Rel. 36, Last annotation update)  RADIATION.NOUCIBLE IMMEDIATE-EARLY RESPONES 3 PROTEIN)  FROTEIN (LIVE) (IMMEDIATE EARLY RESPONES 3 PROTEIN)  FROTEIN (LIVE) (PRCI) PROTEIN)  ENGRE 1 PROTEIN)  ENGR 1 PROTEIN)  ENGR 2 PROTEIN)  ENGR 2 PROTEIN)  ENGR 3 PROTEIN)  ENGR 4 PROTEIN)  ENGR 4 PROTEIN)  ENGR 5 PROTEIN)  ENGR 5 PROTEIN)  ENGR 5 PROTEIN)  ENGR 6 PROTEIN)  ENGR 6 PROTEIN)  ENGR 7 PROTEIN)  ENGR 7 PROTEIN)  ENGR 1 PROTEIN)  ENGR 1 PROTEIN)  ENGR 1 PROTEIN)  ENGR 1 PROTEIN)  ENGR 5 PROTEIN)  ENGR 5 PROTEIN)  ENGR 6 PROTEIN)  ENGR 7 PROTEIN)  ENGR 7 PROTEIN  | NULT 1  X1_HUMAN STANDARD, PRT; 156 AA.  44655; 03044; 02261  01-NOV-1995 (Rel. 32, Created)  30-MAY-2000 (Rel. 39, Last amotation update)  30-MAY-2000 (Rel. 39, Last amotation update)  30-MAY-2000 (Rel. 39, Last amotation update)  RADIATION-INDUCIBLE INMEDIATE-ERRIZ GENE IR-1 (IMMEDIATE BARDIATION-INDUCIBLE INDUCIBLE IN |         |                                         |          |                                          |                  |        |            |                     |                 |
| NALIGUARN  NALIGUARN  STANDARD;  PRT; 156 AA.  164665;  10-0031044; 093691;  10-10V-1996 [Rel. 36, Last sequence update)  15-10L-1996 [Rel. 36, Last sequence update)  15-10L-1996 [Rel. 36, Last andoctation update)  15-10L-1996 [Rel. 36, Last andoctation update)  15-10L-1996 [Rel. 36, Last andoctation update)  RADIATION (DIF-2 PROTEIN)  PROTEIN (DIF-2 PROTEIN)  IRAN OR IEX1 OR PROL NO DIF-2.  HOMO SAPLENG HUMAN).  IRAN OR LEACARNA (DIF-2 PROTEIN)  IRAN ORDINE-96101255; Pubmed-8603392;  KONDINE-96101255; Pubmed-8603392;  KONDINE-96101395; Pubmed-8603310;  IRAN ORDINE-96101395; Pubmed-8603310;  IRAN ORDINE-96101395; Pubmed-8603310;  SCHAEFER H. Trausold A. Slegal E. G. Folsch U.R., Schmitt (DIF-2 PROTEIN)  SCHAEFER A. Macchier (C. Aslandis C., Schmitz G., Marra M., Parcons J. MEDLINE-97330426; Pubmed-9196025;  Identification and characterization of a novel monocytec/maccinficant and characterization (Dippoly)saccharide, ceramide, and lysophosphatidylcholine. T., Induction and characterization (Dippoly)saccharide, ceramide, and lysophosphatidylcholine. T., SECHLINIANY SEQUENCE OF 1-106 FROM N.A.  INILIAE L. CARK N., Dubuque T., Elmico R., Marra M., Parcons J. Milliamson A., Wolldmann P., Wilson R., MILLAN N., M | NALIBANAN STANDARD: PRT; 156 AA.  F46655.093044; 092691.  P46655.093044; 092691.  10.NOV-1995 (Rel. 36, Last sequence update)  10.NOV-1995 (Rel. 36, Last sequence update)  10.NOV-1995 (Rel. 36, Last sequence update)  10.NOV-1995 (Rel. 36, Last and custation update)  10.NOV-1995 (Rel. 36, Last and update)  10.NOV-1996 (Rel. 3 | RESI    | ULT 1                                   |          |                                          |                  |        |            |                     |                 |
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| Scheder H., Trauzold A., Siegel E.G., Folsch U.R., Schmidt W., PRG1: a novel early response gene transcriptionally induced pituttary adenylare cyclase activating polypeptide in a pancrearcinoma cell line."; Cancer Res. 56:2641-2641(1996).  [3] ENGUE FROM N.A.  MEDLINE=9733426; Pubmed=9196025; Pletzsch A., Buechler C., Aslanidis C., Schmitz G.; Indentification and characterization of a novel monocyte/mac; differentiation-dependent gene that is responsive to lipopolysaccharide, ceramide, and lysophosphatidylcholine."; Biochem. Biophys. Res. Commun. 235:4-9(1997).  PRELIMINARY SEQUENCE OF 1-106 FROM N.A. TISSUE-PLACENTA; Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M., HG Hultman M., Kucaba T., Le M., Lennon G., Marra M., Parsons J. Submitted (FEB-1995) to the EMBL/GenBank/DBBJ databases.  "SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (POTEN'TAI. INDUCTION: BY RADIATION, TPA, OKADAIC ACID AND TNF-ALPHA.  "INDUCTION: BY RADIATION, TYPE II MEMBRANE PROTEIN (POTEN'TAI. PTM: GLYCOSYLATED.  "CAUTION: REF. 4 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO FRANESHFTS.  "THIS SMISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformalics and the EMBH                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | Schaefer H., Trauzold A., Siegel E.G., Folsch U.R., Schmidt was proved early-response gene transcriptionally induced pituitary adenylate cyclase activating polypeptide in a pancy carcinoma cell line."; Cancer Res. 56:2641-2641(1996).  (3) SEQUENCE FROM N.A. MEDLINE-97339426; pubMed-9196025; Pietzsch A., Buechler C., Aslanddis C., Schmitz G.; Identification and characterization of a novel monocyte/mac; differentiation-dependent gene that is responsive to differentiation-dependent gene that is responsive to lipopolysaccharied, ceramide, and lysophosphatidylcholine."; Blochem. Biophys. Res. Commun. 235:4-9(1997).  Hilliar L., Clark N., Dubuque T., Elliston K., Hawkins M., Hellitm L., Rohlfing T., Tan F., Trevaskis E., Waterston R., Williamson A., Wohldmann P., Wilson R.; Submitted (FER-1995) to the EMBL/GenBank/DDBJ databases.  I. SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (POTENTIAL). PPIN: GLYCOSYLATED.  I. SUBLISHERTY: STRONG, TO MOUSE ORTHOLOG.  I. CAUTION: BF RADIATION, TPA, OKADAIC ACID AND TNF-ALPHA.  FRAMESHIFTS.  This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | XX.     | MEDLIN                                  | E=9622   | :6611                                    | PubMed*          | 865    | 3710;      |                     |                 |
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| pituitary adenylate cyclase activating polypeptide in a pane carcinoma cell line.;  Cancer Res. 56:2641-2641(1996).  SEQUENCE FROM N.A.  MEDLINE-97339476; Pubmed-9196025;  Pietzsch A., Buechler C., Aslanidis C., Schmitz G.;  Indentification and characterization of a novel monocyte/mac;  Aliferantiation-dependent gene that is responsive to lipopolysaccharide, ceramide, and lysophosphatidylcholine.";  Bloochem. Blophys. Res. Commun. 235:4-9(1997).  PRELIMINARY SEQUENCE OF 1-106 FROM N.A.  TISSUB-PLAGENTA;  Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M., He Hulltam M., Kucaba T., Le M., Lennon G., Marra M., Parsons J. Rifkin L., Rohlfing T., Tan F., Trevaskis E., Waterston R., Williamson A., Wohldmann P., Wilson R.;  Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.  -! SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (POTENTIAL)  -! TINDUCTION: BY RADIATION, TPA, OKADAIC ACID AND TNF-ALPHA.  -! SIMILARITY: STRONG, TO MÖUSE ORTHOLOG.  -! SIMILARITY: STRONG, TO MÖUSE ORTHOLOG.  -! CAUTION: REF. 4 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO FRANESHIFTS.  This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Baichformalics and the EMBI                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | pituitary adenylate cyclase activating polypeptide in a pance carcinoma cell line.;  cancer Res. 56:2641-2641(1996).  SEQUENCE FROM N.A.  MEDLINE-97339405, Pubbwed-9196025,  Pitzsch A., Buechler C., Aslanidis C., Schmitz G.;  Pietzsch A., Buechler C., Aslanidis C., Schmitz G.;  Identification and characterization of a novel monocyte/mac;  differentiation-dependent gene that is responsive to lipopolysaccharide, ceramide, and lysophosphatidylcholine.;  Allipopolysaccharide, ceramide, and lysophosphatidylcholine.;  Allipopolysaccharide, ceramide, and lysophosphatidylcholine.;  Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M., He Hultman M., Kucaba T., Le M., Lennon G., Marra M., Parsons J. Rifkin L., Rohlfing T., Tan F., Trevaskis E., Waterston R., Walliamson A., Wohldmann P., Wilson R., Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | RT      | "PRG1:                                  | a nov    | el ear                                   | ly-resp          | ons    | e gene tr  | ٠,                  | 2               |
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| Cancer kes. 30:2041-2041(199b).  SEQUENCE FROM N.A.  SEQUENCE FROM N.A.  MEDLINE-9733426; Pubmed=9196025; Pietzsch A., Buechler C., Aslanidis C., Schmitz G.; Pietzsch A., Buechler C., Aslanidis C., Schmitz G.; Pietzsch A., Buechler C., Aslanidis C., Schmitz G.; Identification and characterization of a novel monocyte/macj differentiation-dependent gene that is responsive to lipopolysaccharide, ceramide, and lysophosphatidylcholine."; Blochem. Biophys. Res. Commun. 235:4-9(1997).  PRELIMINARY SEQUENCE OF 1-106 FROM N.A.  TISSUE-PLACENTA; Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M., HG Hultman M., Rucaba T., Le M., Lennon G., Marra M., Parsons J. Rifkin L., Rohlfing T., Tan F., Trevaskis E., Waterston R., Williamson A., Wohldmann P., Wilson R.; Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases!- SUBCEILLULAR LOCATION: TYPE II MEMBRANE PROTEIN (POTENTIAI!- SUBCEILLULAR LOCATION: TYPE II MEMBRANE PROTEIN (POTENTIAI!- SUMILARITY: STRONG, TO MÖUSE ORTHOLOG!- CAUTION: REF 4 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO FRAMESHIFTS.  This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the Embin                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | Californ Res. 20:2041-2041(199b).  SEQUENCE FROM N.A. MEDILINE-9733426; PubMed-9196025; Pietzsch A. Buechler C., Aslandis C., Schmitz G.; Pietzsch A., Buechler C., Aslandis C., Schmitz G.; Pietzsch A., Buechler C., Aslandis C., Schmitz G.; Identification and characterization of a novel monocyte/macidification and characterization of and lysophosphatidylcholine."; Biochem. Biophys. Res. Commun. 23:4-9(1997).  TISSUE-PLACENTA: HILLIAR Y. Clark N., Dubuque T., Elliston K., Hawkins M., Hellitman M., Kucaba T., Le M., Lennon G., Marra M., Parsons J. Rifkin L., Rohling T., Tan F., Trevaskis E., Walerston R., Williamson A., Wohldmann P., Wilson R.; Submitted (FER-1995) to the EmbL/GenBank/DDBJ databases                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | 1       | Carcin                                  | יים ביים | 0111                                     |                  | 0      | ,          |                     |                 |
| ESCUENCE FROM N.A.  MEDLINE-97339426; PubMed-9196025;  MEDLINE-97339426; PubMed-9196025;  Pietzsch A., Buechler C., Aslanddis C., Schmitz G.;  "Identification and characterization of a novel monocyte/mac;  Ippopolysaccharide, ceramide, and lysophosphatidylcholine.";  Biochem. Biophys. Res. Commun. 235:4-9(1997).  TISSUB-PILGENTRA,  "ILIJER L., Clark N., Dubuque T., Elliston K., Hawkins M., He Hultman M., Kucaba T., Le M., Lennon G., Marra M., Parsons J. Rifkln L., Rohlfing T., Tan F., Trevaskis E., Waterston R., Williamson A., Wohldmann P., Wilson R., Williamson A., Wohldmann P., Wilson R., Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.  -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (POTENTIAL: INDUCTION: BY RADIATION, TPA, OKADAIC ACID AND TNF-ALPHA.: PTM: GLYCOSYLATED.  -!- SIMILARITY: STRONG, TO MOUSE ORTHOLOG  -!- CAUTION: REF. 4 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO FRAMESHIFTS.  This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | SEQUENCE FROM N.A. MEDLINE-97339426; Pubmed-9196025; Pietzsch A., Buechler C., Aslandis C., Schmitz G.; Identification and characterization of a novel moncyte/mac; differentiation-dependent gene that is responsive to lipopolysaccharide, ceramide, and lysophosphatidylcholine."; Blochem. Blophys. Res. Commun. 235:4-9(1997).  PRELIMINARY SEQUENCE OF 1-106 FROM N.A. TISSUE-PLACENTA; Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M., HG Hultman M., Kucaba T., Le M., Lennon G., Marra M., Parsons J. Rifkin L., Rohlfing T., Tan F., Trevaskis E., Waterston R., Williamson A., Wohldmann P., Wilson R.; Submitted (FEB-1995) to the EMBL/Gendank/DDBJ databases SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (POTENTIAL) INDUCTION: BY RADIATION, TPA, OKADAIC ACID AND TNF-ALPHA PTM: GLYCOSYLATED CAUTION: REF. 4 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO FRAMESHIFTS.  This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | 7 ;     | Cancer                                  | Kes.     | 20:204                                   | 1-7041(          | 133    | . ( )      |                     |                 |
| MEDLINE=9739426; PubMed=9196025; Pietzsch N.A. MeCDLINE=9739426; PubMed=9196025; Pietzsch A., Buechler C., Aslanidis C., Schmitz G.; Indentification and characterization of a novel monocyte/macJefferantiation-dependent gene that is responsive to lipopolysaccharide, ceramide, and lysophosphatidylcholine."; Aslochem. Biophys. Res. Commun. 235:4-9(1997).  TISSUE=PLACENTA.; Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M., Helliar L., Clark N., Dubuque T., Elliston K., Hawkins M., Helliason A., Wohldmann P., Wilson R.; Williamson A., Wohldmann P., Tarevaskis E., Waterston R., Williamson A., Wohldmann P.Y., Wilson R.; Submitted (FEB-1995) to the EMBL/GenBank/DBBJ databases! SUBCEILULAR LOCATION: TYPE II MEMBRANE PROTEIN (POTEN'TAI-P TMIS GLYCOSYLATED! PTM: GLYCOSYLATED! SIMILARITY: STRONG, TO MOUSE ORTHOLOG! CAUTION: REF. 4 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO FRANESHFTS.  This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformalics and the EMPI                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | MEDLINE=973426; PubMed=9196025;  PIECESCH A., BueChler C., Aslanddis C., Schmitz G.; Piectsch A., Buechler C., Aslanddis C., Schmitz G.; Piectsch A., Buechler C., Aslanddis C., Schmitz G.; Piectacht and characterization of a novel monocyte/mac: differentiation-dependent gene that is responsive to lipopolyasccharied, ceramide, and lysophosphatidylcholine.; Blochem. Biophys. Res. Commun. 235:4-9(1997).  TISSUE-PLACENTA: HILLIAR Y. Clark N., Dubuque T., Elliston K., Hawkins M., Hellitar L., Rohlfing T., Tan F., Trevaskis E., Waterston R., Williamson A., Wohldmann P., Wilson R.; Submitted (FER-1995) to the EMBL/GenBank/DDBJ databases                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | Z<br>X  | [3]                                     |          |                                          |                  |        |            |                     |                 |
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| Pietzsch A., Buechler C., Aslanidis C., Schmitz G.; "Identification and characterization of a novel monocyte/maccidificatentiation-dependent gene that is responsive to lipopolysaccharide, ceramide, and lysophosphatidylcholine."; Biochem. Biophys. Res. Commun. 235:4-9(1997).  PRELIMINARY SEQUENCE OF 1-106 FROM N.A. TISSUE-PIACENTA; Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M., HG Hultman M., Kucaba T., Le M., Lennon G., Marra M., Parsons J. Rifkin L., Rohlfing T., Tan F., Trevaskis E., Waterston R., Williamson A., Wohldmann P., Wilson R.; Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases: SUBCELLUAR LOCATION: TYPE II MEMBRANE PROTEIN (POTEN'TIAI-PIMUGIYON: BY RADIATION, TPP. II MEMBRANE ALO AND TNF-ALPHAI-PTM: GLYCOSYLATED: SIMILARITY: STRONG, TO MÖUSE ORTHOLOG: CAUTION: REF. 4 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO FRANESHFFES.  This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | Pietzsch A., Buechler C., Aslanidis C., Schmitz G.; "Identification and characterization of a novel monocyte/maco differentiation-dependent gene that is responsive to lipopolysaccharide, ceramide, and lysophosphatidylcholine."; [4] PRELIMINARY SEQUENCE OF 1-106 FROM N.A. TISSUE-PLACENTA; Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M., He Hultman M., Kucaba T., Le M., Lennon G., Marra M., Parsons J. Rifkin L., Rohlfing T., Tan F., Trevaskis E., Waterston R., Williamson A., Wohldmann P., Wilson R., Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (POTENTIAL) INDUCTION: BY RAITATION, TPA, OKADAIC ACID AND TNF-ALPHA PTM: GLYCOSYLATED SMILLANTY: STRONG, TO MOUSE ORTHOLOG CAUTION: REF-4 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO FRAMESHIFTS. This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | XX.     | MEDLIN                                  | E=9733   | 9426                                     | PubMedia         | 010    | 6025.      |                     |                 |
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| differentiation and characterization of a monocyte/macci<br>lipopolysaccharide, ceramide, and lysophosphatidylcholine.";<br>Blochem. Blophys. Res. Commun. 235:4-9(1997).  [4] PRELIMINARY SEQUENCE OF 1-106 FROM N.A. TISSUS-PLACENTA; Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M., Hc Hultman M., Kucaba T., Le M., Lennon G., Marra M., Parsons J. Rifkin L., Rohlfing T., Tan F., Trevaskis E., Waterston R., Williamson A., Wohldmann P., Wilson R.; Williamson A., Wohldmann P., Wilson R.; Submitted (FER-1995) to the EMBL/GenBank/DDBJ databases SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (POTENTIAL) INDUCTION: BY EARDIATION, TPA, OKADAIC ACID AND TNF-ALPHA PTM: GLYCOSYLATED CAUTION: REF. 4 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO FRAMESHIFTS.  This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EmBI                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | differentiation dend characterization of a monocyte/macci<br>lipopolysaccharide, ceramide, and lysophosphatidylcholine.";<br>Biochem. Biophys. Res. Commun. 235:4-9(1997).<br>[4] PRELIMINARY SEQUENCE OF 1-106 FROM N.A. TISSUE-PIACENTA; Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M., Halliar L., Clark N., Lennon G., Marra M., Parsons J. Williamson A., Wohldman P., Wilson R.; Williamson A., Wohldman P., Wilson R.; Williamson A., Wohldman P., Wilson R.; Submitted (FEB-1995) to the EMBL/Genbank/DDBJ databases SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (POTENTIAL) INDUCTION: BY RADIATION, TPA, OKADAIC ACID AND TNF-ALPHA PTM: GLYCOSYLATED CAUTION: REF. 4 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO FRAMESHIFTS.  This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | S E     | 110001                                  |          | Puecii.                                  | Ler C.,          | A.     | raniois C  | SCHMILEZ            |                 |
| differentiation-dependent gene that is responsive to lipopolysaccharide, ceramide, and lysophosphatidylcholine."; Blochem. Biophys. Res. Commun. 25:4-9(1997).  [4] PRELIMINARY SEQUENCE OF 1-106 FROM N.A. TISSUE-PLACENTA; Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M., HCHIllier L., Roubling T., Le M., Lennon G., Marra M., Parsons J. Rikkin L., Rohlfing T., Tan F., Trevaskis E., Waterston R., Williamson A., Wohldmann P., Wilson R.; Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (POTENITAL: INDUCTION: BY RADIATION, TPA, OKADAIC ACID AND TNF-ALPHA PTM: GLYCOSYLATED SMILARITY: STRONG, TO MOUSE ORTHOLOG CAUTION: REF. 4 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO FRAMESHIFTS.  This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the Emfil                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | differentiation-dependent dene that is responsive to lipopolysaccharide, ceramide, and lysophosphatidylcholine."; Blochem. Biophys. Res. Commun. 235:4-9(1997).  [4] PRELIMINARY SEQUENCE OF 1-106 FROM N.A. TISSUE-PLACENTA; HILLIPE L., Clark N., Dubuque T., Elliston K., Hawkins M., He Hiltman M., Kucaba T., Le M., Lennon G., Marra M., Parsons J. Rifkin L., Rohlfing T., Tan F., Trevaskis E., Walterston R., Williamson A., Wohldmann P., Wilson R.; Submitted (FER-1995) to the EMBL/GenBank/DDBJ databases.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | . E     | ייייייייייייייייייייייייייייייייייייייי | 11100    | TOU WILL                                 | u chara          | cre    | rization   | a novel             | :e/macrophage   |
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| Biochem. Biophys. Res. Commun. 235:4-9(1997).  [4] PRELIMINARY SEQUENCE OF 1-106 FROM N.A. TISSUE-PLACENTA;  TISSUE-PLACENTA;  Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M., Hc Hultman M., Kucaba T., Le M., Lennon G., Marra M., Parsons J.  Rifkin L., Rohlfing T., Tan F., Trevaskis E., Waterston R., Williamson A., Wohldmann P., Wilson R.;  Submitted (FEB-1995) to the EMBL/GenBank/DBBJ databases.  SUBCEILLULAR LOCATION: TYPE II MEMBRANE PROTEIN (POTEN'TAI-  INDUCTION: BY RADIATION, TPA, OKADAIC ACID AND TNF-ALPHA.  PTM: GLYCOSYLATED.  CAUTION: REF. 4 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO FRANTSHIFTS.  This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformalics and the EMBI                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | Biochem. Biophys. Res. Commun. 235:4-9(1997).  [4] PRELIMINARY SEQUENCE OF 1-106 FROM N.A. TISSUE—PLACENTA.  TISSUE—PLACENTA.  Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M., He Hultman M., Kucaba T., Le M., Lennon G., Marra M., Parsons J. Rifkin L., Rohlfing T., Tan F., Trevaskis E., Waterston R., Walliamson A., Wohldmann P., Wilson R.; Submitted (FEB-1995) to the EMBL/GenBank/DBBJ databases.  -! SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (POTENTIAL).  -! INDUCTION: BY RAINATION, TPA, OKADAIC ACID AND TNF-ALPHA.  -! TINDUCTION: BY RAINATION, TPA, OKADAIC ACID AND TNF-ALPHA.  -! SIMILARITY: STRONG, TO MOUSE ORTHOLOG.  -! CAUTION: REF. 4 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO FRAMESHIFTS.  This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | KT      | 11popo                                  | lysacc   | haride                                   | , ceram          | ide    | , and lys  | hosphatidylchol     | ne.             |
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| PRELIMINARY SEQUENCE OF 1-106 FROM N.A.  TISSUB-PLACENTA;  Hiller L., Clark N., Dubuque T., Elliston K., Hawkins M., He Hultman M., Kucaba T., Le M., Lennon G., Marra M., Parsons J. Rifkin L., Fahlfing T., Tan F., Trevaskis E., Waterston R., Williamson A., Wohldmann P., Wilson R., Walliamson A., Wohldmann P., Wilson R., Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.  -! SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (POTENTIAL: INDUCTION: BY RADIATION, TPA, OKADAIC ACID AND TNF-ALPHA-: PTM: GLYCOSYLATED.  -! SIMILARITY: STRONG, TO MOUSE ORTHOLOG.  -! CAUTION: REF. 4 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO FRAMESHIFTS.  This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | PRELIMINARY SEQUENCE OF 1-106 FROM N.A. TISSUE-PLACENTA:  Hiller L., Clark N., Dubuque T., Elliston K., Hawkins M., Hc Hultman M., Kucaba T., Le M., Lennon G., Marra M., Parsons J. Rifkin L., Rohlfing T., Tan F., Trevaskis E., Waterston R., Williamson A., Wohldmann P., Wilson R.; Submitted (FER.1955) to the EMBL/GenBank/DBBJ databases                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | RN      | [4]                                     |          |                                          |                  |        |            |                     |                 |
| TISSUE=PLACENTA; Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M., He Hillier L., Clark N., Le M., Lenon G., Marra M., Parsons J. Rifkin L., Rohlfing T., Tan F., Trevaskis E., Walrerston R., Williamson A., Wohldmann P., Wilson R.; Williamson A., Wohldmann P., Wilson R.; Submitted (FER 1995) to the EMBL/GenBank/DDBJ databases                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | TISSUE-PLACENTA; Hiller L., Clark N., Dubuque T., Elliston K., Hawkins M., Hellitar L., Kucaba T., Le M., Lennon G., Marra M., Parsons J. Rikin L., Rohlfing T., Tan F., Trevaskis E., Waterston R., Wallamson A., Wohldmann P., Wilson R.; Submitted (FEB-195) to the EMBL/GenBank/DDBJ databases SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (POTENTIAL) INDUCTION: BY RADIATION, TPA, OKADAIC ACID AND TNF-ALPHA PTM: GLYCOSYLATED SIMILARIY: STRONG, TO MOUSE ORTHOLOG CAUTION: REF-4 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO FRAMESHIFTS.  This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | RP      | PRELIM                                  | INARY    | SECUEN                                   |                  | -10    | 6 FROM N.  | Ä                   |                 |
| Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M., Hultman M., Kucaba T., Le M., Lennon G., Marra M., Parsons J. Ritkin L., Rohlfing T., Tan F., Trevaskis E., Waterston R., Williamson A., Wohldmann P., Wilson R., Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M., Hultman M., Kucaba T., Le M., Lennon G., Marra M., Parsons J. Rifkin L., Rohlfing T., Tan F., Trevaskis E., Waterston R., Williamson A., Wohldmann P., Wilson R., Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.  -! SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (POTENTIAL: INDUCTION: BY RADIATION, TPA, OKADAIC ACID AND TNF-ALPHA.: PTM: GLYCOSYLATED.  -! SIMILARITY: STRONG, TO MOUSE ORTHOLOG! CAUTION: REF. 4 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO FRAMESHIFTS.  This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | SC      | TISSUE                                  | -PLACE   | N'TA:                                    |                  |        |            |                     |                 |
| Hultman M., Kucaba T., Leavash T., Leavash S., Marra M., Parsons J. Rifkin L., Rohlfing T., Tan F., Trevashis E., Waterston R., Williamson A., Wohldmann P., Wilson R.; Materston R., Submitted (FEB-1955) to the EMBL/GenBank/DDBJ databases SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (POTEN'TAI INDUCTION: BY RADIATION, TPA, OKADAIC ACID AND TNF-ALPHA PTM: GLYCOSYLATED SIMILARITY: STRONG, TO MÖUSE ORTHOLOG CAUTION: REF. 4 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO FRAMESHIFTS.  This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | Hultman M., Kucaba T., Le M., Lennon G., Marra M., Parsons J. Rifkin L., Rohlfing T., Tan F., Trevaskis E., Waterston R., Williamson A., Wohldman P., Wilson R.; Submitted (FEB-195) to the EMBL/Genbank/DDBJ databases                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | RA      | Hillip                                  |          | Clark                                    | 2                | 2      | e          | 4 40                | 2 - 1 - 1       |
| RIKKIN L., Rohlfing T., Ten F., Lennon G., Marra M., Parsons J. Rikkin L., Rohlfing T., Tan F., Trevaskis E., Waterston R., Williamson A., Wohldmann P., Wilson R., Submitted (FEB-1995) to the EMBL/GenBank/DbBJ databases.  -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (POTENTIAL-I INDUCTION: BY RADIATION, TYPE II MEMBRANE PROTEIN (POTENTIAL-I SIMILARITY: STRONG, TO MOUSE ORTHOLOG.  -!- PTM: GLYCOSYLATED.  -!- PTM: GLYCOSYLATED.  -!- CAUTION: REF-4 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO FRAMESHIFTS.  This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | RIKAIN L., Rohlfing T., Tan F., Trevaskis E., Waterston B., Williamson A., Wohldmann P., Wilson R.; Trevaskis E., Waterston R., Williamson A., Wohldmann P., Wilson R.; Waterston R., Williamson A., Wohldmann P., Wilson R.; Bundtted (FEB-1995) to the EmbL/Genaank/DDBJ databases.  -: Submitted (FEB-1995) to the EmbL/Genaank/DDBJ databases.  -: SubcELLULAR LOOPTION: TYPE II MEMBRAND PROTEIN (POTENTIAL)  -: FINDUCTION: BY RADIATION, TPA, OKADAIC ACID AND TNF-ALPHA.  -: SIMILARITY: STRONG, TO MOUSE ORTHOLOG.  -: CAUTION: REF. 4 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO FRAMESHIFTS.  This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the Embl.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | 4 6     | 11.11.10                                |          | CLAIN                                    | a., Dun          | д<br>: |            | con K., Hawi        | HOIMAN M        |
| Milliamson A., Wohldmann P., Wilson R.;  Submitted (FER-1995) to the EMBL/GenBank/DDBJ databases.  SubcElluLAR LOCATION: TYPE II MEMBRANE PROTEIN (POTENTIAL-  INDUCTION: BY EMDIATION, TPA, OKADAIC ACID AND TNF-ALPHA.  SMILARITY: STRONG, TO MOUSE ORTHOLOG.  SMILARITY: STRONG, TO MOUSE ORTHOLOG.  CAUTION: REF. 4 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO FRAMESHIFTS.  This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | MAILIAMSON A., WANDIANG T., TAR F., TREVARKIS E., WALERSTON R., WAILIAMSON A., WANDIAMANN P., WISON R., SUBMITTED A., WANDIAMANN P., WISON R., SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (POTENTIAL: INDUCTION: BY RADIATION, TPA, OKADAIC ACID AND TNF-ALPHA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | Ç 4     | D: 61. 1.                               |          | Aucaba                                   | , ,              | ε      | , Lennon   | , Marra M.,         | ה               |
| Willamson A., Wohldmann P., Wilson R.; Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (POTENTIAL!- PTM: GLYCOSYLATED!- PTM: GLYCOSYLATED!- STMILARITY: STRONG, TO MOUSE ORTHOLOG!- CAUTION: REF. 4 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO FRAMESHIFTS.  This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | Willamson A., Wohldmann P., Wilson R.; Submitted (FEB-195) to the EMBL/Genbank/DDBJ databases SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (POTENTIAL INDUCTION: BY RADIATION, TPA, OKADAIC ACID AND TNF-ALPHA PTM: GLYCOSYLATED SIMILARITY: STRONG, TO MOUSE ORTHOLOG CAUTION: REF.4 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO FRAMESHIFTS.  This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | ž i     | KILKIN                                  | ۲<br>:   | OUTITUO                                  |                  | a<br>a | r., Treva  | is E., Water        | I R.,           |
| Submitted (FER-1995) to the EMBL/GenBank/DBBJ databases SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (POTENTIAL) INDUCTION: BY RADIATION, TPA, OKADAIC ACID AND TNF-ALPHA STMILARITY: STRONG, TO MOUSE ORTHOLOG CAUTION: REF-4 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO FRAMESHIFTS.  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EMBI                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | Submitted (FER-1995) to the EMBL/GenBank/DDBJ databases!- SUBCEILLULAR LOCATION: TYPE II MEMBRANE PROTEIN (POTENTIAL) -!- INDUCTION: BY RADIATION, TPA, OKADAIC ACID AND TNF-ALPHA!- PTM: GLYCOSYLATED!- CAUTION: REF. 4 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO FRANESHIFTS.  This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | ¥.      | WILLIA                                  | mson A   | ., won.                                  | Idmann           | :<br>ط |            |                     |                 |
| -:- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (FOTEN"TAI -:- INDUCTION: BY RADIATION, TPA, OKADAIC ACID AND TNF-ALPHA:- PTM: GLYCOSYLATED -:- SIMILARITY: STRONG, TO MOUSE ORTHOLOG:- CAUTION: REF. 4 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO FRAMESHEYS.  This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (POTENTIAL INDUCTION: BY RADIATION, TPA, OKADAIC ACID AND TNF-ALPHA!- PTM: GLYCOSYLATED!- SIMILARITY: STRONG, TO MOUSE ORTHOLOG!- CAUTION: REF. 4 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO FRAMESHIFTS. This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | RL      | Submit                                  | ted (F   | EB-199                                   | 5) to t          | ě      |            | k/DDBJ datab        |                 |
| -!- INDUCTION: BY RADIATION, TPA, OKADAIC ACID AND TNF-ALPHA -!- PTM: GLYCOSYLATED!- SIMILARITY: STRONG, TO MOUSE ORTHOLOG!- CAUTION: REF. 4 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO FRAMESHIFTS. This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | -!- INDUCTION: BY RADIATION, TPA, OKADAIC ACID AND TNF-ALPHA!- PTH: GLYCOSYLATED!- SIMILARITY: STRONG, TO MOUSE ORTHOLOG!- CAUTION: REF.4 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO FRAMESHIFTS. This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | ပ္ပ     | os -i-                                  | BCELLU   | LAR LOC                                  | CATION:          | ΤY     |            | TEIN                | ENTIAL          |
| -!- PTM; GLYCOSYLATED!- SIMILARITY: STRONG, TO MOUSE ORTHOLOG!- CAUTION: REF. 4 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO FRAMESHIFTS. This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | -!- PTM: GLYCOSYLATED!- SIMILARITY: STRONG, TO MOUSE ORTHOLOG!- CAUTION: REF.4 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO FRANESHETS. This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | ပ္ပ     | NI -i-                                  | DUCTIO   | N: BY                                    | RADIATI          | ON.    |            |                     | ALDHA           |
| -i- SIMILARITY: STRONG, TO MOUSE ORTHOLOG!- CAUTION: REF.4 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO FRANESHIFTS. This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | -1. SIMILARITY: STRONG, TO MOUSE ORTHOLOG1. CAUTION: REF. 4 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO FRAMESHIFTS. This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | ပ္ပ     | -!- PT                                  | M: GLY   | COSYLAT                                  | red.             |        |            |                     |                 |
| -:- CAUTION: REF.4 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO FRAMESHIFTS.  This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | -:- CAUTION: REF.4 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO FRAMESHIFTS.  This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | CC      | 15 -1-                                  | MTLART   | TY. ST                                   | SONG T           | 2      | G          | 0100                |                 |
| FRAMESHETS. This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | FRANCEING NEED TO THE SWISS-PROT ENTRY IS COPYLIGHT. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | ر       | 10                                      | NOT ELL  |                                          | Manoas<br>Manoas | 5 5    | រដូ        |                     |                 |
| This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | )<br>ני |                                         | 10110    | 1 0 8 6                                  | SECOEN.          | 1      | OIFFERS F  | THAI SHOWN          |                 |
| This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EMBI                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | و ر     | 7                                       | AMESHI   | 13.                                      |                  |        |            |                     |                 |
| This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | ນ       | :                                       |          |                                          |                  | 1      |            |                     |                 |
| between the Swiss Institute of Bioinformatics and the EMBI                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | between the Swiss Institute of Bioinformatics and the EMBI                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | S       | v.                                      | WISS-P   | ROT Ant                                  | rry is           | Ċ      | Ticht      | 4000                | •               |
| between the Swiss Institute of Bioinformatics and the EMBL                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | between the Swiss Institute of Bioinformatics and the EMBL                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | ָ<br>ני | o                                       | י מידא   | 102                                      | -1 Y 15          | do     | viigni. I  | anced               | Ø               |
| TOTAL DID CONTRACTOR TO CONTRA |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | ပ္ပ     | betwee                                  | n the    | Swiss                                    | Instit           | ute    | of Bioin   | s and               | 租               |

C2H2-TYPE.

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a litense agreement (See http://www.isb-sib.ch/announce/or send an email to licensedisb-sib.ch).
 R TRANSFAC; T00395; -.

R TRANSFAC; T00395; -.

DR FLYBASE; FBGN0001180; hb.

DR PFAM; PF00096; z CC2H2; 6.

DR PRINTS; PR00048; ZINC_FINGER_C2H2; 3.

R Developmental protein; Gap; Zinc_finger; Metal-binding; DNA-binding;

Depeat; Nuclear protein; Polymorphism.

Propeat; Nuclear protein; Polymorphism.

ZINC FINGERS II.

ZINC FINGERS II.
 EMBL, Y00274; CAA68377.1; --
EMBL, U17742; AAB60232.1; --
EMBL; AE003680; AAF54270.1; --
PIR; A29253; A29253.
 757
69
108
122
262
291
 POLYMORPHISM
 ZN_FING
ZN_FING
DOMAIN
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POLY-GLN.
POLY-HIS.
C2H2-TYPE.
C2H2-TYPE.
C2H2-TYPE.
C2H2-TYPE.
C2H2-TYPE.

DOMAIN ZN\_FING

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RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb D.L.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Parleb J.M.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Sviersas K., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Zheng K.H., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
The genome sequence of Drosophila melanogaster.";
 Tautz D., Nigro L., "Migro L.," "Microevolutionary divergence pattern of the segmentation gene hunchback in Drosophila."; how. Biol. Evol. 15:1403-411(1998).

- FUNCTION: GAP CLASS SEGMENTATION PROTEIN THAT CONTROLS DEVELOPMENT OF HEAD STRUCTURES.
 SUBCELLULAR LOCATION: NUCLEAR.

SUBCELLULAR LOCATION: NUCLEAR.

ISSUE SPECIFICITY: IN EMBRYO, EXPRESSION OF MATERNAL TRANSCRIPT
IS HIGHEST IN ANTERIOR REGION. EXCOTIC TRANSCRIPT IS EXPRESSED IN
ANTERIOR REGION UNTIL FREE MEDINING OF GASTRULATION AND IN
EXPRESSED IN DEVELOPING NERVOUS SYSTEM.

EXPRESSED IN DEVELOPING NERVOUS SYSTEM.

DEVELOPMENTAL STAGE: EXPRESSED MATERALLY AND ZYGOTICALLY

SERPESSION OF THE MATERNAL TRANSCRIPT DECREASES UNTIL EMBRYONIC
STAGE 14, ZYGOTIC TRANSCRIPT IS FIRST DETECTED AT STAGE 11.

SIMILARITY: BELONGS TO THE HUNCHBACK FAMILY OF C2H2-TYPE ZINC.
 SEQUENCE OF 281-349 FROM N-A.

MEDLINE-93066327; PubMed=1438276;

SEMEMER R.J. Retzlaff M., Goerlich K., Sander K., Tautz D.;

SCHOULIONARY CONSERVATION pattern of zinc-finger domains of Drosophila segmentation genes.";

Proc. Natl. Acad. Sci. U.S.A. 89:10782-10786(1992).
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52 PSASRGHRKRSRRVLYPRVVRRQLPVEEPNPAKRLLFLLLTIVFCOILMAEEGVP---- 106
 Gaps
 2 CHSRSCH-----PTWTILQAPTPAPS---TIPGPRRGSGPEIFTFDPLPEPAAAPAGR 51
 107 -----APLPPEDAPNAASLAPTPVSPVLEPFNLTSEPSDYALDLSTFLQQH 152
 Length 758;
 Indels
83113 MW; AD74802EB856ACD7 CRC64;
 26;
 DB 1;
 Score 94.5; DB
Pred. No. 1.5;
9; Mismatches
 11.5%; Sco.
24.6%; Prective 19; 1
 43; Conservative
 Ouery Match
Best Local Similarity
Matches 43; Conserv
 433
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Search completed: January 30, 2001, 23:12:24 Job time: 4005 sec

ERM\_HUMAN P41161;

ERM\_HUMAN

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factors.

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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocgayne J.D.,
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocgayne J.D.,
R.A. Ananatides P.G., Scherer S.E., Li P.W., Hoskins K.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
Baradon R.C., Rogers Y.-H.C., Blazel R.G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
R.A. Baril J.F., Agbayani B.P., Berman B.P., Bhandari D., Bolshakov S.,
R.A. Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
R.A. Borkova D., Botchan M., Butler H., Cadieu E., Center A., Chandra I.,
R.A. Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
R.A. Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
R.A. Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
R.A. Cherry J.M., Cayley S., Dahlke C., Davenport L.B., Davies R.,
A cherry J.M., Cayley S., Dallke C., Davenport L.B., Davies R.,
A cherry J.M., Cayley S., Dallke C., Davenport L.B., Davies R.,
A cherry J.M., Heinan T.J., Herris M., Glasser K.,
R.A. Fosler C., Gabriellian A.E., Garrell J.H., Gu Z., Gelbart W.M., Glasser K.,
R.A. Fosler C., Gabriellian A.E., Garrell J.H., Gu Z., Gelbart W.M., Glasser K.,
A lostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
R.A. Liasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
R.A. Martel B., McIntosh T.C., McLeod M.P., Moshrefi A.,
R.A. Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 Margolis J.S., Borowsky M., Shim C.W., Posakony J.W.;
"A small region surrounding the distal promoter of the hunchback gene directs maternal expression.";
Dev. Biol. 163:381-388(1994).
 Endopterygota; Diptera; Brachycera; Muscomorpha;
 208 PENOYPSEORFOROLSEP-----CHPFPPOPGVPGVPGDNRPSYHROMSEPIV 252
 3 HSRSCHPTMTILQAPTPAPSTIPGPRRGSGPEIFTFDPLPEPAAAPAGRPSASRGHRKRS 62
 Metazoa, Arthropoda; Tracheata; Hexapoda; Insecta;
 107 --APLPPED-----APNAASLAPTPVSPVLEPFNLTSEPSDYALD 144
 253 PAAPPPPQGFKQEYHDPLYEHGVPGMPGPPAHGFQSPMGIKQEPRDYCVD 302
 SEQUENCE FROM N.A.
STRAIN=OREGON R: TISSUE=EMBRYO;
STRAIN=OREGON R: Lehmann R: Schnuerch H.; Schuh R.; Selfert E.;
Kienlin A., Jones K.; Jaeckle H.;
"Finger protein of novel structure encoded by hunchback; a :
 member of the gap class of Drosophila segmentation genes."
Nature 327:383-389(1987):
 Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases
 RRVLYPRVVRRQLPVEEPNPAKRLLFLLLTIVFCQILMAEEGVP
 HUNB_DROME STANDARD; PRT; 758 AA. P05084; 024018; 01-APF-1988 (Rel. 07, Created) 01-OCT-2000 (Rel. 40, Last sequence update) 01-OCT-2000 (Rel. 40, Last annotation update)
 SPECIFICITY.
 Ephydroidea; Drosophilidae; Drosophila.
 Drosophila melanogaster (Fruit fly)
 SEQUENCE FROM N.A., AND TISSUE SP
MEDLINE=94259232; Pubmed-8200478;
 Pterygota; Neoptera;
 SEQUENCE FROM N.A.
 HUNCHBACK PROTEIN.
 REVISION TO 525.
 STRAIN-BERKELEY
 Eukaryota;
 Tautz
 HUNB_DROME
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 MEDLINE-94203669; Pubmed-8152800; Monte D., Baert J.-L., Defossez P.-A., de Launoit Y., Stehelin D.; Monteular cloning and characterization of human ERM, a new member of the Ets family closely.related to mouse PEA3 and ER81 transcription
 Gaps
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 57;
 |[2]
SEQUENCE FROM N.A.
MEDLINE-96299763; PubMed-8661127;
PubMed-8661127
 Length 510;
 Indels
 01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
ETS-RELATED PROTEIN ERM (ETS TRANSLOCATION VARIANT 5).
 ETS-DOMAIN.
B7CE40A33927F46E CRC64;
 62;
 DB 1;
 510 AA.
 Mismatches
 11.5%; Score 94.5; 22.4%; Pred. No. 1;
 PRINTS; PRO0178; Ets; 1.
PRINTS; PRO0454; ETSDOMAIN.
PROSITE; PS000345; ETS_DOMAIN.1; 1.
PROSITE; PS00061; ETS_DOMAIN.2; 1.
PROSITE; PS50061; ETS_DOMAIN.3; 1.
DNA-Binding; Nuclear protein.
DNA_BIND 368 448 ETS-DOMAIN.3; 1.
SEQUENCE 510 AA; 57838 MW; B7CE4(
 EMBL, X96380; CAA65246.1, JOINED. EMBL, X96382; CAA65246.1; JOINED. EMBL, X96379; CAA65246.1; JOINED. EMBL, X96377; CAA65246.1; JOINED. EMBL, X96377; CAA65246.1; JOINED. EMBL, X96375; CAA65246.1; JOINED. PTR, S43692; S43692.
 PRT;
 13;
 EMBL; X76184; CAA53778.1; -. EMBL; X96381; CAA65246.1; -.
 Oncogene 9:1397-1406(1994).
 Ouery Match 11.5
Best Local Similarity 22.4
Matches 38; Conservative
 344 VGPKTEDCKGDPFKRT 359
 STANDARD;
 INTERPRO; IPR000418; -.
 ETV5 OR ERM.
Homo sapiens (Human).
 SEQUENCE FROM N.A.
 TISSUE-TESTIS;
 MIM; 601600;
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 5
"Molecular cloning of chicken myosin-binding protein (MyBP) H (86-kDa protein) reveals extensive homology with MyBP-C (C-protein) with conserved (mmnooglobulin C2 and fibronectin type III motifs."; J. Biol. Chem. 268:3670-3676(1993).

-: FUNCTION: BINDS TO MYOSIN, PROBABLY INVOLVED IN INTERACTION WITH THICK MYOFILAMENTS IN THE A-BAND.
 PRINTS; PRO0014, FNTYPEIII.
PRINTS; PR01217; PRICHEXTENSN.
Immunoglobulin domain; Cell adhesion; Muscle protein; Thick filament;
 69 RVVRRQLPVEEPNPAKRLLFILLTIVFCQILMAEEGVPAPLPPEDAPNAASLAPTPVSPV 128
 93 AAEHAPTPTHEAAPAH------125
 Gaps
 92
 9 PTMTILQAPTPAPSTIPGPRRGSGPEIFTFDPLPEPAAAPAGRPSASRGHRKRSRRVLYP 68
 BE ALSO EXPRESSED
 38 РТРКЕСНАРТРКЕЕНАРРРКЕЕНАР----РРКЕЕНАРАРАВЕТРРАРЕНРРДАЕОРААР
 XP2_XENLA STANDARD; PRT; 439 AA.
17437; Q08044;
01-AUG-1990 (Rel. 15, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-FEB-1995 (Rel. 39, Last annotation update)
SKIN SECRETONY PROTEIN XP2 PRECURSOR (APEC PROTEIN).
Xenopus laevis (African clawed frog).
Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Balrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
 -1- TISSUE SPECIFICITY: SKELETAL MUSCLE, SEEMS TO BE ALSO EXPRES
THE SLOW TONIC ALD MUSCLE, NOT DETECTED IN GIZZARD OR HEART.
-1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
-1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
-1- SIMILARITY: BELONGS TO THE MYBP FAMILY.
 DB 1; Length 537;
 61; Indels
 FIBRONECTIN TYPE-III.
IG-LIKE C2-TYPE DOMAIN.
FIBRONECTIN TYPE-III.
IG-LIKE C2-TYPE DOMAIN.
T -> G (IN AA SEQUENCE).
A -> P (IN AA SEQUENCE).
A -> K (IN AA SEQUENCE).
W, 06C4CF0EFEIDD233 CRC64;
 Score 95.5; DB
Pred. No. 0.89;
5; Mismatches
 SEQUENCE OF 1-25 AND 344-439 FROM N.A.
 MEDLINE-92332564; PubMed-1629230;
Hauser F., Roeben C., Hoffmann W.;
 ;
9
 Ψ
W
 11.68; 27.58;
 EMBL; L05605; AAA21418.1; -.
 129 LEPFNLTSEPSDYALDLS 146
 -EPEKPKEEPPSVPLSLA 142
 15
58678 1
 INTERPRO; IPR001777; ...
INTERPRO; IPR002965; ...
INTERPRO; IPR003006; ...
PFAM; PF00041; fn3; 2.
PFAM; PF00047; ig; 2.
 Conservative
 Kenopodinae; Xenopus.
 Query Match
Best Local Similarity
 9
15
537 AA;
 38;
 CONFLICT
CONFLICT
SEQUENCE
 CONFLICT
 DOMAIN
DOMAIN
 Repeat.
 DOMAIN
 DOMAIN
 Matches
 126
 XP2_XENLA
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 POTENTIAL.

SKIN SECRETORY PROTEIN XP2.

PYROLIDONE CARBOXLIC ACID (PROBABLE).

33 X REPEATS OF G-[GE]-[AP](2,4)-A-E.

P-TYPE 1.

P-TYPE 2.

BY SIMILARITY.

xP2, a new member of the P-domain peptide family of potential growth factors, is synthesized in Xenopus laevis skin.";
J. Biol. Chem. 267:14451-14455(1992).
 TISSUE=SKIN;
MEDLINE=90127399; PubMed=2298293;
Gmachl M., Berger H., Thalhammer J., Kreil G.;
"Dermal glands of Xenopus laevis contain a polypeptide with a highly
 PIR: S07498; SKRAG.
PIR: S07498; SKRAG.
PIR: A37331; A37331.
HSSP; P04155; 1P52.
INTERPRO; IPRO00689; Lrefoil; 2.
PRINTS; PRO00680; PTREFOIL.
PROSITE; PS00025; P_TREFOIL.
S19nal; Growth factor; Alternative splicing; Amphibian skin; Repeat.
S19nal; Growth factor; Alternative splicing; Amphibian skin; Repeat.
 15 QAPTPAP----STIPGPRRGSGPEIFTFDPLPEPAAAPAGRPSASRGHRKRSRRVLYPRV 70
 247 EAPAPAPAEGEAPAPAPAEGEAPA----PAPAEGEAPAPAPAEGEAPAPAEGEAPAPAF
 71 VRRQLPVE-----EPNPAKRLLFLLLTIVFCQILMAEEGVPAPLPPEDAPNAASLAPTP 124
 ------AEGGAPAAAPAEGGAPAPAPVE 343
 57; Indels 38; Gaps
 Score 95; DB 1; Length 439;
Pred. No. 0.8;
 H -> S (IN REF. 2).
C -> W (IN REF. 2).
38C4A4B57CBAE778 CRC64;
 6; Mismatches
 EMBL; M90095; AAA50001.1; -.
EMBL; X51394; CAA35759.1; ALT_FRAME.
 41173 MW;
 11.5%;
25.7%;
 [2]
SEQUENCE OF 3-439 FROM N.A.
 302 AEGEAPAPAPAEGGAPSP----
 Conservative
 125 VSPVLE----PFNLT 135
 18
 AA;
 Query Match
Best Local Similarity
Matches 35; Conserv
 3
18
439 /
 23
23
26
350
397
351
361
361
361
361
361
408
 DISULFID
 CONFLICT
CONFLICT
SEQUENCE
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 ۲,
 9
 69 RVVRRQLPVEEPNPAKRLLFLLLTIVFCQILMAEEGVPAPLP-PEDAPNAASLAPTPVSP 127
 64 RVLY-PRVVRRQLPVEEPNPAKRLLFLLLTIVFCQILMAEEGVPAP-----LPPED 113
 Gaps
 Gaps
 4 SRSCHPTMTILQAPTPAPSTIPGPRRGSGPEIFTFDPLPEPAAAPAGRPSASRGHRKRSR 63
 sequence of the Orgyia pseudotsugata multinucleocapsid nuclear
 9 PTWTILQAPTPAPSTIPGPRRGSGPEIFTFDPLPEPAAAPAGRPSASRGHRKRSRRVLYP
 173 SRHGHPPPPTYAQPPTPIYSPSPQVQPPP---TYSPPPPTHVQPTPSP-PSRGHQPQPP
 45;
 44;
 271 AYAQSPOPSPTYSPPPPTYSPPPPSPIYSPPPPAYSPSPPPTPTFSPPPPA 323
 114 A------PNAASLAPTPVSPVLEPFNLTSEPSDYALDLSTFLQQHPA 154
 Orgyia pseudotsugata multicapsid polyhedrosis virus (OpMNPV).
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
 Score 99.5; DB 1; Length 279;
Pred. No. 0.22;
6; Mismatches 45; Indels 4
3 X APPROXIMATE TANDEM REPEATS. 641DD2278AB28524 CRC64;
 Length 620;
 75; Indels
 MEDLINE-97271300; PubMed-9126251;
Ahrens C.H., Russell R.R., Funk C.J., Evans J., Harwood
Rohrmann G.F.;
 6FA4DAA01009DBF0 CRC64;
 DB 1;
 !- SIMILARITY: TO CORRESPONDING ORF IN ACMNPV.
 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
NOV-1997 (Rel. 35, Last annotation update)
HYPOTHETICAL 29.3 KDA PROTEIN (ORF92).
 12.2%; Scor.
24.3%; Pred. No. v...
've 12; Mismatches
 Score 100; DB 1
Pred. No. 0.46;
 279
 PRT;
 Hypothetical protein.
SEQUENCE 279 AA; 29289 MW;
600 3
65406 MW;
 ch 12.1%;
1 Similarity 27.3%;
36; Conservative
 EMBL; U75930; AAC59091.1; -.
 42; Conservative
 polyhedrosis virus genome.
Virology 229:381-399(1997)
 STANDARD;
 128 TPTPSPTPTPSPTPSP-
 128 VLEPFNLTSEPS 139
 TPSP---TPTPS 172
 Nucleopolyhedrovirus.
499 6
620 AA;
 Query Match
Best Local Similarity
Matches 36; Conserv
 Similarity
 Y091_NPVOP
010341;
DOMAIN
SEQUENCE
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 Best Local
 Y091_NPVOP
 Matches
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 ŵ
 2669 SSRASAASSSGSRARRHRRARSLARATQASATTQGWRPPALPDTVAPVTDFARPPAPPKP 2728
 SEQUENCE FROM N.A.
MEDLINE-88274227; Pubmed=2839594;
MGGeoch D.J., Dalrymple M.A., Davison A.J., Dolan A., Frame M.C.,
MGNab D., Perry L.J., Scott J.E., Taylor P.;
"The complete DNA sequence of the long unique region in the genome of
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
Gallus.
 Gaps
 2 CHSRSCHPTMTILQA--PTPAPSTIPGP------ 48
 herpes simplex virus type 1.";
J. Gen. Virol. 69:1531-1574(1988).
-!- FUNCTION: TEGUMENT PROTEIN.
-!- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL36,
EHV-1 24, EBV BPLF1, HVS-1 64, VZV 22, AND HCMV UL48.
 49 ----AGRPSASRGHRKRSRRVL------RRQLPVEE
 15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
30-MAY-2000 (Rel. 39, annotation update)
MYOSIN-BINDING PROTEIN H (MYBP-H) (H-PROTEIN) (86 KDA PROTEIN).
 2729 PEPAPHALV------SGVPLPLGPQAAGQAS--PALPLDPVPPP 2764
 80 PNPAKRLLFLLLTIVFCQILMAEEGVPAPLPPEDAPNAASLAPTPVSPVLEP 131
 Score 98.5; DB 1; Length 3164; Pred. No. 3.1;
 2911 2980 35 X 2 AA TANDEM REPEATS OF P-Q. 3164 AA; 335857 MW; CC5D31FF4F9FE3F4 CRC64;
 Indels
 SEQUENCE FROM N.A., AND SEQUENCE OF 2-37.
TISSUE-PECTORALIS MUSCLE;
MEDLINE-9115524; PubMed-7679114;
Vaughan K.T., Weber F.E., Einheber S., Fischman D.A.;
 Herpes simplex virus (type 1 / strain 17).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Simplexvirus.
 57;
 01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
LARGE TEGUMENT PROTEIN (VIRION PROTEIN ULJ6).
 3164 AA
 537 AA
 7; Mismatches
 PRT;
 EMBL; X14112; CAA32311.1; -.
 12.0%;
27.3%;
 Conservative
 STANDARD;
 STANDARD;
 Gallus gallus (Chicken).
 Query Match
Best Local Similarity
TEGU_HSV11
P10220;
 47;
 MYPH_CHICK
 SEQUENCE
 Repeat.
 MYPH_CHICK
 ID DTT DTT SERVICE SER
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 9
 PROSITE; PS50014; BROMODOMAIN_2; 1.
Proto-oncogene; Chromosomal translocation; DNA-binding;
Nuclear protein; Zinc-finger: Metal-binding; Transcription regulation;
Alternative splicing; Polymorphism.
 STRAIN=CV. JEMALONG;
MEDILE=9818728; Pubmed-9526510;
Greene E.A., Erard M., Dedicu A., Barker D.G.;
"MtENODI6 and 20 are members of a family of phytocyanin-related early
 57 GHRKRSRRVLYPRVVRRQLPVEEPNPAKRLLFLLTIVFCQILMAEEGVPA-----PLP 110
 Gaps
 ---- PAAAPAGRPS -- ASR 56
 Eukaryota, Viridiplantae, Embryophyta, Tracheophyta, Spermatophyta,
Magnoliophyta; eudicotyledons, core eudicots, Rosidae, eurosids I;
Fabales; Fabaceae, Papilionoideae; Medicago.
 45;
 Length 3866;
 Indels
 ADFC55E14E806F1D CRC64;
 SIMILARITY).
SIMILARITY).
SIMILARITY).
 Plant Mol. Biol. 36:775-783(1998).
 BROMODOMAIN (DIVERGENT)
 MISSING (IN ISOFORM 2).
 DB 1;
 48;
 15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
EARLY NODULIN 20 PRECURSOR (N-20).
 12.5%; Score 102.5; I 26.8%; Pred. No. 1.8; ive 19; Mismatches
 268 AA
 1234 PEPGPEQSKQKKVAPLPSIPVKQ-----KPKD 1260
 PEDAPNAA---SLAPTPVSPVLEPFNLTSEPSD 140
 1.2 TILQAP-TPAPSTIPGPRRGSGPEIFTFDPLPE-
 SET DOMAIN
 HOOK
HOOK
HOOK
 PRO-RICH.
POLY-PRO.
 POLY -GLU
 POLY-GLU
 medic)
 PHD
 A.T
A.T
A.T
PHD
 420976 MW;
 EMBL; X99467; CAA67830.1; -
 Medicago truncatula (Barrel
 41; Conservative
 STANDARD;
 1529
1650
3846
 1238
3536
3697
1505
1497
 469
 AA;
 Nodulation; Signal.
 Best Local Similarity
 SEQUENCE FROM N.A.
 1231
3533
3693
1503
1497
3866
 NO20_MEDTR
 NON_TER
DNA_BIND
DNA_BIND
DNA_BIND
 nodulins
 Query Match
 SEQUENCE
 DOMAIN
DOMAIN
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 VARIANT
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 NO20_MEDTR
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 6
 -!- SUBCELLULAR LOCATION: EXTRACELLULAR MATRIX.
-!- PTM: EXTENSINS CONTAIN A CHARACTERISTIC REPEAT OF THE PENTAPEPTIDE SER-PRO(4). THE PROLINE RESIDUE IS HYDROXYLATED AND THEN GLYCOSYLATED.
 H-A-P-P.
H-A-P-P.
2 X 7 AA TANDEM REPEATS OF T-H-R-H-A-P-P.
 Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I;
Solanales; Solanaceae; Nicotiana.
 65 VLYPRVVRRQLPVEEPNPAKRLLFLLLTIVFCQILMAEEGVPAPLP-----PEDAPNA 117
 179 -----PRSTPI--PHPRKR------SPASPSPSPSLSKSPSPSESP-- 211
 13 ILQAPTPAPS-----TIPGPRRGSGPEIFTFDPLPEPAAAPAGRPSASRGHRKRSRR 64
 01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-MAR-1992 (Rel. 21, Last annotation update)
EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).
 61;
 Length 268;
 CONTAINS THE SER-PRO(4) REPEATS
 PIR; S06733; S06733.
Repeat; Cell wall; Glycoprotein; Signal; Structural protein; SiGNAL
 Indels
 6FA29C5798C75F91 CRC64;
 DB 1;
 31;
 EARLY NODULIN 20.
PLASTOCYANIN-LIKE.
 Score 101.5; DB Pred. No. 0.15; 2; Mismatches
 620 AA.
BY SIMILARITY.
 EXTENSIN
 PRT;
 118 ASLAPTPVSPV -- LEPFNLTSEPSD 140
 Nicotiana tabacum (Common tobacco)
 12;
 212 -SLAPSPSDSVASLAP---SSSPSD
 145 P
28668 MW;
 12.3%;
28.3%;
 Conservative
 STANDARD;
22
268
268
1
23
23
23
136
16 1
268 AA;
 Local Similarity
 EXTN_TOBAC
P13983;
 4];
 DOMAIN
DOMAIN
SEQUENCE
 Query Match
 CHAIN
REPEAT
REPEAT
DOMAIN
REPEAT
REPEAT
 HRGPNT3
 RESULT 9
EXTN_TOBAC
 CHAIN
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 10;
 49 AG----RPSASRGHRKRSRRVLYPRVVRRQLPVEEPNPAKRLLFLLLTIVFCQILMAEEGV 105
 106 PAP-----VSPVLEP-FULTSE 137
 634
 675 PGSSTPGVLPYFPPGLPPPDAGGAPQSSMSESPDVNLVTQQLSKSQVEDPLPPVFSGTPK 734
 Schorey J.S., Holsti M.A., Ratliff T.L., Allen P.M., Brown E.J.;
"Characterization of the fibronectin-attachment protein of
Mycobacterium avium reveals a fibronectin-binding motif conserved
among mycobacteria.";
Mol. Microbiol. 21:321-329(1996).
-!- FUNCTION: PART OF THE BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEM
MODABCD FOR MOLYBDENUW (BY SIMILARITY).
-!- SUBCELGULAR LOCATION: SECRETED.
-!- SIMILARITY: BELONGS TO THE MODD FAMILY.
 (BY SIMILARITY).
PHOSPHORYLATION (ACTIVATES THE KINASE)
(BY SIMILARITY).
POLY ALA.
PROFICE I.
POLY-ARG.
 30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
MOLYBDATE UPTAKE SECRETED PROTEIN PRECURSOR (FIBRONECTIN ATTACHMENT
 Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium
 BY SIMILARITY.
PHOSPHORYLATION (ACTIVATES THE KINASE)
 PRO-RICH 2.
AREGRIRPHRCLCS -> GPVKVEPAHTAASVA (IN
 4 SRSCHPIMILLQAPTPAPSTIPGP------RRGSGPEI----FTFDPLPEPAAAP
 635 PGPAPHP/FGPPG--------PI--PVPAPPQIATSTSLLAAQSLVPPPGL
 70;
 12.6% Score 104; DB 1; Length 815; 24.2%; Pred. No. 0.29; Live 23; Mismatches 57; Indels
 REF. 2).
L -> V (IN REF. 2).
379AD69803207CCF CRC64;
 381 AA.
 PRT;
 MEDLINE=97011577; PubMed-8858587;
 88636 MW;
 EMBL; U53585; AAB50543.1; -.
 735 GSGAGYGVGFDLEEFLNO 752
 138 PS----DYALDLSTFLQQ 151
 Conservative
 STANDARD;
 340
464
523
699
32
 220
 Mycobacterium avium.
 609
815 AA;
 Similarity
48; Conserv
 SEQUENCE FROM N.A.
 PROTEIN) (FAP-A).
 433
520
577
 19
 RESULT WODD_MYCAV NODD_MYCAV A19;
ACT_SITE
MOD_RES
 DOMAIN
 Query Match
 Best Local S
Matches 48
 SEQUENCE
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Molybdenum; Transport; Signal

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 ъ
 70 VVRRQLPVEEPNPAKRLLFLLLTIVFCQILMAEEGVPAPLPPEDAPNAASLAPTPVSPVL 129
 Gaps
 15 QAPTPAP---STIPGPRRGSGPEIFTFDPLPEPA-AAPAGRPS-ASRGHRKRSRRVLYPR 69
 Proc. Natl. Acad. Sci. U.S.A. 90:6350-6354(1993).
-1- FUNCTION: POSSIBLY ACTS AS A TRANSCRIPTIONAL REGULATORY FACTOR.
MAY REGULATE GENES INVOLVED IN SKELETAL FORMATION DURING
 MIL OR HRX OR ALL].
Was musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom!;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 with
 -:- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-:- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; ARE PRODUCED BY ALTERNATIVE SPLICING.
-:- SIMILARITY: BELONGS TO THE TRITHORAX FAMILY OF TRANSCRIPTION
 47;
POTENTIAL.
MOLYBDATE UPTAKE SECRETED PROTEIN.
0DACB9A22AA11D2B CRC64;
 381;
 SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
STRAIN-C57BL/63, AND B6/CBA; TISSUE-SPLEEN, AND LUNG;
MEDLINE-93317679; PubMed-8327517;
MA O., Alder H., Nelson K.K., Chatterjee D., Gu Y., Nakamura Ma O., Alder H., Nelson K.K., Chatterjee D., Gu Y., Nakamura "analysis of the murine All-1 gene reveals conserved domains thuman All-1 and identifies a motif shared with DNA methyltransferases."
 Length
 Indels
 42;
 DB 1;
 FACTORS.
-- SIMILARITY: CONTAINS. 1 BROMODOMAIN.
-- SIMILARITY: CONTAINS 1 'SET' DOMAIN.
-- SIMILARITY: CONTAINS 3 PHD-FINGER DOMAINS.
 01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
2INC FINGER PROTEIN HRX (ALL-1) (FRAGMENT).
 .Pred. No. 0.18;
 3866 AA.
 8; Mismatches
 12.5%; Score 102.5; 30.2%; Pred. No. 0.1
 or send an email to license@isb-sib.ch)
 32 PO
381 MC
38210 MW;
 125 PPPPPADPNAGRIPNSYVL 143
 EP----FNLTSEPSDYAL 143
 EMBL; L17069; AAA62593.1; -.
 EMBRYONIC DEVELOPMENT.
 Query Match
Best Local Similarity 30.29
Matches 42; Conservative
 PF02008; zf-CXXC;
 INTERPRO; IPR001214; -.
 INTERPRO; IPR001965; -.
 PFAM; PF00628; PHD; 3.
PFAM; PF00856; SET; 1.
 MGD; MGI:96995; MLL.
 1
33
381 AA;
 HRX_MOUSE
P55200;
 SEQUENCE
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 HRX_MOUSE
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 6
 Baer R., Bankier A.T., Biggin M.D., Deininger P.L., Farrell P.J., Gibson T.J., Hatfull G., Hudson G.S., Satchwell S.C., Seguin C., Tuffnell P.S., Barrell B.G.; "DNA sequence and expression of the B95-8 Epstein-Barr virus genome.";
 51 RPSASRGHRKRSRRVLY-----PRVVRRQLPVEEPNPAKRLLFLLLIIVFCQILM 100
 | || : ||:|
PVSTIAPSVTPSPRLPLQIPIPLPQAAPSNPKIPLTTPSPSPTAAAA--PTTT------ 534
 --TLSPPI"YQQQPPQSAAPAPSPLLPQQQPTPS------AAPAPSP 572
 ---IPGPRRGSGPEIFTFDPLPEPAAAPAG 50
 PTMTILQAPTPAPS-----TIPGPRRG-SGPEIFTFDPL,PEPAAAPAGRPSASRGHRKRS 62
 SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL36, EHV-1 24, EBV BPLF1, HVS-1 64, VZV 22, AND HCMV UL48.
 109 -LPPEDAPNAASLAPTPVSPVLEPFNLTS---EPSDYALDLSTFLQ---QHPAA 155
 101 AEEGVPAPLPPEDAPNAASLAPTPVSPVLEPFNLTSEPSDYALDLSTFLQQHP 153
 179 PPTHIPSPREPISKPTPPVYIPSPRPPRPPTYIPIPRPPATKPPTHP 231
 58;
 Length 283;
 Length 3149;
 Indels
 51; Indels
 Epstein-barr virus (strain B95-8) (Human herpesvirus 4).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Lymphocryptovirus.
 3149 AA; 337954 MW; 3DD0C576587313D8 CRC64;
 8D7FCD0DA8ED2D90 CRC64;
 Score 112.5; DB 1;
Pred. No. 0.022;
9; Mismatches 81;
 12.8%; Score 105; DB 1; 25.3%; Pred. No. 0.95; ive 21; Mismatches 51.
 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
 PRT; 3149 AA
 POTENTIAL
 EXTENSIN
 SEQUENCE FROM N.A. MEDLINE-84270667; PubMed-6087149;
 6
 24 PO
283 EX
29593 MW;
 re 310:207-211(1984).
FUNCTION: TEGUMENT PROTEIN.
 13.7%;
24.3%;
 EMBL; V01555; CAA24839.1; -.
 9 PTMTILOAPTPAPST ----
 Conservative
 44; Conservative
 STANDARD;
 LARGE TEGUMENT PROTEIN.
 25 283 AA;
 PIR; A03747; QQBE8.
PIR; S32993; S32993.
 Similarity
 Ouery Match
Best Local Similarity
Matches 44; Conserv
 42;
 CHAIN
SEQUENCE
 TEGU_EBV
 Query Match
Best Local 9
 PIR; S329
SEQUENCE
 Nature
 Matches
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 535
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 MK07_HUMAN STANDARD; PRT; 815 AA.
013164, 016634;
101-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
MITOGEN-ACTIVATED PROTOTEIN KINASE 7 (EC 2.7.1.-) (EXTRACELLULAR SIGNAL-REGULATED ARMAY OR PRKM7 OR ERK5 OR ERK4.
 Lee J. D., Ulevitch R.J., Han J.;
"Primary structure of BMK1: a new mammalian map kinase.";
"Primary structure of BMK1: a new mammalian map kinase.";
"Blochem. Biophys. Res. Commun. 213:715-724(1995).

1- FUNCTION: MEKS AND ERKS INTERACT SPECIFICALLY WITH ONE ANOTHER AND NOT WITH MEKI/ERK1 OR MEK2/ERK2 PATHWAYS.

1- FUNCTION: MEKSCHATION: ACTIVATED BY TYROSINE AND THREONINE PHOSPHORYLATION (BY SINILARITY).

1- TISSUE SPECIFICITY: EXPRESSED IN MANY ADULT TISSUES. ABUNDANT IN HEART, PLACENTA, LUNG, KIDNEY AND SKELETAL MUSCLE. NOT DETECTABLE
 PROSITE: PS01351; MARK; 1.
PROSITE: PS0107; PROTEIN KINASE_ATP; 1.
PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
Transferase; Serine/threonine-protein kinase; ATP-binding; Cell cycle;
 -1- DOMAIN: THE SECOND PROLINE-RICH REGION MAY INTERACT WITH ACTIN TARGETING THE KINASE TO A SPECIFIC LOCATION IN THE CELL.
-1- PTM: AUTOPHOSPHORYLATED ON THREONINE AND TYROSINE RESIDUES, WHEN THE C-TERMINAL PART OF THE KINASE, WHICH COULD HAVE A REGULATORY
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelcostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. MAP KINASE FAMILY.
SEQUENCE FROM N.A.
TISSUE=FETAL BRAIN;
MEDLINE=95279403; PubMed=7759517;
Zhou G., Bao Z.Q., Dixon J.E.;
"Components of a new human protein kinase signal transduction
 SIMILARITY)
SIMILARITY)
 Biol. Chem. 270:12665-12669(1995).
 PROTEIN R
ATP (BY S
ATP (BY S
 TISSUE=PLACENTA;
MEDLINE=95374539; Pubmed=7646528;
 EMBL, 025278; AAA81381.1; -
EMBL, 029725; AAA82931.1; -
EMBL, 029726; AAA82932.1; -
EMBL, 029727; AAA82933.1; -
 pkinase; 1.
 INTERPRO; IPR000719; -.
 346
68
83
 Homo sapiens (Human)
 ROLE, IS ABSENT.
 SEQUENCE FROM N.A.
 P24941; 1AQ1
 Phosphorylation.
 INTERPRO; IPROOPFAM; PFOMO69;
 MIM; 602521;
 pathway.";
 NP_BIND
BINDING
 DOMAIN
 HSSP:
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 European Bioinformatics Institute. There are no restrictions on
 THE
 RSRRVLYPRVVRRQLPVEEPNPAKRLLFLLLTIVFCQILMAEEGVPAPLPPEDAPNAASL 120
 61 RSRRVLYPRVVRRQLPVEEPNPAKRLIFILLTIVFCQILMAEGVPAPLPPEDAPNAASL 120
 Signal-anchor.
CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 Gaps
 1 MCHSRSCHPTMTJLQAPTPAPSTIPGPRRGSGPETFTFDPLPEPAAAPAGRPSASRGHRK 60
 1 MCHSRSCHPTMTILQAPTPAPSTIPGPRRCSGPEIFTFDPLPEPAAAPAGRPSASRGHRK 60
 -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (POTENTIAL).
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Rodentla; Sciurognathi, Muridae; Murinae; Mus
 01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
RADIATION-INDUCIBLE IMMEDIATE-EARLY GENE IEX-1 (IMMEDIATE EARLY PROTEIN GLY96) (IMMEDIATE EARLY RESPONSE 3 PROTEIN).
IER3 OR IEX1 OR GLY96.
 N-LINKED (GLCNAC. . .) (POTENTIAL)
A > G (IN REF. 1).
P > R (IN REF. 1).
83C06116C80B9240 CRC64;
 .;
0
 Ouery Match
Best Local Similarity 100.0%; Score 823; DB 1; Length 156;
Best Local Similarity 100.0%; Pred. No. 1.6e-58;
Matches 156; Conservative 0; Mismatches 0; Indels
 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
 AND THE UTERUS. INDUCTION: BY SERUM GROWTH FACTORS AND TPA.
 121 APTPVSPVLEPFNLTSEPSDYALDLSTFLQOHPAAF 156
 153 AA
 -!- SIMILARITY: STRONG, TO HUMAN ORTHOLOG.
 EMBL; X96438; CAA65304.1; -.
EMBL; Y14551; CAA74886.1; -.
EMBL; T49531; -; NOT_ANNOTATED_CDS.
 PRT;
 106
16928 MW;
 Glycoprotein; Transmembrane;
DOMAIN 1 82
 EMBL; S81914; AAB36278.1; -.
 STANDARD;
 -!- PTM: GLYCOSYLATED.
 82
99
 Mus musculus (Mouse)
 AA;
 SEQUENCE FROM N.A.
 100
133
54
106
 83
 MIM; 602996;
 IEX1_MOUSE
P46694;
 DOMAIN
CARBOHYD
 CONFLICT
 TRANSMEM
 CONFLICT
 RESULT 2
FEX1_MOUSE
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
 ;;
 Plant Mol. Biol. 16:365-367(1991).
-!- FUNCTION: STRUCTURAL COMPONENT IN PRIMARY CELL WALL.
-!- PTM: EXTRUCTURAL CONTAIN A CHRARACFERISTIC REPEAT OF THE PENTAPEPTIDE
-SER-PRO(4). THE PROLINE RESIDUE IS HYDROXXLATED AND THEN
 TISSUE=LEAF;
MEDINE=9137082; PubMed=1893107;
REZ R., Cretin C., Puigdomenech P., Martinez-Izquierd T.A.;
"The sequence of a hydroxyproline-rich glycoprotein gene from Sorghum
 61 RSRRVLYPRVVRRQLPTEEPNIAKRVLFLLFAIIFCQILMAEEGVSQPLAPEDATSA--V 118
 RSRRVLYPRVVRRQLPVEEPNPAKRLLFLLLTIVFCQILMAEEGVPAPLPPEDAPNAASL 120
 Signal-anchor.
CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 Gaps
 9
 9
 Spermatophyta;
 1 MCHSRSCHPTWTILQAPTPAPSTIPGPRRGSGPEIFTFDPLPEPAAAPAGRPSASRGHRK
 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
N-LINKED (GLCNAC.) (POTENTIAL).
F4429E3B0120DE11 CRC64;
 8
 PIR; S14449; S14449.
INTERPRO; IPR002965; ...
PRINTS; PR01217; PRICHEXTENSN.
Repeat; Cell wall; Glycoprotein; Signal; Structural protein;
 Length 153;
 Indels
 Eukāryota; Viridiplantae; Embryophyta; Tracheophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; Sorghum.
 63.8%; Score 525; DB 1; Lv 70.3%; Pred. No. 4.2e-35; ive 9; Mismatches 29;
 EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).
 01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
 121 APTPVS----PVLEPFNLTSEPSDYALDLSTFL 149
 283 AA
 Sorghum bicolor (Sorghum) (Sorghum vulgare)
 EMBL; X67644; -; NOT_ANNOTATED_CDS.
PIR; S33363; S33363.
 153 AA; 16875 MW;
 EMBL; X56010; CAA39485.1; -.
 Glycoprotein; Transmembrane;
DOMAIN 1 85
 Query Match 63.8
Best Local Similarity 70.3
Matches 109; Conservative
 STANDARD;
 153
137
 102
 PIR; S33363; S33363.
MGD; MGI:104814; IER3
 SEQUENCE FROM N.A.
 GLYCOSYLATED.
 103
 Repeat; Cell v
Hydroxylation.
 EXTN_SORBI
 CARBOHYD
 SEQUENCE
 TRANSMEM
 vulgare
 EXTN_SORBI
 DOMAIN
 61
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 NAMES OF COLOR OF STREET O
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January 30, 2001, 22:05:39; Search time 43.61 Seconds (without alignments) 115.521 Million cell updates/sec
 US-08-799-910-10
823
1 MCHSRSCHPTMTILQAPTPA......EPSDYALDLSTFLQQHPAAF 156
 88757
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
 Total number of hits satisfying chosen parameters:
 88757 seqs, 32294092 residues
 OM protein - protein search, using sw model
 BLOSUM62 Gapext 0.5
 Title:
Periect score:
 Scoring table:
 Sequence:
 Searched:
 Run on:
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

SwissProt\_39:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

|          | Description           | 1.pc.10:1 | homo sapie | mus mus    | 2 sorghum bic |               |            |            |           | 9 medicago tr |            | orgyia     | herpes     | gallus     | xenopns   | homo sap  | -          | drosophil |            | _          |            |          |            |           |           |            | escherich   | _          |            |           |            | homo as                                 |            |           |            | • |
|----------|-----------------------|-----------|------------|------------|---------------|---------------|------------|------------|-----------|---------------|------------|------------|------------|------------|-----------|-----------|------------|-----------|------------|------------|------------|----------|------------|-----------|-----------|------------|-------------|------------|------------|-----------|------------|-----------------------------------------|------------|-----------|------------|---|
|          | Deer                  | Togor.    | P46695     | P46694     | P24152        | P03186        | 01316      | 048919     | P5520     | P9332         | P1398      | 01034      | P1022      | 005623     | P1743     | P4116     | P0508      | P26675    | 015534     | P41110     | P37370     | P03200   | P30667     | P40602    | 003164    | P14918     | P23367      | 060416     | P49918     | P40603    | P17473     | 091111111111111111111111111111111111111 | 035973     | 002910    | P19275     |   |
| SUMMALES | ID                    | :         | IEX1_HUMAN | IEX1_MOUSE | EXTN_SORBI    | TEGU_EBV      | MK07_HUMAN | MODD_MYCAV | HRX_MOUSE | NO20_MEDTR    | EXTN_TOBAC | Y091_NPVOP | TEGU_HSV11 | MYPH_CHICK | XP2_XENLA | ERM_HUMAN | HUNB_DROME | SOS_DROME | PER1_HUMAN | IF4G_RABIT | VRP1_YEAST | BRL1_EBV | NIFA_AZOBR | APG_ARATH | HRX_HUMAN | EXTN_MA12E | MUTL_ECOL.I | SRE1_CRIGR | CDNC_HUMAN | APG_BRANA | ICP4 HSVEK | TRX2_HUMAN                              | PER1 MOUSE | CPN_DROME | VTP3_TTV1V |   |
|          | DB                    |           |            |            |               |               |            | _          |           |               |            |            |            |            |           | 7         | ٦          | -         | -          | П          | -          | Н        | -          | -         |           |            |             |            | ٦          |           |            |                                         |            |           | П          |   |
|          | Ouery<br>Match Length |           | 156        | 153        | 283           | 3149          | 815        | 381        | 3866      | 268           | 620        | 279        | 3164       | 537        | 439       | 510       | 758        | 1595      | 1290       | 1402       | 817        | 605      | 625        | 534       | 3969      | 267        | 615         | 1133       | 316        | 449       | 1487       | 2715                                    | 1291       | 865       | 474        |   |
| æ        | Ouery<br>Match        |           | 100.0      | n o        | າ ເ           | 12.8          | N          | ~          | 2         | 7             | 2          | ~ (        | 12.0       | 11.6       | 11.5      | 11.5      | 11.5       | 11.5      |            |            |            |          |            | 11.2      |           |            |             |            |            |           |            |                                         |            |           |            |   |
|          | Score                 |           | 823        | 270        | 112.5         | 105           | 104        | 102.5      | 102.5     | 101.5         | 100        | y . v .    |            | 95.5       | 35        | 94.5      | 94.5       | 94.5      | 94         | 93.5       | 69         | 92.5     | 92.5       | 92        | 92        | 91.5       | 91.5        | 91.5       | 06         | 06        | 89.5       | 89.5                                    | 68         | 88.5      | 88         |   |
|          | Result<br>No.         |           | - 0        | <b>v</b> ( | η.            | <b>3</b> * 1. | n 1        | ا ۵        | ~ (       | æ (           | ,<br>D (   | 7.         | Τ.         | 77         | £ [       | 14        | 15         | 16        | 17         | 18         | δ.<br>1.   | 20       | 21         | 22        | 23        | 24         | 25          | 56         | 27         | 28        | 59         | 30                                      | 31         | 32        | 33         |   |

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| P08588 homo sapien Q0209 autographa O08789 mus musculu O43426 homo sapien P08472 homo sapien P28925 equine herp P06487 herpes simp O994427 homo sapien P41479 autographa P07359 homo sapien Q14957 homo sapien Q14957 homo sapien | ALIGNMENTS  LETAL HUMAN LETAL                                                                                                                                                                                                                                                                                                      |
|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| BIAR_HUMAN WAT_MOUSE SYJI_HUMAN P300_HUMAN SREI_RAT ICP4_HSVEN VGLI_HSV11 Y091_HVAN Y091_HVAN Y091_HVAN MME3_HUMAN                                                                                                                | ALIGNMENTS  SULT 1  IEX1_HUMAN STANDARD; PRT; 156 AA. P4665; 033044; 092691; 01-NOV-1996 (Rel. 32, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 30-NOW-1995 (Rel. 36, Last sequence update) 15-JUL-1998 (Rel. 36, Last sequence update) RADIATION-INDICIBLE IMMEDIATE EARLY RESPONSE 3 GENE 1 PROTEIN) (DIF-2 PROTEIN) (DIF-2 PROTEIN) (DIF-SERNITATION CALFACT MEDIATE EARLY RESPONSE 3 PROTEIN) (DIF-SERNITATION CALFACT MEDIATE PROTEIN) (DIF-SERNITATION CALFACT MEDIATE PROTEIN) (DIF-SERNITATION CALFACT MEAN N.A. TISSUE-PLACEMYA; MEDLINE-96181295; Pubmed-8603392; Kondratyev A.D., Chung KN., Jung M.O.; Medentification and characterization of a rad glycosylated human early-response gene."; Cancer Res. 56:1498-1502(1996). Schaefer H., Trauzcold A., Siegel E.G., Folsch PRKI: a novel early-response gene transcript picuitary adenylate cyclase activating polypecarcinoma cell line."; Cancer Res. 56:2641-2641(1996). Schaefer H., Tauazcold A., Siegel E.G., Folsch PRKI: a novel early-response gene transcript picuitary adenylate cyclase activating polypecarcinoma cell line."; Cancer Res. 56:2641-2641(1996). Schaefer H., Tauazcold A., Siegel E.G., Folsch PRKI: a novel early-response gene transcript picuitary adenylate cyclase activating polypecarcinoma cell line."; Cancer Res. 56:2641-2641(1996). SEQUENCE PROM N.A. MEDLINE-97339426; Pubmed-9196025; Pletzsch A., Buechler C., Aslanddis C., Schmifferantidication and characterization of an oval differentiation of ependent gene that is response liopolysaccharide. Ceramide, and lysophospha Blochem. Blophys. Res. Commun. 235:4-9(1997). Hilliamson A., Wohldmann P., Wilson R., Submitted (FRE-1995) to the Embl./GenBank/DDBJSubmitted (FRE-1995) to the Embl./GenBank/DB                                                                                                                                                                                                                                                                                                                  |
|                                                                                                                                                                                                                                   | Careated) Last sequest                                                                                                                                                                                                                                                                                                     |
| 224<br>1334<br>1334<br>1334<br>1234<br>1334<br>1334<br>1333                                                                                                                                                                       | ALIGANDARD; PRT; 39, 12. 36, Last sequence 39, Last annotati LE IMBRIATE FARLY WMEDIATE FARLY PRGI PROTEIN) (DII ROTEIN) ROTEIN PubMed-8653710; ROTEIN-ROTEIN PUBMEd-8653710; ROTEIN-ROTEIN RADIATION, TPA, O SEQUENCE DIFFERS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| 01100.7<br>0100.6<br>0.00100.6<br>0.00100.0<br>0.00100.0<br>0.00100.0                                                                                                                                                             | AN STANI<br>995 (Rel. 36<br>995 (Rel. 36<br>996 (Rel. 36<br>997 (Rel. 36<br>998 (Rel. 36<br>998 (Rel. 36<br>998 (Rel. 36<br>998 (Rel. 36<br>900 (R |
| <br>68 68 88 68 67 7 88 88 68 68 68 68 68 68 68 68 68 68 68                                                                                                                                                                       | ALIGNME  X1_HUMAN  IEXL_HUMAN  FA6695; Q93044; Q92691;  01-NOV-1995 (Rel. 35, Created)  15-JUL-1998 (Rel. 36, Last sequence upple695; Q93044; Q92691;  01-NOV-1995 (Rel. 36, Last sequence upple79700 (Rel. 36, Last sequence upple70 (EDFIL)  FROTEIN GIV96) (IMMEDIATE ERRIY GEFRINGEDENE I PROTEIN) (PRG1 PROTEIN) (DIFFERINGEDENE I RESPONSE (RESPONSE I REAL OFFERINGEDENE)  FROTEIN (DIF-2 PROTEIN) (DIFFERINGEDENE)  FROTEIN (DIFFERINGENE)  FROM (DIFFERINGENE)  FROTEIN (DIFFERINGENE)  FROM (DIFFERINGENE)  FROTEIN (DIFFERINGENE)  FROM (DIFFERINGENE)  FROTEIN (DIFFERINGENE)                                                                                                                                                                                                                                                                                                     |
| 6 8 8 8 8 8 8 9 9 9 9 9 9 9 9 9 9 9 9 9                                                                                                                                                                                           | XILHUM XILHUM XILHUM PAGE PAGE PAGE PAGE PAGE PAGE PAGE PAGE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
|                                                                                                                                                                                                                                   | RESULT FOR THE STANDARD SERVICE COCOCC CCC CCC CCC CCC CCC CCC CCC CC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |

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Search completed: January 30, 2001, 23:09:03
Job time: 6028 sec
 A.Status: preliminary
A.Molecule Lype: mRNA
A.Molecule Lype: mRNA
A.Molecule Lype: mRNA
A.Molecule Lype: mRNA
A.Kolecule Lype: massigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog
E.52-115/Domain: protein kinase homology <KIN>
E.50-68/Region: protein kinase ATP-binding motif
 10;
 7;
A;Title: Components of a new human protein kinase signal transduction pathway.
A;Reference number: A56708; MUID:95279403
A;Accession: B56708
 A; Reference number: 219531
A; Accession: T2216
A; Accession: T2216
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-241 <MIL.
A; Cross-references: EMBL: 283227; PIDN: CAB05726.2; GSPDB: GN00028; CESP: F45B8.3
A; Experimental source: clone F45B8
 T22216
hypothetical protein F45B8.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C:Accession: T22216
 49 AG---RPSASRGHRKRSRRVLYPRVVRRQLPVEEPNPAKRLLFLLLTIVFCQILMAEEGV 105
 635 PGPAPHPTGPPG-------PI--PVPAPPQIATSTSLLAAQSLVPPPGL 674
 106 PAP-----VSPVLEP-FNLTSE 137
 59 RKRSRRVLYPRVVRRQLPVEEPNPAKRLLFLLTIVFCQILMAEEGVPAPLPPEDAPNAA 118
 70; Gaps
 4 SRSCHPTMT1LQAPTPAPSTIPGP------RRGSGPEI----FTFDPLPEPAAAP 48
 131 -------PLVCCKQAPVPE-NPC-------COIVAA-----AMPPPPSAPACC 163
 Gaps
 4 SRSCHPTMTILQAPTPAPSTIP.-GPRRGSGPEIFTFDPLPEPAA---APAGRPSASRGH 58
 12.5%; Score 103; DB 2; Length 241; 30.8%; Pred. No. 0.19; Live 6; Mismatches 48; Indels 38;
 Ouery Match 12.6%; Score 104; DB 2; Length 815; Best Local Similarity 24.2%; Pred. No. 0.53; Matches 48; Conservative 23; Mismatches 57; Indels
 submitted to the EMBL Data Library, December 1996
 735 GŚGAGYGVGFĎĽEEFĽNÓ 752
 138 PS----DYALDLSTFLQQ 151
 Ouery Match 12.55
Best Local Similarity 30.87
Matches 41; Conservative
 A; Map position: X
A; Introns: 21/3; 68/3; 211/2
 164 VAAPVPTNPCCQP 176
 119 SLAPTPVSPVLEP 131
 C.Genetics:
A.Gene: CESP:F45B8.3
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C.Date: 10.Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000 C.Accession: $76953 F.Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajii o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Walanabe, A.; Yamada, M.; DNA Res. 3, 109-136, 1996 A.; Takeuchi, C.; Wada, T.; Walanabe, A.; Yamada, M.; A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synech
 A.Accession: 576953
A.Status: nucleic acid sequence not shown; translation not shown
A.Molecule type: DNA
A.Residues: 1-535 cKAN>
A.Cross-references: EMBL:D90917; GB:AB001339; NID:g1653836; PIDN:BAA18865.1; PID:
A.Cross-references: EMBL:D90917; GB:AB001339; NID:g1653836; PIDN:BAA18865.1; PID:
A.Note: the nucleotide sequence was submitted to the EMBL. Data Library, June 1996
G.Superfamily: Synchocystis sp. protein kinase, 58K; protein kinase homology
C.Keywords: phosphotransferase: protein kinase
F:10-274/Domain: protein kinase homology <KIN>
 A;Title: DNA sequence and expression of the B95-8 Epstein-Barr virus genome. A;Feference number: A03794; MUID:84220667
A;Contents: annotation; protein coding region C;Superfamily: human herpesvirus 4 BPLF1 protein
 extracellular signal-regulated kinase 5 - human
C;Species: Homo sapiens (man)
C;Date: 19-0ct-1995 #sequence_revision 19-0ct-1995 #text_change 24-Sep-1999
C;Accession: B56708
R;Zhou, G; Bao, Z.O.; Dixon, J.E.
J. Biol. Chem. 270, 12665-12669, 1995
 ----LPVEEPNPAKRLLFLLTIVFCQILMAEEGVPAP-- 108
 Gaps
 70 VVRRQLPVEEPNPAKRLLFLLLTIVFCQILMAEEGVPAPLP-PEDAPNAASLAPTPVSPV 128
 457 -----PIISPQPSPTISIPV-----TPAPVPKPSPSPTPKPTVPPQISPT 496
 9 PTMTILQAPTPAPS----TIPGPRRG-SGPEIFTFDPLPEPAAAPAGRPSASRGHRKRS 62
 16 APTPAPSTIPGPRRGSGPEIFTFDP-----LPEPAAAPAGRPSASRGHRKRSRRVLYPR 69
 Synechocystis sp. (strain PCC 6803)
 109 -LPPEDAPNAASLAPTPVSPVLEPFNLTS---EPSDYALDLSTFIQ---QHPAA 155
 DB 1; Length 535;
 Indels
 ----411 SPEPTPSPSPSPETTSSPTEDT1TPMEPEPSLUEPAAPIPEPKRSPS----
 51;
 43;
 DB 1;
 12.7%; Score 104.5; DE 25.6%; Pred. No. 0.32; Live 9; Mismatches
 12.8%; .Score 105; DB 25.3%; Pred. No. 1.7; ive 21; Mismatches
 A; Reference number: S74322; MUID:97061201
 protein kinase (EC 2.7.1.-), 58K - N.Alternate names: protein slr0599 C.Species: Synechocystis sp. A.Variety: PCC 6803
 Conservative
 Conservative
 63 RRVLYPRVVRRQ----
 Ouery Match
Best Local Similarity
Matches 44; Conserv
 Query Match
Best Local Similarity
Matches 32; Conserv
 129 LEPFN 133
 497 PQPSN 501
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 BPLFI protein - human herpesvirus 4 (strain 895-8).

(Species: human herpesvirus 4, Epstein-Barr virus

(Species: human herpesvirus 4, Epstein-Barr virus

(Space: S5-Feb-1985 #sequence_revision 25-Feb-1985 #text_change 16-Jul-1999

(SAccession: 693065; A03747; S32993

R;Bankier, A.T.; Deininger, P.L.; Farrell, P.J.; Barrell, B.G.

Mol. Biol. Med. 1, 21-45, 1983

A;Title: Squence analysis of the 17,166 bp EcoRI fragment C of 895-8 Epstein-Barr virus

A;Reference number: A93065; MUID:85035713
 A;Molecule type: DNA
A;Residues: 1.3149 <BAN>
A;Cross-references: EMBL:VOISSS; NID:g59074; PIDN:CAA24839.1; PID:g1334853
R;Bacr, R.; Bankier, A.T.; Biggin, M.D.; Deininger, P.L.; Farrell, P.J.; Gibson, T.J.;
Nature 310, 207-211, 1984
 proline-rich protein A35L - Chlorella virus PBCV-1
C;Spcies: Chlorella virus PBCV-1
C;Spcies: Chlorella virus PBCV-1
C;Spcies: Chlorella virus PBCV-1
C;Accession: T17525
R;Graves, M.V.; Van Etten, J.L.
submitted to the EMBL Data Library, May 1999
A;Reforence number: 218806
A;Accession: T17525
A;Status: preliminary: translated from GB/EMBL/DDBJ
A;Reforence: T-549 cGRA-A;Residues: 1-549 cGRA-A;Residues: 1-549 cGRA-A;Residues: 1-549 cGRA-A;Residues: 1-549 cGRA-A;Residues: A35L
A;Cross-references: EMBL:U42580; NID:94028896; PIDN:AAC96403.1
A;Experimental source: specific host Chlorella strain NC64A-A;Gene: A35L
 3,
 9
 A; Cross-references: EMBL: L29028; NID: 9530877; PIDN: AAB53954.1; PID: 9530878
 RVVRRQLPVEEPNPAKRLLFLLLTIVFCQILMAEEGVPAPL.P-PEDAPNAASLAPTPVSP 127
 PVEEPNPAKRLLFILLTIVFCQILMAEEGVPAPLP-PEDAPNAASLAPTPV-SPVLEPFN 133
 Caps
 16 APTPAPSTIPGPRRGSGPEIFTFDPLPEPAAAPAGRPSASRGHRKRSRRVLYPRVVRRQL 75
 9 PTMTILQAPTPAPSTIPGPRGSGPEIFTFDPLPEPAAAPAGRPSASRGHRKRSRRVLYP
 44;
 Length 351;
 Length 549;
 36; Indels
 26;
 12.8%; Score 105; DB 2; 24.2%; Pred. No. 0.19; iive 16; Mismatches 56;
 Score 105; DB 2;
Pred. No. 0.3;
 11; Mismatches
 231 KASPVASPQOSPTPSPR----
 12.88; 27.88;
 Query Match
Best Local Similarity 27.89
 Conservative
 Query Match
Best Local Similarity
Matches 30; Conserv
 486 PKPAPKPAPK----
A; Residues: 1-351 <WOE>
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ITSKVS 528
 134 LTSEPS 139
 128 VLEP 131
 27.1 SASP 274
 69
 92
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Audinilke protein - Lymantria dispar nuclear polyhedrosis virus
C;Species: Lymantria dispar nuclear polyhedrosis virus, LdNnPv
C;Date: 29-oct-1999 #sequence_revision 29-oct-1999 #text_change 29-oct-1999
C;Accession: T3051
R;Kuzio, J.; Pearson, M.N.; Harwood, S.H.; Funk, C.J.; Evans, J.T.; Slavicek, J.;
Virology 253, 17-34, 1999
A;Title: Sequence and analysis of the genome of a baculovirus pathogenic for Lym
A;Reference number: 220836; MUID:99124785
A;Accession: T30351
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-1029 <KUZ>
A;Residues: 1-1029 <KUZ>
A;Residues: L1029 <KUZ>
A;Cross-references: EMBL:AF081810; PIDN:AAC70189.1
 hypothetical protein WP6 - Chlamydomonas eugametos
C;Species: Chlamydomonas eugametos
C;Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jul-2000
C;Accession: S50754
R;Woessner, J.P.; Molendijk, A.J.; van Egmond, P.; Klis, F.M.; Goodenough, U.W.;
Plant Mol. Biol. 26, 947-960, 1994
A;Title: Domain conservation in several volvocalean cell wall proteins.
 A;Molecule type: mRNA
A;Residues: 1-1323 <OHA>
A;Residues: 1-1323 <OHA>
A;Cross-references: EMBL:AB006622; NID:dl170675; PIDN:BAA22953.1; PID:dlC23829
A;Experimental source: brain
C;Genetics::
A;Note: KIAA0284
 4,7 APAGRPSASRGHRKRSRRVLYPRVVRRQLPVEEPNPAKRLLFLLLTIVFCQILMAEEGVP 106
 PRVVRRQLPVEEPNPAKRLLFLLTIVFCQILMAEEGVPAPLPPEDAPNAASLAPTPVSP 127
 3 HSRSCHPTMTILQAPTPA-----PSTIPGPRRGSGPEIF-----TFDPL--PEPAA 46
 16 APTPAPSTIPGPRRGSGP-EIFTF-----DPLPEPAAAPAGRPSASRCHRKRSRRVLY 67
 128 VLEPFNLTSE------PSDYALDL-----STF-----LQQHPAA 155
 726 ALEPGESTAEAASELAVERPAQPAPDLISDSAVESTFGHKSTVASELAARPAA 778
 Length 1323;
 Length 1029;
 107 APLPPEDAPNAASLA--PTPVSPVLEPFNLT----SEPSDYALDLSTF 148
 468 PVLPAPLTPHGTSPVGPPTPPPAPTDP-QLTKARKQEEDDSLSDAGTY 514
 Indels
 Indels
 428 RTPARPFGSVGRRSRLAODFMAQCLRESSPAARPSPEK------
 Score 106.5; DB 2;
Pred. No. 0.54;
1; Mismatches 67;
 52;
 Score 106; DB 2;
Pred. No. 0.46;
6; Mismatches 52
 preliminary; translated from GB/EMBL/DDBJ
 13;
 12.9%;
26.8%;
 Query Match
Best Local Similarity 29.5%;
Matches 51; Conservative 6
 Conservative
 Query Match
Best Local Similarity
 A; Accession: S50754
A; Statús: preliminary
A; Molecule type: mRNA
 45;
 Matches
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 R; Yeung, M.K.
Infect: Immun. 61, 109-116, 1993
A; Title: Complete nucleotide sequence of the Actinomyces viscosus T14V sialidase gene:
A; Contents: T14V
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 Seki, N.; Nomura,
 9
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8
 C.Species: Homo sapiens (man)
C.Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 05-Nov-1999
C.Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 05-Nov-1999
C.Accession: T00037
A.Data. O.; Nagase, T.; Ishikawa, K.; Nakajima, D.; Ohira, M.; Seki, N.; Nomulsubmitted to the EMBL Data Library, August 1997
A.Description: Prediction of the coding sequences of unidentified human genes.
A.Reference number: 214073
 C:Species: Actinomyces viscosus
C:Date: 19·Dec-1993 #sequence_revision 18·Nov·1994 #text_change 22·Oct-1999
C:Accession: A49227
 76 PVEEPNPAKRLLFILLTIVFCQILMAEEGVPAPLP-----PEDAPNAASLAP----- 122
 A. Accession: A49227
A. Status: preliminary
A. Molecule type: nucleic acid
A. Residues: 1-901 < YED>
A. Residues: 1-901 < YED>
A. Cross-references: GB:L06898; NID:g289087; PIDN:AAA21932.1; PID:g141852
A. Note: sequence extracted from NCBI backbone (NCBIN:121598, NCBIP:121599)
 69 RVVRRQL, PVEEPNPAKR--LL.FLLLTIVFCQILMA--EEGVP----APLPPEDAPNAASL, 120
 16 APTPAPSTIPGPRRGSGPEIFTFDPLPEPAAAPAGRPSASRGHRKRSKRVLYPRVVRRQL, 75
 9 PTMT1LQAPTPAPSTIPGPRRGSGPEIFTFI)PLPEPAAAPAGRPSASRGHRKRSRRVLYP 68
 771 SVEPTQAPGAQPSSAPKPGATGRAPSVVNPKATGAATEPGTPSSSASPAPSRNA-----
 Length 901;
 PIDN:AAC96773.1
strain NC64A
 ; Score 107; DB 2; Length 49; Pred. No. 0.19; 20; Mismatches 57; Indels
 Indels
 123 ----TPVSPVLE------PFNLTSEPSDYALDLSTFLQ 150
 DB 2;
 12.9%; Score 106.5; DB 2; 29.0%; Pred. No. 0.37; Live 19; Mismatches 64;
A;Status: preliminary; translated from GB/EMBL/DDBJ
 121 APTPVSPVLEPFNLTSEPSDYALDLSTFLQQHPAA 155
 hypothetical protein KIAA0284 - human (fragment)
 A; Wolecule type: DNA
A; Residues: 1.496 < GRA>
A; Cross.references: EMBL:U42580; NID:94028896;
A; Experimental source: specific host Chlorella C; Genetics:
A; Note: A405R
 13.0%; 22.8%;
 sialidase - Actinomyces viscosus
 Best Local Similarity 22.89
Matches 37; Conservative
 Ouery Match
Best Local Similarity 29.0°
Matches 45; Conservative
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64; Gaps

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NID:g1655829; PTDN:AAC08051.1; PID:g1655830 of Svalofs Karat; immature seed, 30 days after \rho
 A;Cross-references: EMBL:277662; PIDN:CAB01192.1; GSPDB:GN00023; CESP:F47B8.5
A;Experimental source: clone F47B8
 proline/lysine-rich protein A405R - Chlorella virus PBCV-1
C;Species: Chlorella virus PBCV-1
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T17908
R;Graves, M.V.; Van Etten, J.L.
submitted to the EMBL Data Library, May 1999
A;Reference number: 218806
A;Accession: T17908
 hypothetical protein F4788.5 - Cacnorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 413 PPADAAPAPPAPPEPVPA------PAPAPEAAPVAPSADAGGYAAAAPAGGG 459
 GHRKRSRRV-----LYPRVVRRQLPVEEPNPAKRLLFLLLTIVFCQILMAEEGVPAP 108
 460 SYPAKKRRVARDYAEGEAAPAAPAEPAPAPAPAPAPA--------PEAAPAPEPAPAP 509
 GHRKRSRRVLYPRVVRRQLPVEEPNPAKRLLFLLLT1VFC01LMAEECVPAPLP---PED 113
 ----- PGPAPGOGPHP 380
 9 PTMTILQAPTPAPSTIPGPRRGSGPEIFTFDPLPEPAAAP-----AG-RPSASR 56
 53;
 55;
 Length 581;
 Length 552;
 A;Map position: 5
A;Introns: 37/3; 82/3; 122/3; 148/3; 194/1; 217/3; 298/2; 368/1
 Indels
 Indels
 552
 LP-----PEDAPNAASLAPTPV----SPVLEPFNLTSEPSDYA 142
 PTMTILQAPTPAPSTIPGPRRGSGPEIFTFDPLPEPAAAP-----
 90;
 DB 2;
 42;
 DB 2;
A;Accession: T08148
A;Status: preliminary; translated from GB/EMBL/DDBJ
 A,Status: preliminary; translated from GB/EMBL/DDBJ
 Score 107,5; DB
Pred. No. 0.2;
9; Mismatches
 Score 109.5; Di
Pred. No. 0.13;
6; Mismatches
 C;Accession: T22341
R;BerKs, M.; McMurray, A.
submitted to the EMBL Data Library, July 1996
A;Reference number: 219551
A;Accession: T22341
 349 GPGPR-----PAPAPAPACQGPRPA--
 114 APNA----ASLAPTPVSPVLEP 131
 6
 381 APAAAPGTSATPAPAPTTTKIGP
 13.1%;
ilarity 25.3%;
Conservative
 Ouery Match
Best Local Similarity 29.4%;
Matches 42; Conservative
 A; Molecule Lype: mRN/
A; Residues: 1-552 <TAL>
A; Cross-references: EMBL: U59446;
A; Experimental source: cv. 20516
 A; Molecule type: DNA
A; Residues: 1-581 <WIL>
 Similarity
 CESP: F47B8.5
 Query Match
Best Local Simi
Matches 42;
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 57
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 109
 A;Gene:
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 C,Accession: 708148
R,Taipalensuu, J.; Falk, A.; Fk, B.; Rask, I..
Rur. J. Blochem. 243, 605-611, 1997
A:Title: Myrosinase-binding proteins are derived from a large wound-inducible and repeti
 hydroxyproline-rich glycoprotein - sorghum
C; Species: Sorghum bicolor (sorghum)
C; Species: Sorghum bicolor (sorghum)
C; Species: 19-May-1994 #text_change 24-Sep-1999
C; Accession: S1383; S14449
R; Raz, R.; Cretin, C.; Pulgdomenech, P.; Martinez-Izquierdo, J.A.
Plant Mol. Biol. 16, 365-367, 1991
A; Titler The Sequence of a hydroxyproline-rich glycoprotein gene from Sorghum vulgare. A; Reference number: S13383; MUID:91370882
A; Molecule type: DNA
A; Residues: 1-283 < RAZ1>
A; Residues: 1-283 < RAZ1>
A; Residues: 1-283 < RAZ1>
A; Note: the source is designated as Sorghum vulgare
 4
 5,
 proline-rich myrosinase-binding protein homolog - rape (fragment)
N;Alternate names: myrosinase-binding protein related protein
C;Species: Brassica napus (rape)
C;Species: 21-May-1999 #sequence_revision 21-May-1999 #text_change 08-Oct-1999
 61 RSRRVLYPRVVRRQLPTEEDNIAKRVLFLLFAIIFCQILMAEEGVSQPLAPEDATSA--V 118
 --- PRVVRRQLPVEEPNPAKRLLFLLLTIVFCQILM 100
 RSRRVLYPRVVRRQLPVEEPNPAKRLLFLLTTVFCQTLMAEEGVPAPLPPEDAPNAASI, 120
 Gaps
 Gaps
 ----IPGPRRGSCPEIFTFDPLPEPAAAPAG 50
 A; Molecule type: DNA
A; Residues: 1-238, YY, 240, OAH', 244-283 <RAZ2>
A; Cross-references: EMBL:X56010; NID:g21626; PIDN:CAA39485.1; PID:g21627
C; Superfamily: hydroxyproline-rich glycoprotein
C; Keywords: glycoprotein; hydroxyproline
 1 MCHSRSCHPTMTILQAPTPAPSTIPGPRRGSGPEIFTFDPLPEPAAAPAGRPSASRGHRK
 .
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 101 AEEGVPAPLPPEDAPNAASLAPTPVSPVLEPFNLTSEPSDYALDLSTFLQQHP 153
 179 РРТНТРЅРКРРТЅКРТРРVYТРЅРКРРКРSРРТYТРТРКРРАТКРРТSТРТНР 231
 13.7%; Score 112.5; DB 2; Length 283; 24.3%; Pred. No. 0.039; Live 9; Mismatches 81; Indels 41
 Length 153;
 Score 525, DB 2; Length 15
Pred. No. 3.1e-35;
9; Mismatches 29; Indels
 121 APTPVS-----PVLEPFNLTSEPSDYALDLSTFL 149
 Submitted to the EMBL Data Library, October 1990 A; Reference number: S14449 A; Accession: S14449
 63.8%;
70.3%;
 9 PTMTILOAPTPAPST----
 109; Conservative
 Conservative
 51 RPSASRGHRKRSRRVLY-
 Best Local Similarity
Matches 42; Conserv
 Similarity
 Query Match
Best Local S
Matches 109,
 Query Match
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Gaps

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January 30, 2001, 21:28:35; Search time 21.17 Seconds (without alignments) 500.354 Million cell updates/sec
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823
I MCHSRSCHPTMTILQAPTPA......EPSDYALDLSTFLQQHPAAF 156
 195891
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
 Total number of hits satisfying chosen parameters:
 195891 seqs, 67900655 residues
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 OM protein - protein search, using sw model
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 Minimum DB seq length: 0
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           | Description   | differentiation-de | gly96 protein - mo | hydroxyproline-ric | proline rich myros | hypothetical prote | ysin | sialidase - Actino | hypothetical prote | 3        | tica   | _      | rotein | Ψ      | extracellular sign |        | Q.     | All-1 protein -GTE | All-1 protein +GTE | proline-rich prote | hydroxyproline-ric | hypothetical prote | · _  | hetical p | proline-rich prote | -rich | prote  | extensin-like prot | arabinoqalactan-li | proline rich prote |
|-----------|---------------|--------------------|--------------------|--------------------|--------------------|--------------------|------|--------------------|--------------------|----------|--------|--------|--------|--------|--------------------|--------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|------|-----------|--------------------|-------|--------|--------------------|--------------------|--------------------|
| SUMMARIES | QI            | 33                 | 533363             | m                  | T08148             | m                  | 9    | A49227             | T00037             | T30351 . | S50754 | T17525 | QQBE8  | 576953 | B56708             | T22216 | T17737 | B48205             | A48205             | T17636             | S06733             | T10361             | 哥    | S50755    | T17815             | -     | T42761 | T10741             | S52994             | 051                |
|           | DB            | 7                  | 7                  | ď                  | ď                  | 7                  | ~    | a                  | ~                  | 7        | 7      | 7      | -      | Н      | 7                  | 7      | 7      | ~                  | 7                  | 7                  | ~                  | 7                  | -    | 7         | ~                  | 7     | ~      | 7                  | 7                  | 7                  |
|           | Length        | 15                 | 153                | 283                | 552                | 581                | 496  | 901                | 1323               | 1029     | 351    | 549    | 3149   | 535    | 815                | 241    | 288    | 3866               | 3869               | 339                | 620                | 279                | 3164 | 473       | 225                | 2157  | 3938   | 461                | 168                | 185                |
| æ         | Query         | 9.                 |                    | ä,                 | 13.3               | ω,                 | ش    | 12.9               |                    |          | ď      |        | ď.     | ď      | ς.                 |        |        |                    |                    |                    |                    |                    |      |           |                    |       |        |                    |                    |                    |
|           | Score         | 81.9               | 525                | 112.5              | 109.5              | 107.5              | 107  | 106.5              | 106.5              | 106      | 105    | 105    | 105    | 104.5  | 104                | 103    | 102.5  | 102.5              | 102.5              | 101                | 100                | 99.5               | 98.5 | 98        | 97.5               | 97.5  | 97.5   | 97                 | . 5 . 96           | 96                 |
|           | Result<br>No. | 1                  | 7                  | ٣                  | 4                  | ស                  | 9    | 7                  | ထ                  | άν       | 10     | 11     | 12     | 13     | 14                 | 15     | 16     | 17                 | 18                 | 19                 | 20                 | 21                 | 22   | 23        | 24                 | 25    | 26     | 27                 | 28                 | 29                 |

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| A NO CONTROLL OF C | · · · · თთთთთ · · · თთთ ·                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | entiatio les: Hom les: Hom les: O2-Sep szshon: A les: A le                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | protein ies: Mus is: 13. 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 Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J., Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic and physical map for the 8 mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
EMBL. AL131469, CAB3180.1;
INTERPRO, IPRO005963.
 77 VEEPNPAKRILFLLTIVFCQILMAEGVPAPLPPEDAP----NAASLAPTP----VSP 127
 ----TPAPTPPPVRPAAPAPAPSVTPTPRPSLSP 160
 15 OAPTPAPSTIPGPRRGSGPEIFTFDPLPEPAAAPAGRPSASRGHRKRSRRVLYPRVVRRQ 74
 17 PTPAPSTIPGPRRGSGPEIFTFDPLPEPAAAPAGRPSASRGHRKRSRRVLYPRVVRRQLP 76
 Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
 37;
 75 LPVEEPNPAKRLLFLLLTIVFCQILMAEEGVPAPLP-PEDAPNAASLAPTPVSP 127
 55;
 Length 233;
 Length 203;
 STRAIN=A3(2);
Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
 Indels
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 Brown S.P., Harris D.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
 D5C494019C45BFE2 CRC64;
 B34A7C01CFDF782A CRC64;
 01-MXY-2000 (TrEMBLrel. 13, Last sequence update) 01-JUN-2000 (TrEMBLrel. 14, Last annotation update) PUTATIVE SECRETED PROLINE-RICH PROTEIN.
 13.2%; Score 108.5; DB 2; 28.1%; Pred. No. 0.011; iive 10; Mismatches 35;
 Score 107.5; DB 2;
Pred. No. 0.012;
6; Mismatches 28;
 203 AA
 Created)
 PRT;
 233
24514 MW;
 PRINTS; PRODO21; PRORICH.
PRINTS; PRO1217; PRICHEXTENSN.
PRINTS; PRO1218; PSTLEXTENSIN.
SEQUENCE 203 AA; 20511 MW;
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28.2%;
EMBL; AF255902; AAF70092.1;
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Matches 32; Conservative
 Query Match 13.1'
Best Local Similarity 28.2'
Matches 35; Conservative
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 Streptomyces coelicolor
 233 AA;
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 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 NCBI_TaxID-1902;
 121 APEPSPTP-
 STRAIN=A3(2);
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Coulson A.,
 57 GHRKRSRRV-----LYPRVVRRQLPVEEPNPAKRLLFLLLTIVFCQILMAEEGVPAP 108
 Caenorhabditis elegans.
Eukaryota, Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
 ----- AGRPSASR 56
 55;
 Length 581;
 Indels
 Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
 109 LP-----PEDAPNAASLAPTPV----SPVLEPFNLTSEPSDYA 142
 62838 MW; 0663409C9615CCB4 CRC64;
 Last sequence update)
Last annotation update)
 13.1%; Score 107.5; DB 5; 25.3%; Pred. No. 0.033; tive 9; Mismatches 60;
 9 PTMTILQAPTPAPSTIPGPRRGSGPEIFTFDPLPEPAAAP----
 Search completed: January 30, 2001, 23:11:29
Job time: 3994 sec
 Created)
 01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-JUN-2000 (TrEMBLrel. 14,
 EMBL, 277662, CAB01192.1,
INTERPRO, IPR002485, -,
PFAM, PF01482, DUF13; 1.
PRODOM, PD002726, -; 1.
 Query Match 13.1
Best Local Similarity 25.3
Matches 42; Conservative
 Nature 368:32-38(1994)
 SEQUENCE FROM N.A.
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 1078 SASPPREVPVPTPAPVEVPVPERVAGSPV---TPLPEQEASPA-RPAGPTEESPPSAPL 1133
 1134 RPP----EPPAGPPAPAPRDERPSSPIPLLPPPKKRRKTVSFSAI----EVVPAPEPP 1184
 Nagase T., Ishikawa K., Nakajima D., Ohira M., Seki N., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
"Prediction of the coding sequences of unidentified human genes. VII. The complete sequences of 100 new cDNA clones from brain which can DNA Res. 4:11-150(1997).

EMBL: AB00237: BAA20797.2; -.
 60 KRSRRVLYPRVVRRQLP-VEEPNPAKRILFLLLTIVFCQ1LMAEEGVPAPLPPEDAPNAA 118
 66 LYPRVVRRQLPVEEPNPAKR-----LLFLL.-----LTLVFCQILMAEEGVPAPLPP 111
 Gaps
 1 MCHSRSCHPTMT1LQAPTPAP-STIPGPRGSGPEIFTFDPLPEPAAAPAGRPSASRGHR 59
 Ramon A., Gil R., Burgal M., Sentandreu R., Valentin E.;
"A novel cell wall protein specific to the mycelial form of Yarrowia
 SCHPTMTILQAPTPAPSTIPGPRRGSGPEIFTFDPLPEPAAAPAGRPSASRGHRKRSRRV
 Homo saplens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
 13.2%; Score 109; DB 4; Length 1709; 32.6%; Pred. No. 0.069; ive 10; Mismatches 53; Indels 2
 13.2%; Score 109; DB 3; Length 285; larity 28.4%; Pred. No. 0.012; Conservative 11; Mismatches 62; Indels
 DCF2E0FF716B672C CRC64;
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0BA7FF1C515CD57D CRC64;
 01-JAN-1998 (TrEMBLrel. 05, Created)
U-MXY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
KIAA0339 PROTEIN (FRAGMENT).
 PRT; 1709 AA
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MEDLINE-97127825; PubMed-8972576;
 1709 AA; 186231 MW;
 16 PC
285 PC
30036 MW;
 219 SLRS---SPSLPPLPLPPSPS 236
 119 SLAPTPVSPVLEPFNLTSEPS 139
 PR01217; PRICHEXTENSN.
 lipolytica.";
Yeast 12:1535-1548(1996).
EMBL; 281006; CAB02634.1;
 Conservative
 PRELIMINARY;
 PFAM; PF00076; rrm; 1. PFAM; PF00856; SET; 1.
 INTERPRO; IPR001214; -
 285' AA;
 Local Similarity
nes 40; Conserv
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Matches 44; Conserv
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2859 PAPKPKPPP-----TPDSKPSPAPKPKSPSASKPLPVPFPNSDSKTSPV 2902
 2802 SPAPKPSPAPKPPPPDPD----FKPSPASKPSPASKPSPASKPSPASKPSPASKPS 2858
 PVEEPNPAKRLLFLLLTIVFCQ1LMAEEGVPAPLPPEDAPNAASLAPTP-----VSPV 128
 Gaps
 16 APTPAPSTIPGPRRGSGPEIFTFDPLPEPAAAPAGRPSASRGHRKRSRRVLYPRVVRRQL 75
 Jones D., Lee L., Liu J.L., Kung H.J., Tillotson J.K.; "Marek disease virus encodes a basic-leucine zipper gene resembling the fos/jun oncogenes that is highly expressed in lymphoblastoid
 Streptococcus pneumoniae.
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
 Lee L.F., Wu P., Sui D., Ren D., Kung H.J.;
Lee C.F., Wu P., Sui D., Ren D., Kung H.J.;
"The Complete UL Sequence of Serotype I Marek's Disease Virus.";
Proc. Natl. Acad. Sci. U.S.A. 0:0-0(2000).
EMBL; AFI47805, AAF65771.1;
SEQUENCE 3325 AA; 365698 MW; 5D4A84EF719BB9FD CRC64;
 Length 3325;
 Indets
 Beall B.W.;
Beal B.W.;
"pspA sequence types from multiresistant pneumococci":
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
 no RNA stage; Herpesviridae
 Created)
Last sequence update)
Last annotation update)
 Last sequence update)
Last annotation update)
 52;
 Proc. Natl. Acad. Sci. U.S.A. 89:4042-4046(1992)
 13.2%; Score 109; DB 12; 25.2%; Pred. No. 0.13; tive 14; Mismatches 52;
 3325 AA
 AA
 Created)
 MEDLINE-92237304; PubMed-1315048;
 01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15,
 15,
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 Best Local Similarity 25.2%
Matches 31; Conservative
 1185 PATPPOAKF-PGPAS 1198
112 EDAPNAASLAPTPVS 126
 PRELIMINARY;
 01-OCT-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
MAJOR TEGUMENT PROTEIN.
 Viruses; dsDNA viruses,
 Turkey herpesvirus
 SEQUENCE FROM N.A.
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 SEQUENCE FROM N.A.
 NCBI_TaxID=10390;
 NCBI_TaxID-1313;
 PSPA (FRAGMENT)
 Streptococcus
 2903 PNP 2905
 129 LEP 131
 STRAIN-GA;
 Query Match
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 65 VLYPRVVRRQLPVEEPNPAKRLLFLLLTIVFCQILMAEEGVPAPLPPEDAPNAASLAPTP 124
 PIMIILQAPIPAPSTIPGPRRGSGPEIFTFDPLPEPAAAP-----AG-RPSASR 56
 7 CHPTMTILQAPTPAPSTIPGPRRGSG--PEIFTFDPLPEPAAAPAGRPSASRGHRKRSRR 64
 Eukaryóta; Viriáiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.
NCBI_TaxID=4577;
 GHRKRSRRVLYPRVVRRQLPVEEPNPAKRLLFLLLTIVFCQILMAEEGVPAPLP---PED
 Stratford S., Barnes W., Golubiewski A., Cotter R., McCormick S., Hohorst D., Gao M., Showalter A., Bedinger P.A.;
Hohorst D., Gao M., Showalter A., Bedinger P.A.;
"Pollen Extensin-like (Pex) Genes in a Monocot and a Dicot.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF159297; AAD55980.1;
INTERRO; IPR001998;
INTERRO; IPR001998;
PRINTS: PR01217; PRICHEXTENSN.
PROSITE; PR01217; PRICHEXTENSN.
PROSITE; PS00172; XYLOSE_ISOMERASE_1; UNKNOWN_1.
SEQUENCE 1315 AA: 134401 MM; 64C97A2A01F0936F CRC64;
 Yarrowia lipolytica (Candida lipolytica).
Ekbaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
Dipodascaceae; Yarrowia.
NCBL_TaxID+4952;
 Query Match 13.3%; Score 109.5; DB 10; Length 1315; Best Local Similarity 24.6%; Pred. No. 0.048; Matches 33; Conservative 14; Mismatches 50; Indels 37;
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Last annotation update)
 01-WAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 285 AA.
 349 GPGPR-----PAPAPAPGOGPRPA----
 Created)
 PRT;
 114 APNA----ASLAPTPVSPVLEP 131
 SEQUENCE FROM N.A.
STRAIN-CX39-74A; TISSUE-PINA240;
 . 1140 -----PPPTPVSSPPPELK---
 13,
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 CELL WALL PROTEIN PRECURSOR
 PRELIMINARY;
 1175 APVSLPPPEVKSSP 1188
 PRELIMINARY;
 01-MAY-2000 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
01-JUN-2000 (TrEMBLrel.
 125 VSPVLEPFNLTSEP 138
 EXTENSIN-LIKE PROTEIN.
 SEQUENCE FROM N.A.
 Zea mays (Maize)
 TISSUE-POLLEN;
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 STRAIN-20516 OF SVALOFS KARAT;
STRAIN-20516 OF SVALOFS KARAT;
MEDLINE-9721078; Pubmed-905982;
Taipaleansuu J., Falk A., Ek B., Rask L.;
"Myrosinase-binding proteins are derived from a large wound-inducible and repetitive transcript.";
and repetitive transcript.";
Eur. J. Biochem. 243:605-611(1997).
EMBL: U59446; AAC08051.1;
HSSP; P18674; JJOT.
MENDEL: 14865; Brana; 2388;14865.
 RKRSRRVLYPRVVRRQLPVEEPNPAKRLLFLLLTIVFCQILMAEEGVPAPLPPEDA---- 114
 722 EPTSEPTPQPAPPQPAPPQPAPQP------APQPAPQPAPQPPQPAPPQPAPPQPAPPQPAPPQP
 Gaps
 mouse
 Brassica napus (Rape).
Eukaryota; Viridiplantac; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
 4 SRSCHPIMTILQAPTPAPSTIPGPRRGSGPEIF -- -- TFDPLPEPAAAPAGRPSASRGH
 53;
 Lee L.H., Gigliotti F., Wright T.W., Simpson-Haidaris P.J., Weinberg G.A., Haidaris C.G.; "Molecular characterization of KEXI, a kexin-like protease in indemocystic carini."; "Gene 242:141-150(2000).

EMBL; AF093132; AAF32493.1; -.
 DB 3; Length 1011;
 Length 552;
 Pneumocystis carinii f. sp. muris.
Eukaryota, Fungi, Fungi incertae sedis, Pneumocystidaceae;
 42; Indels
 Indels
 1011 AA; 112020 MW; FBE472C8F65864E8 CRC64;
 096343;
01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-UIN-2000 (TrEMBLrel. 14, Last annotation update)
MYROSINASE-BINDING PROTEIN RELATED PROTEIN (FRAGMENT).
 5FE51A3718FBD0FA CRC64;
 Last sequence update)
Last annotation update)
 13.3%; Score 109.5; DB 10; 29.4%; Pred. No. 0.021;
 73;
 115 -----PNAASLAPTPVSPVLEPFNLTSEPSDYALDLST 147
 764 VPPQPVPPQPMPSRPAPPKPTPQP---TSEPAPQPTSEST
 13.4%; Score 110.5; DE
25.0%; Pred. No. 0.03;
tive 10; Mismatches
 6; Mismatches
 Created)
 PRT;
 552 AA; 59270 MW;
 01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15,
 PFAM; PF01419; Jacalin; 3.
NON_TER 1 1 1
SEQUENCE 552 AA; 59270 M
 KEXIN-LIKE PROTEASE KEX1.
 Conservative
 Query Match 13.3
Best Local Similarity 29.4
Matches 42; Conservative
 PRELIMINARY;
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Best Local Similarity
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 SEQUENCE FROM N.A
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37; Gaps

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RASAMENEEREEN, STAIN-WERKELEN, CENINKELEN, CENINKERS S.E. HOLT R. Anabutner M., Henderson S.N., Shandton R.C., Norteman J.R., Yandala M.D., Zhang O., Chen L.X., Radardon R.C., Norteman J.R., Yandala M.D., Zhang O., Chen L.X., Brandon R.C., Norgers Y.-H.C., Blazel, R.G., Champe M., Pfeiffer B.D., RADILO G., Wortman J.R., Yandala M.D., Bandart D., Belankavo S.M., Beneson K.Y., Benos P.V., Berman B.P., Bhandart D., Bolankavo S.M., Beneson K.Y., Benos P.V., Berman B.P., Bhandart D., Bolankavo S.M., Borkova D., Botchen M.R., Bouck J., Brokstein P., Brottier P., Borderson M.D., Bollike C., Davenport L.B., Daviss P., Radelland M.C., Capten B.C., Champer C.C., Ferraz C., Dunn P., RADOSON K., Boughlista C.C., Ferraz C., Perriera S., Fleischmann W., RADOSON K., Doup L.B., Downes M. Dugan Rocha S., Dunkov B.C., Dunn P., RADOSON K., Doup L.B., Downes M., Dugan Rocha S., Ploitov B.C., Dunn P., RADOSON K., Doup L.B., Gongrey, Gorle C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K., RADOSON K., Doup L.B., McIntel B.C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K., Alalai M., Kalush F., Kaleren G.H., Ke Z., Kennison J.A., Ketchum K.A., Alani M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Houth M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., RAMMEL B.E., Kodira C.D., Kraft C., Morison J.A., Malson D.L., R., Nalson M., Pittman G.S., Pan S., Pollard J., Purl V., Wang X., R., Balazollo M., Pittman G.S., Pan S., Pollard J., Purl W., Wang C.Y., Wassenbach J., Wang C.Y., Wassenbach G., Scheeler E., Spradling A.C., Staplecon M., Stupski N., Stupski N., Shong K., Shong W., Shong K., Shong W., Wang C.Y., Wassenbach G., Scheeler E., Shong R.,
 Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
 68 P-----TIVECQILMAEEGVPAP 108
 | :| :| :| :| :| 399 PLSQLETFKDMLLYNAQLYIKENVPHPPKILIGRLKDEDPEEHT-----VL1PQSPKPSP 453
 10 TMTILQA--PTPAPSTIPGPRRGSGPEIFTFDPLPEPAAAPAGRPSASRGHRKRSRRVLY 67
 109. LPPEDAPNAASLAPTPVSPVLEPFNLTSEPSDY------ALDLSTFLQQHPAAF 156
 Indels 39;
 Length 649;
 6471AC52B49F9AE9 CRC64;
 13.7%; Score 112.5; DB 5; 25.8%; Pred. No. 0.013; iive 26; Mismatches 67;
 PRT; 1011 AA
 74414 MW;
 EMBL; AE003802; AAF577911; -
 Query Match
Best Local Similarity 25.8%
Matches 46; Conservative
 PRELIMINARY;
 649 AA;
 SEQUENCE FROM N.A.
 SEQUENCE
 09P944
 RESULT
 Q9P944
ID Q9
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 2760 -GARKSLPAAQPR--QRLL------RSRSPASVPAPGSELVPP---PSGGALGSPP 2803
 69 RVVRRQLPVEEPNPAKRLLFLLLTIVFCQILMAEEGVPAP----LPPEDAPNAASLAPTP 124
 Gaps
 9 PTMTILQAPTPAPSTIPGPRRGSGPEIFTFDPLPEPAAAPAGRPSASRGHRKRSRRVLYP 68
 Schwyzer M., Vloek C., Lowery D.E., Bello L.J., Meyer G., Misra V., Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
 Schwyser M., Vicek C., Lowery D.E., Bello L.J., Meyer G., Misra V.,
Thiry E., Paces V.;
 Schwyzer M., Styger D., Vogt B., Lowery D.E., Simard C.,
LaBoissiere S., Misra V., Vlcek C., Paces V.;
"Gene contents in a 31-kb segment at the left genome end of bovine
 30;
 DB 12; Length 3247;
 Ouery Match
13.9%; Score 114; DB 12; Length 32
Best Local Similarity 31.1%; Pred. No. 0.045;
Matches 41; Conservative 12; Mismatches 49; Indels
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 Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
 3AEAA72F8F001F6A CRC64;
 Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases
 to the EMBL/GenBank/DDBJ databases
 Simard
 Bovine herpesvirus 1.
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Varicellovirus.
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 Created)
Last sequence update)
Last annotation update)
 Schwyzer M., Styger D., Vogt B., Lowery D.E.,
LaBoissiere S., Misra V., Vlcek C., Paces V.;
Vet. Microbiol. 0:0-0(1996).
 649 AA.
 STRAIN---.
Schwyzer M.;
Schwyzer M.;
EMBL: 278205; CAB01605.1; -.
EMBL: AJ004801; CAA06097.1; -.
 PRT;
 MEDLINE-97164286; PubMed-9010999;
 Microbiol. 53:67-77(1996).
 09/884;
01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-JUN-2000 (TrEMBLrel. 13,
CG18635 PROTEIN.
 SEQUENCE OF 1-179 FROM N.A.
 SEQUENCE OF 1-179 FROM N.A.
 PRELIMINARY;
 2804 SFVPSRPPSLEP 2815
 125 V----SPVLEP 131
 SEQUENCE FROM N.A. STRAIN-COOPER;
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 NCBI_TaxID=10320;
 STRAIN-COOPER;
 STRAIN-COOPER;
 herpesvirus-1
 Schwyzer M.;
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 STRAIN-JURA;
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Length 1668;

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; Score 114.5; DB 4;
; Pred. No. 0.021;
12; Mismatches 50;
 SEQUENCE FROM N.A.
MEDLINE-99278407; Pubmed-10347196;
 PRINTS; PROJESS, THOOK.
PRINTS; PRO1217; PRICHEXTENSN.
PRINTS; PRO 2971 AA; 315641 MW;
 TRANSCRIPTIONAL ACTIVATOR SRCAP.
 2242 PPPACTPPPAHTPPPAQTCL 2261
 13.9%;
29.3%;
 124 PVSPVLEPFNLTSEPSDYAL 143
 PPPACTPPPAHTPPPAQTCL 958
 INTERPRO; IPR002965; -- PFAM; PF00176; SNF2_N; 1. PFAM; PF00271; helicase_C; 1.
 124 PVSPVLEPFNLTSEPSDYAL 143
 01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01,
 Ouery Match 13.9%
Best Local Similarity 29.3%
Matches 41; Conservative
 Conservative
 PRELIMINARY;
 PRELIMINARY;
 Homo sapiens (Human).
 NTERPRO; IPR001650;
 Ouery Match
Best Local Similarity
 INTERPRO;
 Q9Y5L9;
 065553;
 09Y5L9
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Matanabe K., Kumagai A., Itakura S., Yamazaki M., Tashiro H., Ota T.,
Buzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T.,
Nakamura Y., Isogai T., Sugano S.;
"NEDO human cDNA sequencing project.";
Submitted (FER-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AKO00252; BAA91032.1; -.
 Nagase T., Ishikawa K., Nakajima D., Ohira M., Seki N., Miyajima N., Tanaka A., Koɗani H., Nomura N., Ohara O.; Prodiction of the coding sequences of unidentified human genes. VII. The complete sequences of 100, new cDNA clones from brain which can
 Gaps
 19 PAPSTIP-GPRRG-SGPEIFTFDPLPEPAAAPAGRPSASRGHRKRSRRVLYPRVVRRQLP 76
 Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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 DB 4; Length 423;
 14.9%; Score 122.5; DB 4; Length 42.2%; Pred. No. 0.001; Live 9; Mismatches 34; Indels
 PFAM: PF00271; helicase_c; 1.
PFAM: PF02178; AT hook: 3.
PRINTS; PR00929; ATHOOK.
NON-TER
SEQUENCE: 1668 AA; 175162 MW; 7717C8FC6A396C49 CRC64;
 41032.1; -.
46942 MW; F3F52BC058CAD51E CRC64;
 01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
CDNA FLJ20245 FIS, CLONE COLF6454.
 Last sequence update)
Last annotation update)
 423 AA
 PRT; 1668 AA
 77 -VEEPNPAKRLLFLILTIVFCQILMAEEGV 105
 Created)
 code for large proteins in vitro.";
DNA Res. 4:141-150(1997).
EMBL, BA002307; BAA20768.1; -.
INTERPRO; IPRO00637; -.
 PRT;
 TISSUE-BRAIN;
MEDLINE-97349984; PubMed-9205841;
 (TrEMBLrel. 05, (TrEMBLrel. 05, (TrEMBLrel. 15,
 38; Conservative
 PRELIMINARY;
 PRELIMINARY;
 015026;
01-JAN-1998 (TrEMBLrel.
01-JAN-1998 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
181 DLSTFLQQHPAAF 193
 Homo sapiens (Human).
 Homo sapiens (Human).
 NTERPRO; IPRO01650;
 KIAA0309 (FRACMENT).
 Best Local Similarity
Matches 38; Conserv
 423 AA;
 SEQUENCE FROM N.A.
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 Query Match
 K1AA0309
 O9NXHB
O9NXHB;
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2198 --LVPVPVSAPVPISAPNP------ITILPVHIL------PSPPPPSQIPPCSSPACT 2241
 64 RVLYPRVVRRQLPVEEPNPAKRLLFLLTIVFCQILMAEEGVPAPLPPEDAPNAASLAPT 123
 64 RVLYPRVVRRQLPVEEPNPAKRLLFLLTIVFCQILMAEEGVPAPLPPEDAPNAASLAPT 123
Gaps
 6 SCHPTMTILQAP--TPAPSTIPGPRRGSGPEIFTFDPLPEPAAAPAGRPSASRGHRKRSR 63
 SCHPIMTILQAP - - TPAPSTIPGPRRGSGPEIFTFDPLPEPAAAPAGRPSASRGHRKRSR 63
 Johnston H., Kneer J., Chackalaparampil I., Yaciuk P., Chrivia J.; "Identification of a novel SNF2/SW12 protein family member, SRCAP, which interacts with CREB-binding protein."; J. Biol. Chem. 274:16370-16376(1999).

EMBL; AF143946; AAD39760.1; -...
INTERPRO; IPRO00330; -...
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
 2157 SAHQTRSTTTPPRCSPARERVPRP----APR-----PRPTPASAPAAIPA-----
37;
 37;
 13.9%; Score 114.5; DB 4; Length 2971; 29.3%; Pred. No. 0.037; Live 12; Mismatches 50; Indels 37:
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 F9F7EE70304B78A3 CRC64;
 01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 Created)
Last sequence update)
 PRT; 2971 AA
 PRT; 3247 AA.
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us-08-799-910-10.rspt

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Q96AXB homo saplen
Q9553 homo saplen
Q6553 bovine herp
Q9884 drosophila
Q96343 brassica na
Q96343 brassica na
Q96347 yarrowia li
Q15Q47 homo saplen
Q91568 streptococc
Q91568 streptococc
Q91568 streptococc
Q91547 drosophila
Q90yt7 drosophila
Q98457 paramecium
Q944562 actinomyces
 January 30, 2001, 22:04:55; Search time 64.84 Seconds (without alignments) 281.993 Million cell updates/sec
 075353 homo sapien
09nxh8 homo sapien
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
 1 MCHSRSCHPTMTILQAPTPA......EPSDYALDLSTFLQQHPAAF 156
 Description
GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
 Total number of hits satisfying chosen parameters:
 374700 seqs, 117207915 residues
 SUMMARIES
 Listing first 45 summaries
 OM protein - protein search, using sw model
 Q9Y5L9
Q65553
Q9V884
 Q9P944
Q96343
Q9SPM0
P78977
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 015047
091BT9
 Q9LAY5
Q98457
Q44562
 Q9L568
Q9RCX9
Q20517
Q9VYT7
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sp_vertebrate:*
sp_unclassified:*
 sp_invertebrate:*
sp_mammal:*
 Post-processing: Minimum Match 08
Maximum Match 1008
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 Minimum DB seq length: 0
Maximum DB seq length: 200000000
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sp_bacteria:*
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 sp_rodent:*
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 sp_fungi:*
sp_human:*
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089379 chlamydomon
089370 paramecium
091567 streptococc
091565 streptococc
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0915745 synchoryst
096716 chlorella v
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099738 drosophila
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Q89370
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## ALIGNMENTS

| SULT 1<br>5353<br>075353 PRELIMINARY;<br>075353;<br>01-NOV-1998 (TrEMBLEEL: 08, 0 | DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  101-NAY-1999 (TrEMBLrel. 10, Last annotation update)  E ANTI-DEATH PROTEIN.  GN IEX-1L.  OS Homo sapiens (Human).  C EUKaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  OX NCBI_TaxID=9606; | RP SEQUENCE FROM N.A.  RX MEDLINE-98369175; PubMed-9703517;  RA WU M.X. A0 2., Prasad K.V.S., Wu R., Schlossman S.F.;  RT "IEX-1L, an apoptosis inhibitor involved in NF-kappaB-mediated cell  RT survival.;  R. Schence 281:998-1001(1998).  B. Schence 281:998-1001(1998).  DR EMBL: AF039067; AAC72558.1;  DR EMBL: AF039067; AAC72558.1;  SCQUENCE 193 AA; 21028 MW; 7927D9D3FFBC7C57 CRC64; | Ouery Match Best Local Similarity 78.8%; Pred. No. 8.1e-64; Matches 152; Conservative 1; Mismatches 3; Indels 37; Gaps Oy I MCHSRSCHPTWILQAPTPAPSTIPGPREGGGEIFTFDPLPEPAAAPAGRPSASRGHRK 60 | OY 61 RSRRVLYPR | 84 KRLEFLLTIVECO | Qy 144 DLSTFLQQHPAAF 156 |
|-----------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------|------------------|--------------------------|
|-----------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------|------------------|--------------------------|

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21 LTIVFCQILMA-----EGVPAPLPPEDAPNAASLAPTPVSPVLEPFNLTSEP-SDYAL 73
 Detection of modulators of Mena and Ena-VASP-like genes and proteins - used in control of cytoskeletal dynamic events in normal and abnormal cell morphology, adhesion, motility, growth and
 Mena protein; mammalian Ena; Enabled; Evl protein; cytoskeleton; cell morphology; cell adhesion; cell differentiation; cell growth; cell motility; mouse.
 This polypeptide comprises murine Mena (mammalian Ena) that shows significant amino acid similarity to Drosophila Ena and which exhibits a broad pattern of tissue distribution in neurons,
 'note= "Ena-VASP homology domain 1 (EVH1)"
 /note= "mediates binding to profilin" 316..321
 /note= "mediates binding to profilin"
 Soriano P, Wehland J;
 (GBFB) GES BIOTECHNOLOGISCHE FORSCHUNG MBH. (HUTC-) HUTCHINSON CANCER RES CENT FRED.
 /note= "O-phosphorylated"
305..310
 "LERER repeat"
 207..211
/note= "LERER repeat"
 "LERER repeat"
 "LERER repeat"
 "LERER repeat"
 "LERER repeat"
 Example 1; Page 54-56; 77pp; English.
 Location/Qualifiers
 W37148 standard; Protein; 541 AA.
 97WO-US11669.
 06-JUL-1998 (first entry)
 170
 .180
 . 203
 160
 Gertler FB, Niebuhr K,
 /note=
199..20
 'note=
 |:| ||:|
853 ilttgeaghpsa 864
 Mammalian Ena (Mena).
 74 DLSTFLQQHPAA 85
 WPI; 1998-101197/09.
 differentiation
 N-PSDB; V02996
 Modified-site
 Mus musculus.
 Binding-site
 Binding-site
 WO9801755-A1
 03-JUI.-1997;
 05-JUL-1996;
 15-JAN-1998
 Peptide
 W37148;
 Pept:1de
 Peptide
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 Peptide
 Peptide
 Domain
 15
 RESULT
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6 PVEEPNPAKRLLFLLTIVFCQILMAEEGVPAPLPPEDAPN----AASLAPTPVSPVLEP 61
haematopoletic cells. Its amino acid sequence was deduced from a mouse embryonic stem conditions of the condition of conditio
 genes and proteins, a variety of methods and compositions are provided for screening, isolating and characterising endogenous and exogenous. Factors, drugs and therapeutic agents useful to evaluate and/or control cytoskeletal dynamic events involved in normal and abnormal cell morphology, adhesion, mothlity, growth and/or differentiation. A method of detecting a modulator of Mena
 20;
 Ouery Match
15.2%; Score 67; DB 19; Length 541;
Best Local Similarity 29.9%; Pred. No. 25;
Matches 20; Conservative 4; Mismatches 23; Indels ;
 Search completed: January 30, 2001, 22:05:37 Job time: 11886 sec
 activity/expression is claimed
 268 paesptpqglvl--
 541 AA;
 312 lpstgpp 318
 62 FNLTSEP 68
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 The present invention a method for detecting the presence or absence of mutations in the E-cadherin gene, which is indicative of a predisposition to cancer. The method can be used to identify predisposition to cancers such as breast cancer, colorectal cancer, pastric cancer, prostate cancer, thyroid cancer, kidney cancer, bladder cancer, and liver cancer. The method is particularly useful for identifying predisposition to rereditary diffuse gastric cancer (HDCC). Compounds which increase the expression or prevent the decrease of E-cadherin would be potential cancer chemopreventative agents. Gene therapy can also be used to supply wild-type E-cadherin. The key to cancer treatment is early detection.
an cDNA clone (T05764) derived from human liver. The extracellular domain of E-cadherin is used to generate peptides that specifically bind to heterotypic cognates of E-cadherin and which inhibit adhesion of intra-epithelial T-lymphocytes to E-cadherin-expressing epithelial or endothelial cells in vitro or in vivo, thereby modulating mucosal immune responses. Such peptides are also specifically reactive with a monoclonal antibody (E4.6 or E6.1) that binds to E-cadherin and that can inhibit T-cell binding.
 Gaps
 E-cadherin, Maori, familial gastric cancer; germline mutation; detection; human; breast cancer; colorectal cancer; prostate cancer; thyroid cancer; kidney cancer; bladder cancer; liver cancer;
 1 VRROLPVEEPNPAKRLLFLLLTIVFC-----51LMAKEGVPAPLPPEDAPNAASLA--- 51
 Determining predisposition to cancer by detecting a mutation in the
 33;
 Length 878;
 Indels
 31;
 52 ------PrPVSPVLEPFNLTSEPSDYALDLSTFLQQH 82
 DB 16;
 Local Similarity 25.7%; Pred. NO. JV...
hes 26; Conservative 11; Mismatches
 15.5%; Score 68.5; 25.7%; Pred. No. 30;
 hereditary diffuse gastric cancer; HDGC
 Disclosure, Page 35-37; 55pp; English.
 LTD.
 (TEWH-) TE WHETU WHANAU TRUST
 Y09375 standard; Protein; 882
 98WO-NZ00160
 97NZ-0328994
 14-JUL-1999 (first entry)
 Guilford PJ, Reeve AE;
 Wild-type E-cadherin.
 WPI; 1999-288129/24
 878 AA;
 UNIV OTAGO
 E-cadherin gene
 N-PSDB; X56022
 Homo sapiens
 WO9920168-A2
 19-OCT-1998;
 17-OCT-1997;
 29-APR-1999
 Sequence
 Query Match
 (UYOT-)
 Y09375;
 Matches
 RESULT
 109375
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5
The method allows the identification of individuals with a predisposition to cancer, particularly to hereditary cancer, which enables detection before the appearance of clinical symptoms, and thus allows treatment, or other courses of action, to commence as soon as possible. Also, families with histories of familial cancer will be able to undergo tests to search for E-cadherin gene mutations. The present sequence represents
 2;
 588 vndnapipepr----tiffcernpkpgvinl---idadippntspftaelthga 634
 A cDNA clone was obtd. (see T06027) from a HeLa cell cDNA library that encoded a novel density-enhanced Type III receptor-like PTP, designated hubEp-1 (R85203). hubEp-1 is useful for the study of PTPs and for the development of therapeutic or prophylactic cpds. e.g. for prevention of abnormal or malignant cell growth.
 Gaps
 Density enhanced Type III receptor-like protein tyrosine phosphatase;
 1 VRRQLPVEEPNPAKRLLFLLLTIVFC-----51
 Gaps
 develop
of
 33;
 .:
 Length 1337;
 Length 882;
 New density enhanced protein tyrosine phosphatase - used to prods. to modify transcription, translation and/or activity
 Indels
 Indels
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 52 ----- PTPVSPVLEPFNLTSEPSDYALDLSTFLQQH 82
 DB 20;
 DB 16;
 33;
 11; Mismatches
 15.5%; Score 68.5; D
29.2%; Pred. No. 50;
Live 11; Mismatches
 15.5%; Score 68.5; 1
25.7%; Pred. No. 30;
 Claim 4; Page 34-38; 51pp; English.
 Ā
 (COLD-) COLD SPRING HARBOR LAB.
 95WO-US05512
 94US-0237940.
 (first entry)
 Query Match
Best Local Similarity 29.2%
Matches 21; Conservative
 Conservative
 tyrosine phosphatase(s).
 Tonks NK;
 wild-type E-cadherin
 WPI; 1995-393079/50.
 Best Local Similarity
Matches 26; Conserv
 882 AA;
 R85203 standard;
 N-PSDB; T06027
 Homo sapiens
 WO9530008-A1
 03-MAY-1995;
 03-MAY-1994;
 12-FEB-1996
 09-NOV-1995.
 Oestman A,
 Sequence
 Query Match
 Sequence
 huDEP-1.
 R85203;
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 RESULT 14
 R85203
 88666666888
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 7
 A37022 to A37144 encode the new isolated human transmcmbrane, receptor or secreted PRO polypeptides given in Y99340 to Y99462. The transmembrane and receptor PRO proteins can be used for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interactions. The polypeptides and nucleotide sequences encoding then have various industrial applications, including uses as pharmaceutical and diagnostic agents. A37145 to A37330 represent PCR primers and hybridisation probes used in the isolation of the PRO polypeptides from the present invention.
secreted PRO polypeptides, useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interactions
 E-cadherin is a cell adhesion molecule that is also known as uvomorulin, L-CAM and Cell CAM 120/80. The DNA encoding hEC was obtd. by screening normal human liver and hepatocellular carcinoma cDNA libraries and a colonic epithelial cell CDNA library. The following sequences are specifically claimed: AAS 1-878; 151-878; 30 sequential AAS from AAS 108-878; AAS 1-150; AAS 178-289; AAS 290-401; AAS 402-513; AAS 178-513; AAS 151-703; AAS 1-1703; AAS 728-878; AAS 704-878; nucleotide sequences comprising nucleotide numbers 116-2749; 566-2749; 1-1053; 10-26696; 1332-3000; 540-1500; 348-9066; 890-1648; 384-1208; 641-2046; 685-1336; 880-1661; 1199-1742; 1373-1742;
 Gaps
 E-cadherin; cell adhesion molecule; CAM;
 Purified human E-cadherin protein and nucleic acid - used to develop prods. for diagnosis, prognosis, therapy and prophylaxis of t-cadherin disorders, e.g. mallgnancies
 ..
6
 Length 370;
 32 EEGVPAPLPPEDAPNA-ASLAPTPVSPVLEPFNLTSEPSDYALDLSTFL 79
 Indels
 21;
 6; Mismatches 15;
 ĎВ
 Score 68.5; I
Pred. No. 11;
 Sequence of human liver E-cadherin.
 Human epithelial-cadherin; E-cadher
uvomorulin; L-CAM; Cell CAM 120/80.
 59-63; 97pp; English
 Claim 12; Fig 178; 773pp; English
 R55060 standard; Protein; 878 AA.
 15.5%;
38.8%;
 92US-0978897.
 93WO-US11097
 (first entry)
 Conservative
 Rimm DL;
 WPI; 1994-183426/22.
 Query Match
Best Local Similarity
Matches 19; Conserv
 370 AA;
 (UYYA) UNIV YALE.
 N-PSDB; Q65487
 Claim 1; Page
 16-NOV-1993;
 17-NOV-1992;
 08-NOV-1994
 WO9411401-A
 26-MAY-1994
 Morrow JS,
 Seguence
 R55060;
 11
 Ношо
 RESULT
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Gaps
 1. VRROLPVEEPNPAKRLLFLLLTIVFC-----51LMAEEGVPAPLPPEDAPNAASLA--- 51
 /label= Extracellular_domain
/label= Extracellular_domain (amino acids 1-552
/note= "the extracellular domain (amino acids 1-552
of the mature protein) is the preferred
region for generation of peptides of the
 Inhibiting adhesion of T lymphocytes with E-cadherin - useful for isolating agents to treat auto-immune diseases e.g. Crohn's disease, psoriasis, etc
1705-2204; 2458-2775; DNA encoding at least 30 AAs selected from AAs 308-878. The prods. can be used in the diagnosis, prognosis, therapy and prophylaxis of conditions involving improper E-cadherin expression. Suitable dosages for i.v. admin. of a protein are 20-500 mcg/kg body wt.
 E-cadherin; T-lymphocyte; alpha-E,beta-7 integrin; cell adhesion; autoimmune disease; Crohn disease; psoriasis.
 ρλ
 33;
 Length 878;
 The human E-cadherin protein precursor (R85487) is expressed
 Indels
 š
 631 vpnwtiqyndptqesiilkp-kmalevgdykinlklmdngn 670
 DB 15;
 31;
 ------PTPVSPVLEPFNLTSEPSDYALDLSTFLQQH 82
 /label- Transmembrane_domain 727..876
/label- Cytoplasmic_domain
 ; Score 68.5; D); Pred. No. 30; 11; Mismatches
 Disclosure; Page 70-75; 103pp; English.
 |...|50
|/abel=_Sig_peptide
 Location/Qualifiers
 (BGHM) BRIGHAM & WOMENS HOSPITAL.
 R85487 standard; Protein; 878
 15.5%;
 95WO-US05518
 94US-0237919
 Human E-cadherin precursor.
 Query Match
Best Local Similarity 25.79
Matches 26; Conservative
 Brenner MB, Cepek KL;
 WPI; 1995-392921/50.
N-PSDB; T05764.
 AA;
 Homo sapiens
 WO9529693-A1
 03-MAY-1995;
 03-MAY-1994;
 18-MAR-1996
 09-NOV-1995
 Seguence
 Peptide
 R85487;
 Domain
 Domain
 Domain
 12
 52
 R85487
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mammalian DNA sequences encoding transmembrane, receptor or
 Watanabe
 Smith V,
 AL,
 Gurney
 980'S - 010880'I
980'S - 010880'S
980'S - 010880'S
980'S - 010886'7
980'S - 010884'B
980'S - 010884'B
980'S - 010884'B
980'S - 010885'D
980'S - 010885'D
98US-0102570.
98US-0102571.
98US-0102687.
98US-0103687.
98US-0103149.
98US-01031314.
98US-01031314.
98US-01031318.
98US-01031318.
98US-01031318.
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98US-01031318.
98US-0103679.
98US-0103679.
98US-0105687.
98US-0105687.
98US-01056882.
98US-01056882.
98US-0105882.
98US-0105983.
98US-0105938.
98US-0105938.
 98US-0108858
98US-0108904
 (GETH) GENENTECH INC
 Baker K, Goddard A,
 WPI; 2000-237871/20.
N-PSDB; A37110.
30.5EP-1998;
30.05F-1998;
30.05T-1998;
01.0CT-1998;
02.0CT-1998;
07.0CT-1998;
07.0CT-1998;
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31.7.NOV-1998;
31.8.NOV-1998;
31.8.NOV-1998;
31.8.NOV-1998;
31.8.NOV-1998;
 New
 Human; PRO polypeptide; membrane bound protein; receptor; diagnosis; transmembrane; sccretion; immunoadhesion; pharmaceutical; screening.
 Human PRO1431 (UNQ737) amino acid sequence SEQ ID NO:315.
 9805.0098749
9805.0098750
9805.00988730
9805.00988730
9805.00998731
9805.0099538
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9805.0099816
 99WO-US20111
08-AUG-2000 (first entry)
 40200012708-A2
 Homo sapiens.
 23-SEP-1998;
23-SEP-1998;
23-SEP-1998;
 01-SEP-1999;
 24 - SEP-1998
24 - SEP-1998
 24-SEP-1998
 09-MAR-2000
 -SEP-1
-SEP-1
-SEP-1
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Wood WI;

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Streptococcus pneumoniae surface protein PspC and truncated PspA used in vaccines for protecting animals against S.pneumoniae
 pneumococcal surface protein; vaccine; otitis media;
 Streptococcus pneumoniae PspA central region.
 Streptococcus pneumoniae strain Rctl23.
 meningitis; bacteraemia; pneumonia.
 W14578 standard; Protein; 204 AA.
 (UABR-) UAB RES FOUND.
 WPI: 1997-202002/18
 Misc-difference 8
 Misc-difference
 WO9709994-A1
 6-SEP-1996;
 5-SEP-1995;
 McDaniel LS,
 28-OCT-1997
 20-MAK-1997.
 Briles DE,
 infection
 Seguence
 W14578;
 ó
 7
 This protein is encoded by gene 036 (see T91708), which was identified by differential display analysis as being expressed at a higher level in normal colon tissues than in cancerous colon tissues. Gene 036 is a candidate tumour suppressor gene. A correlation was found between an increase in the expression level of gene 036 and a decrease in a colon cell's tumour potential. Hence, methods that increase the level of expression of gene 036 may inhibit or slow the progression to tumours and cancer. e.g. colon cancer. The 036 protein is used in claimed methods for treating a patient suffering from a disorder associated with insufficient expression of gene 036 protein, and for identifying compounds that modulate 036 protein activity. Such compounds are useful in the diagnosis, prevention and treatment of tumours and
 Gaps
 Gene 036 product differentially expressed in colon tumour cells.
 .
6
 Colon tumour; colon cancer; differential expression; gene 036; human; diagnosis; gene therapy; tumour suppressor.
 Length 739; .
 Gene 036 with reduced or amplified expression in tumour cells used, optionally with genes 097, 030 and 056 or their protein products, for diagnosis and treatment of colonic cancer
 Indels
 11;
 DB 18;
 36 PAPLP-----PEDAPNAASLAPTPVSPVLEPFNLTSEPS 69
Best Local Similarity 45.0%; pred. No. 9.5; Matches 18; Conservative 2; Mismatches
 Score 69.5; 1
Pred. No. 19;
 W25790 standard; Protein; 739 AA
 Claim 38; Fig 2; 117pp; English.
 Query Match
Best Local Similarity 37.8%;
Matches 17; Conservative 8
 97WO-US04191
 96US-0013438
 11-MAR-1998 (first entry)
 (MILL-) MILLENNIUM PHARM.
 WPI; 1997-470615/43.
N-PSDB; T91708.
 739 AA;
 14-MAR-1997;
 15-MAR-1996;
 Homo sapiens
 W09733551-A2
 18-SEP-1997,
 Shyjan AW;
 Sequence
 W25790;
 œ
 RESULT
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Hollingshead J;

r A, Crain MJ, Tart R, Yother

Brooks-Walter A,

Swiatlo E,

96WO-US14819. 95US-0529055

/note= "unidentified amino acid" /note- "unidentified amino acid"

Location/Qualifiers

(first entry)

```
of the alpha-hellx region and some of the proline rich region, of pneumococcal surface protein A (PspA) of Streptococcus pneumoniae strain comparison of the N-terminal and central regions (W14533-57 and W14562-91) of PspA polypeptides from different pneumococcal strains can be used to divide the strains into several families based on sequence homologies. PspA polypeptides, or fragments of them, can be used in vaccines to protect animals against S. pneumoniae infection and hence for the prevention of diseases such as otitis media, meningitis, bacteraemia and pneumonia. The sequence of the 3' half of the PspA alpha-helical region and the immediate 5' tip of the coding sequence are likely to be the critical sequences for predicting PspA cross-reactions and vaccine
 Gaps
 This sequence shows the central portion, including the C-terminus
 61
 13;
 6 PVEEPNPAKRLLFLLLTIVFCQILMAEEGVPAPLPPEDAPNAASLAPTPVSPVLEP
 Length 204;
 Indels
 22;
 DB 18;
 Ouery Match
Best Local Similarity 32.1%; Pred. No. 5.4;
Matches 18; Conservative 3; Mismatches
Example 6; Fig 13; 296pp; English.
 Y99428 standard; Protein; 370 AA.
 204 AA;
 composition.
 Y99428;
 RESULT 10
Y99428
 XXXX
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Gaps

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Indels

8; Mismatches 19;

25 FCQILMAEEGVPAPLPPEDAPNAASLAP-TPVSPVLEPFNLTSEP 68

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RESULT W14578

NX K

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W18201 standard; protein; 610 AA.
 W18201;
 Region
 Region
 Reg ton
 Region
W18201
 3
 Gaps
 DNA encoding platelet glyco:protein 1b alpha mutant Phe57 - introduced into platelets to reduce aggregation and reactivity with you Willebrand factor, also probe for diagnosis of Bernard-Soulier
 Platelet glycoprotein-Ib-alpha; GPIba; mutagenesis; point mutation; von Willebrand factor; blood disorder; platelet disorder; protein engineering; Bernard-Soulier disease.
 A substitution of T for C at position 259 in the DNA sequnce of GPIb-alpha leads to the replacement of Phe for Leu at residue 57 of the mature GPIb-alpha molecule. This mutated GPIb-alpha molecule. This mutated GPIb-alpha protein is less reactive with von Willebrand factor, a characteristic of the autosomal recessive bleeding disorder, Bernard-Soulier disease.
 6
 Length 610;
 Mutated platelet glycoprotein-Ib-alpha GPIba protein sequence
 /note- "substitution from Phe in wild-typ GPIb-alpha"
 .220
e= "flanking region to Leu rich area"
 Indels
 DB 17;
 11;
 36 PAPLP----PEDAPNAASLAPTPVSPVLEPFNLTSEPS 69
 Lyle VA, Miller JL;
 Match 16.2%; Score 71.5; DB Local Similarity 45.0%; Pred. No. 9.5; es 18; Conservative 2; Mismatches
 "Ser/Thr rich area"
 Disclosure, Column 21-26; 20pp; English.
 36..200
 NEW YORK STATE RES FOUND.
 /note= "hinge region"
310..420
 Location/Qualifiers
 R89436 standard; Protein; 610 AA
 92US-0821717.
91US-0770968.
93US-0119262.
 91US-0770968
 (first entry)
 Finch CN,
 ..310
 /note=
 /note=
 WPI; 1996-128585/13.
 610 AA;
 Misc-difference
 Cunningham D,
 (UYNY) UNIV
 07-0CT-1991;
 Homo sapiens
 15-JAN-1992;
07-0CT-1991;
 09-SEP-1993;
 02-SEP-1996
 JS5492809-A
 20-FEB-1996
 Sequence
 Ouery Match
 R89436;
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Matches
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 R89436
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The present sequence represents the naturally-occuring wild-type platelet glycoprotein Ib alpha (GPIb alpha). The polypeptide can have a mutation which makes it more reactive with von Willebrand factor (WWF) chan the wild-type. Preferably the mutation is a substitution of within residues 228 to 238. The preferred mutation is a substitution of within residues 228 to 238. The preferred mutation a substitution of the wild-type Gly at position 233. The mutation a beta-bend conformation to an alpha helix conformation, and also creates an amphipathic region within the polypeptide. The DNA encoding mutant platelet GPIb alpha polypeptides (Where the mutation is between the patelet GPID alpha polypeptides (Where the mutation is between the useful for production of recombinant mutant GPIb alpha polypeptides, which can be used to inhibit platelet adhesion and aggregation (e.g. in anithrombotic medicaments or on medical devices or vascular prostheses), or can be labelled and used as imaging agents, or can be prosthese or thrombolytic agent for targeting to sites of thrombus or millaring an probes for diagnosis of platelet contact or anithrombolytic agent for targeting to sites of diagnosis of the platelet contact or an elementary and a probes for diagnosis of
 ______Preferred mutation; substitution of Val for Gly' 310..420 /label= Serine/threonine_rich
 /note= "A major binding site for von Willebrand factor" 228..238
 /note= "preferred sites for mutations that result
in a mutant polypeptide having more reactivity
with von Willebrand factor"
 DNA encoding mutant platelet glyco:protein Ib alpha - for production of recombinant polypeptide(s) useful as antithrombotic agents, etc.
 Platelet glycoprotein Ib alpha naturally-occurring wild-type.
 GPIb alpha; recombinant polypeptide; antithrombotic; platelet adhesion; platelet aggregation; thrombus formation; platelet-type von Willebrand disease.
 Finch CN, Lyle VA, Miller JL, Pincus MR;
 Disclosure; Column 27-32; 20pp; English.
 (UYNY) UNIV NEW YORK STATE RES FOUND.
 platelet-type von Willebrand disease.
 36..200
/label-_Leucine_rich
 Location/Qualifiers
 /label= Hinge
 91US-0770968
94US-0234265
 91US-0770968
 (first entry)
 310
 WPI; 1997-258215/23.
 Misc-difference 233
 610 AA;
 Cunningham D,
 07-OCT-1991;
 07-OCT-1991;
 28-APR-1994;
 Homo sapiens
 US5624817-A.
18-AUG-1997
 29-APR-1997
 Sequence
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us-08-799-910-10\_copy\_71\_156.rag

610 AA;

Seguence

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9
 three-dimensional coordinates obtained from the crystals, is useful for identifying an agent that stabilizes the Ras-Sos complex. The crystals are also useful for identifying agents that inhibit the formation of Ras-Sos complex. Ras and Sos fragments are useful for growing a crystal of a protein-ligand complex. Agents that stabilize or inhibit the formation of Ras-Sos complex are useful in the treatment of cancer. The present sequence represents a Drosophila
 Gaps
 A substitution in platelet glycoprotein Ib alpha (Leucine 57 to Phenylalanine) underlies a form of Bernard-Soulier disease. The mutated glycoprotein can be used in compositions to inhibit platelet aggregation/adhesion. The glycoprotein may be labelled and agent, preferably tissue plasminogen activator (IPA), (PrO) urokinase, streptokinase, anisoylated plasminogen streptokinase activator complex, tPA analogues or a protease, allowing localisation of the thrombolytic agent to a thromboly.
 53
 Platelet; glycoprotein; imaging; thrombolytic agent;
tissue plasminogen activator; tPA; pro-urokinase; urokinase;
streptokinase; Bernard-Soulier disease; thrombus; aggregation;
anisoylated plasminogen-streptokinase activator complex; adhesion;
 VRRQL,PVE-----EPNPAKRLLFLLLTIVFCQILMAEEGVPAPL,PPFDAPNAASLAPT
 25;
 factor,
 Length 1596;
 Platelet glycoprotein Ib alpha with an amino acid substn at position 57 - has reduced reactivity with Von Willebrand factor and can be used to inhibit platelet aggregation and inhibition
 Indels
 1478 tspltpamspmspnipshpvestsssyahglrmrqqqqqthpaiy 1523
 54 -- PVSPVLEPF--NLTSEP----SDYALDLSTFLQQ----HPAAF 86
 37;
 DB 21;
 Miller JL;
 Ouery Match
Best Local Similarity 28.3%; Pred. No. 4.2;
Matches 30; Conservative 14; Mismatches
 (UYNY) UNIV NEW YORK STATE RES FOUND.
 Claim 1; Columns 3-8; 20pp; English.
 VA,
 R51116 standard; protein; 610 AA
 Platelet glycoprotein Ib alpha,
 Lyle
 92US-0821717
 91US-0770968
 91US-0770968
 (first entry)
 Cunningham D, Finch CN,
 1596 AA;
 WPI; 1994-100287/12.
 Sos protien.
 23-SEP-1994
 Homo sapiens
 7-0CT-1991;
 07-OCT-1991;
 29-MAR-1994.
 15-JAN-1992;
 US5298239-A
 Sequence
 R51116;
 RESULT
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Gaps
 A substitution in platelet glycoprotein ib alpha (Leucine 57 to Phenylalanine) underlies a form of Bernard-Soulier disease. The mutated glycoprotein can be used in compositions to inhibit platelet aggregation/adhesion. The glycoprotein may be labelled and used as an imaging agent and may also be bound to a thrombolytic agent, preferably tissue plasminogen activator (LPA), (PrO) urokinase, streptokinase, anisoylated plasminogen-streptokinase activator complex, tPA analogues or a protease, allowing localisation of the thrombolytic agent to a thrombus.
 Gaps
 Platelet; glycoprotein; imaging; thrombolytic agent;
tissue plasminogen activator; tPA; pro-urokinase; urokinase;
streptokinase; Bernard-Soulier disease; thrombus; aggregation;
anisoylated plasminogen-streptokinase activator complex; adhesion;
 Platelet glycoprotein Ib alpha with an amino acid substn at position 57 - has reduced reactivity with Von Willebrand factor, and can be used to inhibit platelet aggregation and inhibition
 6
 6
 Length 610;
 Length 610;
 Indels
 Indels
 11;
 36 PAPLP-----PEDAPNAASLAPTPVSPVLEPFNLTSEPS 69
 366 ptpspttsepvpepapnmttleptpspttpep---tsepa 402
 DB 15;
 36 PAPLP----PEDAPNAASLAPTPVSPVLEPFNLTSEPS 69
 Lyle VA, Miller JL;
 Pred. No. 9.5;
2; Mismatches
 16.2%; Score 71.5; DF
45.0%; Pred. No. 9.5;
iive 2; Mismatches
 Score 71.5;
 Mutant platelet glycoprotein Ib alpha.
 (UYNY) UNIV NEW YORK STATE RES FOUND
 Ş
 R56664 standard; protein; 610
 16.2%;
nilarity 45.0%;
Conservative
 91US-0770968.
 91US-0770968
92US-0821717
 23-SEP-1994 (first entry)
 Finch CN,
 Claim 1; ; 20pp; English.
 Conservative
Ouery Match
Best Local Similarity
 WPI; 1994-100287/12.
 Query Match
Best Local Similarity
Matches 18; Conserv
 610 AA;
 Cunningham D,
 07-OCT-1991;
 07-OCT-1991;
15-JAN-1992;
 US5298239-A.
 inhibition.
 29-MAR-1994
 Sequence
 R56664;
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Gaps

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Indels

Length 156;

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expressed in different cardiovascular disease states. Compositions which ear modify TGF-beta signalling pathway are identified by screening. These are used therapeutically to treat fibroproliferative and oncogenic disorders, especially TGF (Transforming growth factor)-beta related disorders, including diabetic retinopathy, artherosclerosis, pancreatic cancer, angiogenesis, inflammation, fibrosis, tumour growth and vascularisation. The present sequence is the protein product of fchd605 gene which is up-regulated in monocytes treated with oxidised LDL (low density lipoprotein) can be used to design cardiovascular disease treatment strategies. Depending on whether the up-regulation has a pathogenic or protective effect treatment methods can be designed to increase or decrease the activity of the protein product of the gene.
 Sos contacting region of a Ras protein and at least a Son of sevenless (Sos) protein catalytic region fragment, that effectively diffracts x-rays. Ras and Sos form a tight complex. Sos does not impede the binding sites for the nucleotide base and the ribose of GTP or GDP and thus the Ras-Sos complex maintains a structure that permits nucleotide release and rebinding. The crystals are used for the determination of the atomic coordinates of the complex to a resolution of more than 5.0 Angstrom. The crystals, or a dataset comprising the
 Novel crystals comprising a Ras-Son of sevenless complex, useful for screening drugs useful in cancer treatment
 Amino acid sequence of a Drosophila Son of sevenless (Sos) protein.
 The specification describes a crystal complex comprising at least a
 Ras; Son of sevenless; Sos; crystal; Ras-Sos complex; cancer;
 100.0%; Score 442; DB 21;
100.0%; Pred. No. 1.5e-39;
ive 0; Mismatches 0;
 Bar-Sagi
 Disclosure; Page 169-175; 224pp; English.
 Y68821 standard; protein; 1596 AA
 Boriack-Sjodin A, Margarit SM,
 61 PFNLTSEPSDYALDLSTFLQQHPAAF
 98US-0119794.
 99WO-US16348
 16-MAY-2000 (first entry)
 Query Match 100.
Best Local Similarity 100.
Matches 86; Conservative
 (UYRQ) UNIV ROCKEFELLER
 protein coordinate data.
 Drosophila melanogaster
 WPI; 2000-182647/16.
 156 AA;
 WO200005258-A1.
 20-JUL-1999;
 21-JUL-1998;
 03-FEB-2000
 Seguence
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 fchd605 gene; human; cardiovascular disease; oncogenic disorder; diabetic retinopathy: libroproliferative disorder; artherosclerosis; TGF-beta signalling pathway; TGF; Transforming growth factor; pancreatic cancer; anglogenesis; inflammation; fibrosis; tumour growth;
 symptoms of fibroproliferative
 This protein is encoded by the novel human fchd605 gene (see 794471) that is up-regulated in monocytes treated with oxidised low density lipoproteins that simulate the conditions under which foam cells develop during atherogenesis. The protein has sequence similarity to the mouse gly96 gene and to EST T49532. Novel fchd511, fchd540, fchd602 and fchd605 genes (see T94467-71) provide a fingerprint for the study of cardiovascular diseases, including atheroscierosis, ischaemia/reporfusion, hypertension, restenosis and arterial inflammation. Methods are provided for the diagnosis, monitoring in clinical trials, screening for therapeutically effective compounds, and treatment of cardiovascular diseases based on discoveries regarding the expression patterns of these novel genes.
 Gaps
 1 VRRQLPVEEPNPAKRLLFLLLTTVFCQILMAEEGVPAPLPPEDAPNAASLAPTPVSPVLE 60
 The patent discloses methods for the treatment and diagnosis of
 0
 Length 156;
 disease, e.g. atherosclerosis, restenosis, hypertension, etc
 vascularisation; cytostatic; antidiabetic; opthalmological.
 Indels
 100.0%; Score 442; DB 18; 100.0%; Pred. No. 1.5e-39;
 .
,
 0; Mismatches
 Jdentifying substances for ameliorating diseases or oncogenic related disorders
 61 PFNLTSEPSDYALDLSTFLQQHPAAF 86
 Example 6; Fig 5; 163pp; English.
 Protein encoded by fchd605 gene.
 Example; Fig 5; 214pp; English.
 Y45017 standard; Protein; 156
 (MILL-) MILLENNIUM PHARM INC
 99WO-US17394.
 31-MAY-2000 (first entry)
 86; Conservative
 WPI; 2000-205414/18.
 Similarity
 156 AA;
 N-PSDB; 250711.
 WO200006206-A1.
 Homo sapiens
 30-JUL-1999;
 30-JUL-1998;
 10-FEB-2000.
 Sequence
 Query Match
Best Local 9
 Falb DA;
 Y45017;
 Matches
 Y45017
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Kuriyan J;

Cole P,

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Mammalian Ena (Men Mouse neural Mena+ Mouse neural Mena+

Homo sap

Wild-type E-cadher

Secreted protein A Human secreted pro

Mouse neural Mena

Streptococcus pneu

Mycobacterium Mycobacterium

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Fchd605 gene; differential expression; monocyte; humap; foam cell; cardiovascular disease; atherosclerosis; Ischaemia; reperfusion; hypertension; restenosis; arterial inflammation; therapy; diagnosis; drug screening; marker.
 ALIGNMENTS
 Y39033
R66460
W36984
Y68748
R60799
W14584
 W03566
W03565
 W64322
Y39083
 Y38945
Y17067
 W64379
Y32063
 W27646
 W44082
 W32350
 Y39225
Y39082
 Y39081
 W81683
 W36006 standard; Protein; 156 AA.
 (MILL-) MİLLENNIUM PHARM INC
96US-0011787.
 97WO-US02291.
 97US-0799910.
 Human Fchd605 gene product.
 03-MAR-1998 (first entry)
 5522

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 802
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Homo sapiens
 WO9730065-A1
 14-FEB-1997;
 13-FEB-1997;
 16-FEB-1996;
 21-AUG-1997
 64 .
 Falb DA;
 W36006;
RESULT
 W36006
 Human Fchd605 gene
Protein encoded by
 Amino acid sequenc
Platelet glycoprot
Mutant platelet gl
 Mutated platelet g
Platelet glycoprot
Gene 036 product d
 Search time 54.97 Seconds (without alignments) 53.496 Million cell updates/sec
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 86
 Description
 442
1 VRRQLPVEEPNPAKRLLFLL......EPSDYALDLSTFLQQHPAAF
 / cgn2_2/gcgdata/geneseq/geneseqp/AA1983.DAT:
/ cgn2_2/gcgdata/geneseq/geneseqp/AA1983.DAT:
/ cgn2_2/gcgdata/geneseq/geneseqp/AA1985.DAT:
/ cgn2_2/gcgdata/geneseq/geneseqp/AA1985.DAT:
/ cgn2_2/gcgdata/geneseq/geneseqp/AA1987.DAT:
/ cgn2_2/gcgdata/geneseq/geneseqp/AA1989.DAT:
/ cgn2_2/gcgdata/geneseq/geneseqp/AA1989.DAT:
/ cgn2_2/gcgdata/geneseq/geneseqp/AA1989.DAT:
/ cgn2_2/gcgdata/geneseq/geneseqp/AA1989.DAT:
/ cgn2_2/gcgdata/geneseq/geneseqp/AA1999.DAT:
/ cgn2_2/gcgdata/geneseq/geneseqp/AA1999.DAT:
 Jeydata/geneseg/genesegp/AA1989.DAT:*/dccddta/geneseg/genesegp/AA1990.DAT:*
 . DAT: *
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/cgn2_2/gcgdata/geneseq/geneseqp/AA1999
 /gcgdata/geneseq/geneseqp/AA1999
 A_Geneseq_36:*
: /cgn2_2/gcgdata/geneseq/geneseqp/AA1980.
: /cgn2_2/gcgdata/geneseq/geneseqp/AA1981.
 /cgn2_2/gcgdata/geneseq/geneseqp/AA1982.
 GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
 hits satisfying chosen parameters:
 268485 seqs, 34193795 residues
 US-08-799-910-10_COPY_71_156
 SUMMARIES
 January 30, 2001, 22:05:37
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 OM protein - protein search, using sw model
 X45017
X68821
R51116
R56664
R89436
W18201
 Gapop 10.0 , Gapext 0.5
 W36006
 Minimum DB seq length: 0
Maximum DB seq length: 200000000
 Query
Match Length DB
 156
156
1596
610
610
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18 .0
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16 .2
16 .2
16 .2
15 .7
15 .5
15 .5
15 .5
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114 115 116 119 119 119 119

Score

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Total number

Database

Searched:

Title: Perfect score:

Run on:

Sequence:

Scoring table:

Streptococcus pneu Amino acid sequenc

genes differentially expressed in cardiovascular disease - used diagnosis, drug screening and treatment of cardiovascular

WPI; 1997-424966/39. N-PSDB; T94471.

New

Streptococcus pneu Human PRO1431 (UNO Sequence of human Human E-cadherin p

Y99428 R55060 R85487

79.77 71.5 71.5 71.5 69.5 68.5 68.5 68.5

5 6 7 10 11 12

Mycobacterium tube

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MICROBACTERIAL PROTEINS, MICROORGANISMS PRODUCING THEM AND THEIR USE FOR VACCINES AND FOR THE DETECTION OF TUBERCULOSIS
 Gaps
 DB 1; Length 286;
 11; Indels
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: THEN PC compatible
OCHENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/641,356
FILING DATE:
 LIKET: 1755 S. Jefferson Davis Highway, Suite 400 CITY: Arlington STATE: Virginia COUNTRY: U.S.A. MPINTER: U.S
 Sequence 3, Application US/08641356
; Patent No. 5866130
; GENERAL INFORMATION:
 APPLICANT:
 TITLE OF INVENTION: MICROBACTERIAL PROTEINS,
 TITLE OF INVENTION: MICROBACTERIAL PROTEINS,
 TITLE OF INVENTION: MICROBACIEN PRODUCING THEM FITTLE OF INVENTION: MICRORGANISMS PRODUCING THEM FITTLE OF INVENTION: AND FOR THE DETECTION OF TUBERG; NUMBER OF SEQUENCES: 3
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & ADDRESSEE: OBLON, SPIVAK,
 STREET: 1755 S. Jefferson Davis Highway, Suite 40
 Score 65.5; DB; Pred. No. 5; 3; Mismatches
 29 LMAEEGVPAPLPPEDAP---NAASLAPTPVSP 57
 CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ILING DATE: 01-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REFERNCE/DOCKET NUMBER: 22640720
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
 22640720
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 22640
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3200
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
 Ouery Match
Best Local Similarity 46.9%;
Matches 15; Conservative
 TELEFAX: 703-413-2220 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acid
STRANDEDNESS:
 TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
 TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
US-08-641-356-3
 STRANDEDNESS
 US-08-382-184-3
 US-08-641-356-3
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Search completed: January 30, 2001, 22:06:26 Job time: 9705 sec

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 21 LTIVFCQILMA-----EEGVPAPLPPEDAPNAASLAPTPVSPVLEPFNLTSEP-SDYAL 73
 1 VRRQLPVEEPNPAKRLLFLLLTIVFC-----QILMAEEGVPAPLPPEDAPNAASLA--- 51
 Sequence 2, Application US/08854585
Patent No. 6114140
GENERAL INFORMATION:
APPLICANT: Tonks, Nicholas K. and stman, Arne
TITLE OF INVENTION: Density Enhanced Protein Tyrosine Phosphatase
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
33;
 DB 3; Length 1337;
 E: Marshall, O'Toole, Gerstein, Murray & Borun
233 South Wacker Drive, Suite 6300
 31; Indels
 APPLICANT: Tonks, Nicholas K. and stman, Arne
TITLE OF INVENTION: Density Enhanced Protein Tyrosine
TITLE OF INVENTION: Phosphatase
 631 VPNWTIQYNDPTQESIILKP-KMALEVGDYKINLKLMDNON 670
 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
 ------PTPVSPVLEPFNLTSEPSDYALDLSTFLQQH 82
 Mismatches
 15.5%; Score 68.5; D
29.2%; Pred. No. 15;
tive 11; Mismatches
 27866/31954
 PRIOR APPLICATION DATA: APPLICATION NUMBER: US/08/237,940
 STATE: Illinois
COUNTRY: United States of America
 APPLICATION NUMBER: US/08/854,585
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
 Sequence 2, Application PC/TUS9505512
GENERAL INFORMATION:
 ATTORNEY AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 278
TELECOMMUNICATION INFORMATION:
 312-474-6300
 21; Conservative
 Conservative
 protein
 COMPUTER READABLE FORM:
 |:| | ||:|
853 ILTTGEAGHPSA 864
 74 DLSTFLQQHPAA 85
 Best Local Similarity
Matches 21; Conserve
 amino acid
 Chicago
 MOLECULE TYPE:
 FILING DATE:
 90909
 ADDRESSEE:
 PCT-US95-05512-2
 TOPOLOGY
 STREET:
 Query Match
 ò
 q
 ò
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MICROBACTERIAL PROTEINS,
MICROORGANISMS PRODUCING THEM AND THEIR USE FOR VACCINE
AND FOR THE DETECTION OF TUBERCULOSIS
 21 LIIVFCQILMA-----EEGVPAPLPPEDAPNAASLAPTPVSPVLEPFNLTSEP-SDYAL 73
 7;
 E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30 (EPO)
 CORRESPONDENCE S. 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPITAR, MCCLELLAND, MAIER &
ADDRESSEE: NEUSTADT, P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05512
FILING DATE:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray ADDRESSEE: Borun
 233 South Wacker Drive, Suite 6300
 11; Mismatches
 Score 68.5; 1
Pred. No. 15;
 FILING DATE: 01-FEB-1995
CLASSIFICATION: 435
 STATE: Illinois
COUNTRY: United States of America
2IP: 60606
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 Sequence 3, Application US/08382184 Patent No. 5714593 GENERAL INFORMATION: APPLICANT:
 NAME: Borun, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 276
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
 15.5%;
29.2%;
 ATTORNEY/AGENT INFORMATION:
 Conservative
 CURRENT APPLICATION DATA:
 TELEFAX: 312-474-0448
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
 ; MOLECULE TYPE: protein PCT-US95-05512-2
 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
 COMPUTER READABLE FORM:
 853 ILTIGEAGHPSA 864
 COMPUTER: IBM PC OPERATING SYSTEM:
 74 DLSTFLQQHPAA 85
 Query Match
Best Local Similarity
Matches 21; Conserva
 TITLE OF INVENTION:
TITLE OF INVENTION:
 amino acid
 STATE: Virginia COUNTRY: U.S.A.
 CITY: Arlington
 Chicago
 TOPOLOGY:
 US-08-382-184-3
 LENGTH:
 g
 ò
```

```
TITLE OF INVENTION: Methods and Compositions for Modulating Heterotypic TITLE OF INVENTION: E-cadherin Interactions with T Lymphocytes NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSEE: Wolf, Greenfield & Sacks P.C.
 1 VRRQLPVEEPNPAKRLLFLLTIVFC-----GILMAEEGVPAPLPPEDAPNAASLA--- 51
 33;
 Length 878;
 Indels
 631 VPNWTIQYNDPTQESIILKP-KMALEVGDYKINLKLMDNQN 670
 52 -----PIPVSPVLEPFNLTSEPSDYALDLSTFLQQH 82
 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05518
FILING DATE: herewith
 DB 1;
 DB 4;
 15.5%; Score ou...
25.7%; Pred. No. 9;
+ive 11; Mismatches
 NAME: Plumer, Elizabeth R
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0801/7023
 PCT-US95-05518-2; Sequence 2, Application PC/TUS9505518; GENERAL INFORMATION:
 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/237,919
FILING DATE: 3 May 1994
ATTORNEY/AGENT INFORMATION:
 REFERENCE/DOCKET NUMBER: B08
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-3441
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 878 amino acids
TYPE: amino acid
 36,637
 TELECOMMUNICATION INFORMATION TELEPHONE: 617-720-3500
 15.5%;
25.7%;
 NAME: Plumer, Elizabeth REGISTRATION NUMBER: 36,
 Floppy disk
 Query Match
Best Local Similarity 25.78
Matches 26; Conservative
 : 878 amino acids
amino acid
 TELEFAX: 617-720-2441 INFORMATION FOR SEQ ID NO:
 SEQUENCE CHARACTERISTICS
 ; MOLECULE TYPE: protein US-08-237-919-2
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
 linear
 Query Match
Best Local Similarity
 STREET: 600 A
 ; MOLECULE TYPE:
PCT-US95-05518-2
 02210
 Ψ
 TOPOLOGY:
 STATE: M.
 APPLICANT:
 ò
 δ
 APPLICANT: Brenner, Michael B
APPLICANT: Brenner, Michael B
APPLICANT: Cepek, Karyn L
TITLE OF INVENTION: Methods and Compositions for
TITLE OF INVENTION: Modulating Heterotypic E-cadherin Interactions with T lymphocy
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks P.C.
STREET: 600 Atlantic Avenue
 DB 3; Length 739;
 25 FCQILMAEEGVPAPLPPEDAPNAASLAP-TPVSPVLEPFNLTSEP 68
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/237,919
 OPERATING SYSTEM: Windows95
STEMBRES EASLSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/035,648
 15.7%; Score 69.5; Dilarity 37.8%; Pred. No. 5.6; Conservative 8; Mismatches
 07334/003001
 CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
 NAME: Meiklejohn, Ph.D., Anita L. REGISTRATION NUMBER: 35,283

REFERENCE/POCKET NUMBER: 07334/00:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/818,829
FILING DATE:
ATTORNEY/AGENT INFORMATION:
 Sequence 2, Application US/08237919
Patent No. 5610281
GENERAL INFORMATION:
 TELEX: 200154
INFORMATION FOR SEQ 1D NO: 24:
SEQUENCE CHARACTERISTICS:
 IBM Compatible
 : 739 amino acids
amino acid
 Diskette
 617-542-8906
 MOLECULE TYPE: protein
FRAGMENT TYPE: internal
 COMPUTER READABLE FORM:
 FILING DATE:
CLASSIFICATION: 424
NUMBER OF SEQUENCES:
 OPERATING SYSTEM:
 linear
 Query Match
Best Local Similarity
Matches 17; Conserv
 COUNTRY: US
ZIP: 02110-2804
 ADDAL
STREET: ZZZ
'mv: Boston
 CITY: Boston
STATE: MA
 USA
 MEDIUM TYPE:
 FILING DATE:
 TOPOLOGY:
 TELEFAX:
 US-09-035-648-24
 LENGTH:
 COUNTRY:
 US-08-237-919-2
 qq
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COMPOSITIONS AND METHODS FOR THE DIAGNOSIS, PREVENTION, AND TREATMENT OF NEOPLASTIC CELL GROWTH AND PROLIFERATION
 Gaps
 Gaps
 ..
 6
 Length 610;
Score 71.5; DB 1; Length 610; Pred. No. 2.7;
 APPLICANT: Cunningham, David
APPLICANT: Lyle, Vicki A.
APPLICANT: Finch, Clara N.
APPLICANT: Pincus, Matthew R.
TITLE OF INVENTION: Mutations in the Gene Encoding the
TITLE OF INVENTION: Chain of Platelet Glycoprotein Ib
 Indels
 OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
 36 PAPLP-----PEDAPNAASLAPTPVSPVLEPFNLTSEPS 69
 366 PIPSPITSEPVPEPAPNMTTLEPIPSPITPEP---TSEPA 402
 DB 1;
 ,11;
 36 PAPLP-----PEDAPNAASLAPTPVSPVLEPFNLTSEPS 69
 Pred. No. 2.,,
2; Mismatches
 2; Mismatches
 16.2%; Score 71.5;
ilarity 45.0%; Pred. No. 2.7
Conservative 2; Mismatches
 NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ALDRESSEE: Nixon, Hargrave, Devans 6 |
STREET: Clinton Square, P.O. Box 1051
 28-APR-1994
 Sequence 24, Application US/09035648
Patent No. 6100031
GENERAL INFORMATION:
APPLICANT: Shyjan, Andrew W.
TITLE OF INVENTION: COMPOSITIONS APPLICE OF INVENTION: DIAGNOSIS, PREY TITLE OF INVENTION: GROWTH AND PROI
 20884/24
 Sequence 11, Application US/08234265A Patent No. 5624817 GENERAL INFORMATION:
 APPLICANT: Miller, Jonathan L.
 NAME: Timian, Susan J. REGISTRATION NUMBER: 34,103
 COMPUTER: IBM PC compatible
 REFERENCE/DOCKET NUMBER: 20
FELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1636
 (716) 263-1636
(716) 263-1600
 16.2%;
 ATTORNEY/AGENT INFORMATION:
 610 amino acids
 TELEFAX: (716) 263-160
TELEX: 978450
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
 Conservative
 protein
 ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
 APPLICATION NUMBER:
 amino acid
 CITY: Rochester STATE: New Y
 Best Local Similarity
Matches 18; Conserv
 Ouery Match
Best Local Similarity
Matches 18; Conserva
 linear
 FILING DATE: 28 CLASSIFICATION:
 , MOLECULE TYPE:
US-08-234-265A-11
 USA
 US-09-035-648-24
 ropology:
 RESULT 8
US-08-234-265A-11
 COUNTRY:
 Query Match
 ò
 g
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 δ
 factor to the
 7
 Gaps
 6
 Alpha
 Length 610;
 von Willebrand
 APPLICANT: Cuningham, David
APPLICANT: Lyle, Vicki A.
APPLICANT: Lyle, Vicki A.
APPLICANT: Finch, Matthew R.
TITLE OF INVENTION: Mutations in the Gene Encoding the TITLE OF INVENTION: Chain of Platelet Glycoprotein Ib NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
 Mismatches 11; Indels
 6: FROM 0 TO 610
 6: FROM 0 TO 293
 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
 366 PIPSPITSEPVPEPAPNMITLEPTPSPITPEP---TSEPA 402
 36 PAPL,P-----PEDAPNAASLAPTPVSPVLEPFNLTSEPS 69
 DB 1;
 ADDRESSEE: Nixon, Hargrave, Devans & Doyle STREET: Clinton Square, P.O. Box 1051
 PUBLICATION INFORMATION:
AUTHORS: Zimmerman, Theodore S.
AUTHORS: Ruggeri, Zaverio M.
AUTHORS: Houghten, Richard A.
AUTHORS: Wincete, Vincete
AUTHORS: Mohri, Hiroshi
TITLE: Proteolytic fragments and synthetic
 Score 71.5; D
Pred. No. 2.7;
 APPLICATION NUMBER: US/08/135,929A FILING DATE: 14-OCT-1993 CLASSIFICATION: 514
 20884/23
 TITLE: that block the binding of
TITLE: membrane glycoprotein Ib
DOCUMENT NUMBER: EP 0 317 278 A2
FILLIG DATE: 16-NOV-1989
PUBLICATION DATE: 24 MAY-1989
RELEVANT RESIDUES IN SEQ ID NO: 6:
US-08-119-262B-6
 MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOSTWARE: Patentin Policy
 Sequence 11, Application US/08135929A Patent No. S593959 GENERAL INFORMATION:
 RESIDUES IN SEQ ID NO:
 NAME: Timian, Susan J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 2088.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1636
TELEFAX: (716) 263-1600
 16.2%; Sco
ilarity 45.0%; Pro
Conservative 2;
 11:
 APPLICANT: Miller, Jonathan APPLICANT: Cunningham, David APPLICANT: Lyle, Vicki A.
 ATTORNEY/AGENT INFORMATION:
 LENGTH: 610 amino acids TYPE: amino acid
 TELEX: 978450
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
 , MOLECULE TYPE: protein US-08-135-929A-11
 ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
 linear
 Best Local Similarity
Matches 18; Conserv
 CITY: Rochester
STATE: New York
 US-08-135-929A-11
 COUNTRY:
 RELEVANT
 TITLE:
TITLE:
 Query Match
 ò
 qq
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5615-5619
 GENERAL INFORMATION:
 USA
 TYPE: amino
STRANDEDNESS
 ; RELEVANT F
US-07-821-717B-6
 US-08-119-262B-6
 AUTHORS:
AUTHORS:
AUTHORS:
AUTHORS:
 TITLE: ΢
JOURNAL:
VOLUME: 8
 COUNTRY:
 PAGES:
 QQ
 ò
 Integrated the state of the sta
 platelet glycoprocein Ib: A transmembrane protein with homology to leucine-rich alpha-2-glycoprotein .. Proc. Natl. Acad. Sci. U.S.A.
 APPLICANT: Miller, Jonathan L.
APPLICANT: Cunningham, David
APPLICANT: Lyle, Vicki A.
APPLICANT: Lyle, Vicki A.
APPLICANT: Lyle, Vicki A.
TITLE OF INVENTION: MUTA*IONS RENDERING PLATELET
TITLE OF INVENTION: GLYCOPROTEIN ID ALPHA LESS REACTIVE
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle
STREET: Clinton Square P.
 1478 TSPLTPAMSPMSPNIPSHPVESTSSYAHQLRMRQQQQQTHPAIY 1523
54 -- PVSPVLEPF--NLTSEP----SDYALDLSTFLQQ----HPAAF 86
 6: FROM 0 TO 610
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/821,7176
FILLIG DATE: 15-JAN-1992
CLASSIFICATION: 424
 RS: Lopez, Jose A.
RS: Chung, Dominic W.
RS: Fujikawa, Kazuo
RS: Hagen, Frederick S.
RS: Papayannopoulou, Thalia
RS: Roth, Gerald J.
RS: Roth, Gerald J.
RS: Cloning of the alpha chain of human
 ATTORNEY/AGENT INFORMATION:
NAME: Timain, Susan J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 20884/21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1636
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 610 amino acids
TYPE: amino acid
 RELEVANT RESIDUES IN SEQ ID NO:
 Sequence 6, Application US/07821717B Patent No. 5298239
 UBLICATION INFORMATION:
 TOPOLOGY: linear
MOLECULE TYPE: protein
PUBLICATION INFORMATION:
 GENERAL INFORMATION:
APPLICANT: Miller,
 5615-5619
AUG-1987
 CITY: Rochester
STATE: New York
 TITLE: platelet
DOCUMENT NUMBER:
 USA
 STRANDEDNESS:
 COUNTRY: U
 JOURNAL:
VOLUME: 8
PAGES: 56
 US-07-821-717B-6
 AUTHORS:
AUTHORS:
AUTHORS:
 AUTHORS:
AUTHORS:
AUTHORS:
AUTHORS:
 AUTHORS:
 AUTHORS:
 AUTHORS
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with ha
 Gaps
 6
 DB 1; Length 610;
 APPLICANT: Miller, Jonathan L.
APPLICANT: Cunningham, David
APPLICANT: Lyle, Vicki A.
APPLICANT: Linch, Clara N.
TITLE OF INVENTION: MUTATIONS RENDERING PLATELET
TITLE OF INVENTION: GLYCOPROTEIN ID ALPHA LESS REACTIVE
 Indels
 6: FROM 0 TO 293
 Roth, Gerald J.
Cloning of the alpha chain of human
glycoprotein Ib: A transmembrane protein
leucine-rich alpha-2-glycoprotein
Proc. Natl. Acad. Sci. U.S.A.
 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
FILING DATE: US/08/119,262B
FILING DATE: 09-SEP-1993
CLASSIFICATION: 424
 16.2%; Score 71.5; DB 1;
ilarity 45.0%; Pred. No. 2.7;
Conservative 2; Mismatches 11;
 36 PAPLP-----PEDAPNAASLAPTPVSPVLEPFNLTSEPS 69
 E: Nixon, Hargrave, Devans & Doyle
Clinton Square, P.O. Box 1051
 FILING DATE: 09-SEP-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/821,717
FILING DATE: 15-JAN-1992
ATTORNEY/ABORT INFORMATION:
 20884/22
 Fujikawa, Kazuo
Hagen, Frederick S.
Papayannopoulou, Thalia
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
FILING DATE: 16-NOV-1988
PUBLICATION DATE: 24-MAY-1989
RELEVANT RESIDUES IN SEQ ID NO:
 . Sequence 6, Application US/08119262B
; Patent No. 5492809
 NAME: Timain, Susan J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 2088/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1636
TELECAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
 LENGTH: 610 amino acids TYPE: amino acid
 ZIP: 14603
COMPUTER READABLE FORM:
 NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Ha
 Query Match
Best Local Similarity
Matches 18; Conserv
 STREET: Clinton
CITY: Rochester
STATE: New York
```

```
GENERAL INFORMATION:
APPLICANT: FALB, Dean A.
ITILE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASF;
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASF;
FILE REFERENCE: 7853-126
CURRENT APPLICATION NUMBER: 08/09/126,640A
CURRENT FILING DATE: 1999-07-30
EARLIER APPLICATION NUMBER: 08/799,910
EARLIER FILING DATE: 1997-02-13
EARLIER FILING DATE: 1997-02-14
EARLIER FILING DATE: 1996-02-16
NUMBER OF SEO ID NOS: 44
SOFTWARE: FASTSEO for Windows Version 4.0
 1 VRRQLPVEEPNPAKRLLFLLLTIVFCQILMAEEGVPAPLPPEDAPNAASLAPTPVSPVLE 60
 Sequence 11, Application US/09126640A
Patent No. 6099823
 Query Match
Best Local Similarity 100.(
Matches 86; Conservative
 ORGANISM: Homo sapiens
 US-09-126-640-11
 LENGTH: 156
 US-09-126-640-11
 US-09-356-952-3
 TYPE: PRT
 SEQ ID NO 3
 TYPE: PRT
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 11 VRRQLPVEEPNPAKRLLFLLLTIVFCQILMAEEGVPAPLPPEDAPNAASLAPTPVSPVLE 130
 1 VRRQLPVEEPNPAKRLLFLLLTIVFCQILMAEEGVPAPLPPEDAPNAASLAPTPVSPVLE 60
 1 VRROLPVEEPNPAKRLLFLLTTVFCQILMAEEGVPAPLPPEDAPNAASLAPTPVSPVLE 60
 .;
0
 0
 Length 156;
 Length 156;
 Indels
 Indels
 Sequence 10, Application US/0894495
Patent No. 6087477
GENERAL INFORMATION:
APPLICANT: Falb, Dean
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: CARDIOVASCULAR DISEASE
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
 0
 100.0%; Score 442; DB 3; ilarity 100.0%; Pred. No. 1.1e-42; Conservative 0; Mismatches 0;
100.0%; Score 442; DB 3;
100.0%; Pred. No. 1.1e-42;
ive 0; Mismatches 0;
 NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-067-999
TELECOMUNICATION INFORMATION:
TELEPHONE: (212)7909090
 E: PENNIE & EDMONDS LLP
1155 Avenue of the Americas
 OPERATING SYSTEM: DOS
SOSTWARE: FASLESO VERSION 2.0
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,495
 131 PFNLTSEPSOYALDLSTFLQQHPAAF 156
 61 PFNLTSEPSDYALDLSTFLQQHPAAF 86
 61 PFNLTSEPSDYALDLSTFLQQHPAAF 86
 PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/799,910
 TELEX: 66141 PENNIE
INFORMATION FOR SEQ 1D NO: 10:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPALIDE
 ATTORNEY/AGENT INFORMATION:
 156 amino acids
 Conservative
 unknown
 MOLECULE TYPE: protein FRAGMENT TYPE: internal
 (212)8699741
 SEQUENCE CHARACTERISTICS
 unknown
 Ouery Match
Best Local Similarity
Matches 86; Conserva
 TYPE: amino acid
STRANDEDNESS: unl
 Similarity
 CLASSIFICATION:
 New York
 USA
 FILING DATE:
 FILING DATE
 ADDRESSEE:
 US-08-944-495-10
 86;
 US-08-944-495-10
 TELEFAX:
 COUNTRY:
 LENGTH:
 STREET:
 STATE:
 Query Match
Best Local 5
 131
 Matches
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Gaps

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Length 156; Indels

100.0%; Score 442; DB 3; 100.0%; Pred. No. 1.1e-42; ive 0; Mismatches 0;

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1 VRRQLPVE-----EPNPAKRILFLLLTIVFCQILMAEEGVPAPLPPEDAPNAASLAPT 53
 GENERAL INFORMATION:

APPLICANT: Borlack-Sjodin, Ann
APPLICANT: Bargarit, S. M.
APPLICANT: Bor-Soqi, Dafna
APPLICANT: Cole, Philip
APPLICANT: Kuriyan, John
TITLE OF INVENTION: A CRYSTAL OF A RAS-SOS COMPLEX AND WETHODS OF USE
FILE REPRENEUS: 600-1-228N
CURRENT APPLICATION NUMBER: US/09/356,952
CURRENT FILING DATE: 1999-07-19
 25;
 Length 1596;
 18.0%; Score 79.5; DB 3; 28.3%; Pred. No. 1.1;
 Mismatches
 EARLIER APPLICATION NUMBER: 60/093,631
EARLIER FILING DATE: 1998-07-21
NUMBER OF SEQ ID NOS: 14
 131 PFNLTSEPSDYALDLSTFLQQHPAAF 156
61 PFNLTSEPSDYALDLSTFLQQHPAAF 86
 , ORGANISM: Drosophila melanogaster
US-09-356-952-3
 Sequence 3, Application US/09356952
Patent No. 6117663
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 SOFTWARE: PatentIn Ver. 2.0
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 Query Match
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Matches 30; Conserv
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US-07-935-311A-2
US-08-360-079-2
US-08-360-545B-6
US-09-262-653A-6
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 E: PENNIE & EDMONDS LLP
1155 Avenue of the Americas
 UMBER: US/08/826,246
28-MAR-1997
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COPERATING SYSTEM: DOS
SOFTWARE: FASTEGQ VECSION 2.0
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Patent No. 6048709
GENERAL INFORMATION:
APPLICANT: Falb, Dean
 CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/799,910
FILING DATE: 13-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/011,787
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TOPOLOGY: unkr
 USA
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January 30, 2001, 22:06:25 ; Search time 36.91 Seconds (without alignments) 41.840 Million cell updates/sec
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 Score
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 Database
 Run on:
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 A:Suclectie type: protein
A:Residues: 224-227;262-270;277-282 <HES>
R:Lopez, J.A.: Ludwig, B.H.; McCarthy, B.J.
J. Biol. Chem. 267, 10055-10061, 1992
A:Title: Polymorphism of human glycoprotein Ib alpha results from a variable number of
 A; Molecule type: protein
A; Residues: 17-315 <TIT>
R; Hess. D.; Schaller, J. 31. Rickli, E.E.; Clemetson, K.J.
Eur. J. Biochem. 199, 389-383, 1991
A;Title: Identification of the disulphide bonds in human platelet glycocalicin.
A;Reference number: S16945; MUID:91301149
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Gaps

14;

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C; Accession: A94174; A60435; A94173; S16945; IS5355; A27075; A27102
R; Lopez, J.A.; Chung, D.W.; Fujikawa, K.; Hagen, F.S.; Papayannopoulou, T.; Roth Proc. Natl. Acad. Sci. U.S.A. 84, S615-5619, 1987
A; Title: Cloning of the alpha-chain of human platelet glycoprotein Ib: a transment Reference number: A94174; MUID:87289655
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A;Residues: 1-626 <LOP>
A;Residues: 1-626 <LOP>
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R;Wicki, A.N.; Walz, A.; Gerber-Huber, S.N.; Wenger, R.H.; Vornhagen, R.; Clemet-
Thromb. Haemost, 61, 448-453, 1989
 R.Titani, K.; Takio, K.; Handa, M.; Ruggeri, Z.M.
Proc. Natl. Acad: Sci. U.S.A. 84, 5610-5614, 1987
A.Title: Amino acid sequence of the von Willebrand factor-binding domain of plat
 A;Title: Isolation and characterization of human blood platelet mkNA and construe
 C;Species: Erwinia chrysanthemi
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 21-Jul-2000
C;Accession: S28013; S23885
F;Condemine, G: Dorel, C: Hugouvieux-Cotte-Pattat, N.; Robert-Baudouy, J. Mol. Mcrobiol. 6, 3199-3211, 1992
A;Title: Some of the out genes involved in the secretion of pectate lyases in A;Reference number: S28011; MUID:93086427
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N.Alternate names: membrane glycoprotein Ib alpha chain
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30.1%; Pred. No. 5.6;
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 d cloning of a GPIb coding cDNA insert.
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 61 PFNLTSEPSDYAL 73
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Best Local Similarity
Matches 22; Conserv
 A; Accession: S28013
 A; Accession: A94174
 A; Accession: A60435
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S28013
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 C; Accession: T30351
R; Kuzio, J.; Poarson, M.N.; Harwood, S.H.; Funk, C.J.; Evans, J.T.; Slavicek, J.M.; Rohr
V; rology 253, 17-34, 1999
A; Title: Sequence and analysis of the genome of a baculovirus pathogenic for Lymantria of A; Reference number: 220836; MUID:99124785
A; Recession: T30351
 :Title: Sequence variation of cytotoxic T cell epitopes in different isolates of Epstei
Reference number: A49034; MUID:92111623
Accession: G49253
 Cross references: EMBL:M34440; NID:g330407; PIDN:AAA45893.1; PID:g330408
Apolloni, A.; Moss, D.; Stumm, R.; Burrows, S.; Suhrbier, A.; Misko, I.; Schmidt, C.;
Ir. J. Immunol. 22, 183-189, 1992
 A;Molecule type: DNA
A;Residues: 314-338 <AP2>
A;Cross-references: GB:S79234; NID:g242899; PIDN:AAB20989.1; PID:g242900
A:Experimental source: human B-type strain AG876JS; human B-type strain L4MR
A;Note: sequence extracted from NCBI backbone (NCBIN:79237, NCBIP:79254, NCBIN:79234,
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 nuclear antigen EBNA-3A - human herpesvirus 4 C;Species: human herpesvirus 4, Epstein-Barr virus C;Species: human herpesvirus 4, Epstein-Barr virus C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jul-2000 C;Accession: S27920; 649253; H49253; F9253 R;Sample, J.; Young, L.; Martin, B.; Chatman, T.; Kieff, E.; Rickinson, A.; Kieff, submitted to the EMBL Data Library, July 1990 A;Reference number: S27920 A;Reference number: S27920
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C;Species: Lymantria dispar nuclear polyhedrosis virus, LdMNPV
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
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 Accession: H49253
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A47021
pectic enzyme secretion protein OutC - Erwinia chrysanthemi
C;Species: Erwinia chrysanthemi
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C;Species: 24-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 16-Feb-1997
C;Accession: A47021
C;Accession: A47021
J; Collmer, A
J; Bacteriol. 174, 7385-7387, 1992
A;Title: Analysis of eight out genes in a cluster required for pectic enzyme sec
 zinc finger protein wizL - mouse
C:Species: Mus musculus (house mouse)
C:Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 05-Nov-1999
C;Accession: T00248
R:Matsumoto, K.; Ishii, N.; Yoshida, S.; Shiosaka, S.; Wanaka, A.; Tohyama, M.
Submitted to the EMBL Data Library, March 1998
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 4 QLPVEEPNPAKRLLFLLITIVFCQ---ILMAEEGVPAPI,PPEDAPNAASLAPTPVSPVLE 60
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Best Local Similarity
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Matches 18; Conserv
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R;Tettclin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J., Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A. fi, H.; Oin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M.; Science 287, 1809-1815, 2000

A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; V. A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.

A;Reference number: A81000; MuID:20175755
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 63
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R:Prasad, R: Zhadanov, A.B.; Sedkov, Y.; Bullrich, F.; Druck, T.; Rallapalli, R
Oncogene 15, 549-560, 1997
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Matches 21, Conserv
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 C; Genetics
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 Cross-references: Flybase:FBgn0001965
Superfamily: CDC25-type guanine nucleotide exchange activator homology; pleckstrin rep
479-586/Domain: pleckstrin repeat homology <PLK>
825-1066/Domain: CDC25-type guanine nucleotide exchange activator homology <SOS>
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R; Simon, M.A.; Bowtell, D.D.L.; Dodson, G.S.; Laverty, T.R.; Rubin, G.M.
R; Title: Ras1 and a putative guanine nucleotide exchange factor perform crucial steps
A; Reference number: A41216; MUID:92034991
 2;
 ä
 9
 Cross-references: EMBL:AF099001; PIDN:AAC68734.1; GSPDB:GN00028; CESP:R160.5; Experimental source: strain Bristol N2; clone R160
 C.Species: Caenorhabditis elegans
C.Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 18-Feb-2000
C.Accession: T33565
 C;Species: Drosophila melanogaster
C;Date: 28-May-1992 #sequence_revision 28-May-1992 #text_change 24-Sep-1998
C;Accession: A41216
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 11;
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 Length 102;
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:Residues: 1-1596 <SIM>
:Cross-references: GB:M7501; NID:9158470; PID:9158471
 14;
 28;
 C)Accession.
S.NoLson, J.; Gattung, S.
Submitted to the EMBL Data Library, October 1998
Submitted to The EMBL Data Library, October 1998
 37;
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 DB 2;
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 30; Conservative
 Ouery Match
Best Local Similarity
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 A; Gene: CESP:R160.5
 A; Accession: A41216
 FlyBase: Sos
 Map position: X :Introns: 25/2
58;
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Gaps

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Gaps

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January 30, 2001, 23:09:03; Search time 21.17 Seconds (without alignments) 275.836 Million cell updates/sec
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Listing first 45 summaries
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 Database :
 Searched:
 Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| riptio        | 1 6    | enciation.                              | gly96 protein - mo | hypothetical prote | o    | ALR protein - huma |    | I COA thioe | P-glycoprotein E - | zinc finger protei |        | ic enzym | nuclear antiqen EB | mucin-like protein | outC protein - Erw | platelet glycoprot | hypothetical prote | hypothetical prote | ⊂      | probable acyl-CoA | .0     | fatty-acid synthas | ത      |        | nascent polypeptid | hypothetical prote | ч      | n    | protein-tyrosine-p | hypothetical prote |
|---------------|--------|-----------------------------------------|--------------------|--------------------|------|--------------------|----|-------------|--------------------|--------------------|--------|----------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------|-------------------|--------|--------------------|--------|--------|--------------------|--------------------|--------|------|--------------------|--------------------|
| SUMMARIES     |        |                                         | _                  |                    |      |                    |    |             |                    |                    |        |          | _                  |                    |                    |                    |                    |                    | _      |                   |        |                    | _      |        |                    |                    |        |      | _                  |                    |
| ۵             | 105527 | ,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,, | 5333503            | T33565             | 4121 | T03455             | 03 | A81141      | T18344             | T00247             | T00248 | A47021   | S27920             | T30351             | \$28013            | NBHUIA             | T33756             | D83477             | QQBE29 | E81878            | T37045 | S61703             | T19800 | I46707 | T30826             | T08793             | IJHUCE | 5094 | 138670             | 0195               |
| DB            |        | 4 (                                     | 7                  | ~                  | ~    | N                  | ~  | ~           | ~                  | ~                  | 7      | 7        | 7                  | ~                  | ~                  | _                  | ~                  | 7                  | -      | 7                 | 7      | ~                  | ~      | 7      | ~                  | ~                  | ~      | 7    | -                  | ~                  |
| Length        | 156    | 2 .                                     | 103                | 102                | 59   | 4957               | 26 | 148         | 1677               | 95                 | 1561   | 272      | 925                | 1029               | 272                | 626                | 359                | 235                | 605    | 148               | 23     | 1887               | -      | 1402   | ന                  | 181                | æ      | 1072 | 3                  | 4                  |
| ery           | 1000   | 0.5                                     |                    | 18.4               | •    |                    |    | 17.2        | •                  |                    | •      |          | 9                  | ė.                 | ė.                 |                    | ė.                 | è.                 | 9      | 15.8              | 'n.    |                    |        |        | 'n                 | 'n.                | 'n     | 15.5 | ري                 |                    |
| Score         | . <    |                                         | ,                  | 81.5               | 6    |                    |    | 97          |                    | 74                 | 74     | 73.5     | ب                  | 7                  | 72.5               | _                  |                    | 70.5               | 0      | 70                |        | 69.5               | 69     | 69     |                    | 8                  | æ      | 68.5 | Ф                  | æ                  |
| Result<br>No. | -      | 4 (                                     | 7 (                | m                  | 4    | 2                  | 9  | 7           | æ                  | 0                  | 10     | 11       | 12                 | 13                 | 14                 | 15                 | 16                 | 17                 | 18     | 19                | 20     | 21                 | 22     | 23     | 24                 | 25                 | 56     | 27   | 28                 | 59                 |

|    | 30<br>31                                                                                                                                                                                                                                                         | 68.5                                                                                                                                     | ω.<br>                                                                        | 2649                                             | 000                                    | T51023<br>T22216                                                          | hypothetical prote                                                                                                                                     |         |
|----|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------|--------------------------------------------------|----------------------------------------|---------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------|---------|
|    | 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2                                                                                                                                                                                                                            | 68<br>67<br>67<br>67<br>66.5                                                                                                             |                                                                               | 267<br>1396<br>283<br>586<br>3566<br>169         | 222222                                 | A49068<br>A44453<br>S13381<br>S19381<br>A40701<br>A72466<br>A00BE8        | craniosynotosis-as<br>translation initia<br>hydroxyproline-ric<br>hypothetical prote<br>tenascin-x precurs<br>hypothetical prote<br>BPLF1 protein - hu | 4       |
| ÷  | 0 0 4 4 4 4 4 4 0 0 0 0 1 0 1 0 1 0 1 0                                                                                                                                                                                                                          | 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6                                                                                                    | 11111111111111111111111111111111111111                                        | 101<br>187<br>621<br>5149<br>325<br>325<br>424   | 0000000                                | 745506<br>C75558<br>C75558<br>F83345<br>D70666<br>S28442<br>T43468        | hypothetical prote<br>acetyl-CoA carboxy<br>acetolactate synth<br>probable non-ribos<br>probable modD prot<br>cxbB protein - Pse<br>hypothetical prote |         |
|    |                                                                                                                                                                                                                                                                  |                                                                                                                                          |                                                                               |                                                  |                                        | ALIGNMENTS                                                                |                                                                                                                                                        |         |
|    | RESULT 1<br>UC5537<br>differentiation-dependent protein<br>C:Species: Homo sapiens (man)<br>C:Date: 02-Sep-1997 #sequence_re<br>C;Accession: UC5537<br>R:Pietzsch, A.: Buechler, C.: As<br>Biochem. Blophys. Res. Commun. 2<br>A:Title: Identification and char. | l<br>ntiation<br>es: Homo<br>02-Sep-<br>sion: JC<br>sch, A.;<br>Blophy<br>Identi                                                         | -depende<br>sapiens<br>11997 #se<br>5537<br>Buechle<br>s. Res.                | ent pro<br>(man)<br>equence<br>er, C.;<br>Commun | rotein [ n) ce_revis .; Aslar un, 235, | ore - tuman sion 05-Sep-1997 ridis, C.; Schmit 4-9, 1997 erization of a n | text_change 07-May-1999<br>, G.<br>vel monocyte/macrophage                                                                                             | diff    |
|    | A; Melere<br>A; Molecu<br>A; Residu<br>A; Experi<br>A; Note:                                                                                                                                                                                                     | eletence number: Juccession: JC5537<br>olecule type: MRNA<br>esidues: 1-156 <pie<br>xperimental source:<br/>ote: the authors tr</pie<br> | ber: JC:<br>5537<br>: mRNA<br>56 <pie><br/>source:<br/>hors tra</pie>         | JC5537; MUID VA PIE> ce: monocyte translated t   | te<br>d the                            | .339426<br>codon CCG for res                                              | 1due 106 as Arg                                                                                                                                        |         |
|    | Query  <br>Best Lo<br>Matche                                                                                                                                                                                                                                     | Matc)<br>ocal<br>s {                                                                                                                     | Similarity<br>36; Conserv                                                     | 100.0%;<br>/ 100.0%;<br>:vative (                | 80.                                    | Score 442; DB 2;<br>Pred. No. 6.2e-36;<br>0; Mismatches 0;                | Jength 156;<br>1ndels 0; Gaps                                                                                                                          | .;<br>0 |
|    | Qy<br>Db 7                                                                                                                                                                                                                                                       | 1 VRROLI<br>        <br>71 VRROLI                                                                                                        | PVEEPNPA<br>                                                                  | KRLLFL<br>        <br> KRLLFL                    | 1111                                   | VRROLPVEEPNPAKBLIELLLTIVFCOILMAEEGVPAPLPPEDAPNASLAPTPVSPVLE<br>           | DAPNAASLAPTPVSPVLE 60<br>                                                                                                                              |         |
|    | Oy 6<br>Db 13:                                                                                                                                                                                                                                                   | PFNLT<br>                                                                                                                                | SEPSDYALDLSTFLQQHPAAF<br>                                                     | DLSTFL<br>       <br> DLSTFL                     | HOO HOO                                | 9AAF 86<br>    <br>9AAF 156                                               | ذ                                                                                                                                                      |         |
|    | RESULT<br>S33363<br>91y96 pr<br>C;Specie<br>C;Date:                                                                                                                                                                                                              | 2<br>octein -<br>ss: Mus r<br>13-Jan-                                                                                                    | mouse<br>musculus<br>1995 #se                                                 | eouenba                                          | e j<br>E é                             | e mouse)<br>_revision 13-Jan-1995 #                                       | #text_change 16-Feb-1997                                                                                                                               |         |
|    | R;Charles, C.H.; Yoon, J.K.; Sin<br>Oncogene 8, 797-801, 1993<br>A;Title: Genomic structure, cDN<br>A;Reference number: S33363; MUIS<br>A;Accession: S33363<br>A;Status: preliminary<br>A;Moleoule Type: mRNA<br>A;Residnes: 1-153, CHAA                         | s, C.H. Senomic Genomic ince num ince s3: prelin: prelin le type                                                                         | 7000,<br>7000,<br>801, 19<br>c struct<br>ber: 833<br>3363<br>minary<br>minary | J.K.;<br>193<br>.ure, c<br>1363; M               | Sims<br>CDNA<br>MUID:                  | Simske, J.S.; Lau, L.F.<br>DNA sequence, and expres<br>UID:93173526       | ision of gly96, a growth                                                                                                                               | fac     |
| 10 | A; Cross-C; Geneti<br>A; Intron<br>C; Keywor                                                                                                                                                                                                                     | references:<br>cs:<br>s: 70/3<br>ds: tran                                                                                                | ces: EMB                                                                      | L:X676<br>ne pro                                 | 67644<br>protein                       |                                                                           |                                                                                                                                                        |         |
|    | Query<br>Best L                                                                                                                                                                                                                                                  | / Match<br>Local Sin                                                                                                                     | Similarity                                                                    | 61.<br>68.                                       | 28%;                                   | Score 273; DB 2;<br>Pred. No. 1.3e-19;                                    | Length 153;                                                                                                                                            |         |

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Run on:

Searched:

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 Sequence
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APPLICANT: Falb, Dean
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: THE TREATMENT AND DIAGNOSIS OF
TITLE OF INVENTION: CARDIOVASCULAR DISEASE
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
 US-08-329-704-1
US-08-486-117-1
US-08-865-337A-3
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US-08-462-014-2
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 ALIGNMENTS
 NAME: COTUZZI, LAURA A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-078-999
TELECOMMUNICATION INFORMATION:
TELEFHONE: (212)7909090
TELEFRAX: (212)78699741
 MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/826,246
FILING DATE: 28-WAR-1997
 E: PENNIE & EDMONDS LLP
1155 Avenue of the Americas
 5248670-4
 CLASSIFICATION 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/799,910
FILING DATE: 13-FEB-1997
PRIOR APPLICATION NUMBER: 60/011,787
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
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Patent No. 6048709
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 TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 9
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STATE: NY
COUNTRY: USA
ZIP: 10036-2711
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Maximum Match 100%
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Maximum DB seq length: 200000000
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 1100 Peachtree Street, Suite 2800
 Bell, Leonard
Squinto, Stephen
FRYTION: Universal Donor Cells
 Genbank HUMDAF; HUMDAFC1
Human DAF cDNA
 Sims, Peter J.
Bothwell, Alfred L.M.
Elliott, Eileen A.
Flavell, Richard A.
 CLASSIFICATION: 435
ATTORREY/AGENT INFORMATION:
NAME: Pabst, Patrea L. 284
REFERENCE/DOCKET NUMBER: 31.284
REFERENCE/DOCKET NUMBER: OMRE'
TELEPHONE: 404-815-6500
TELEPHONE: 404-815-6555
 Sequence 2, Application US/08087007
Patent No. 5705732
Patent No. 5705732 5684223
 Kilpatrick & Cody
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 Rollins, Scott
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LOCATION: 1.819
OTHER INFORMATION: /not
OTHER INFORMATION: end
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 Madri, Joseph
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ZIP: 30309-4530
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STRANDEDNESS: single
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CORRESPONDENCE ADDRESS:
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MOLECULE TYPE: CD
 Georgia
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STATE: Georgia
 IMMEDIATE SOURCE
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 HYPOTHETICAL:
 ADDRESSEE:
 ORGANISM:
 ANTI-SENSE:
 Query Match
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181 CCCTTTAATCTGACTTCGGAGCCCTCGGACTACGCTCTGGACCTCAGCACTTTCCTCCAG 240
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SOFTWARE: PATENTIN RELEASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
 APPLICANT: DORNER, F.
APPLICANT: SCHETELINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SIQUENCES: 52
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
 30472/114 IMMU
 STREET: 1800 Diagonal Road, Suite 500 CITY: Alexandria
 APPLICATION NUMBER: EP 91 114 300.6 FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REFISTHATION NUMBER: 30472/114 1
 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
 Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL, INFORMATION:
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INFORMATION FOR SEQ 1D NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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IBM PC compatible
 TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
 451 caacacccygccgccttc 468
 241 CAACACCCGCCCGCCTTC 258
 (703)683-4109
 ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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 USA
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 FILING DATE:
 COUNTRY:
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ORGANISM: Homo saplens
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Best Local Similarity
Matches 258; Conserv
 Similarity
 RESULT 9
US-09-699-998-9797
 258;
 Query Match
Best Local Si
Matches 258
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 61 CTCACCATCGTCTTCTGCCAGATCCTGATGGCTGAAGAGGGTGTGCCGGGGGCGCCCTGCCT 120
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 Length 657;
 APPLICANT: Genering, David P.
APPLICANT: Genering, David P.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A
TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A
TITLE OF INVENTION: HUMAN MAMMARY EPITHELIUM LIBRARY
FILE REFERENCE: 1600.1086.001
CURRENT FOLLOTION NUMBER: 85/09/522,303
CURRENT FILING DATE: 2000-03-08
EARLIER APPLICATION NUMBER: 60/123,393
EARLIER FILING DATE: 1999-03-08
NUMBER OF SEQ ID NOS: 1353
SOFTWARE: FastSED for Windows Version 3.0
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 APPLICANT: Williamson, Mark
APPLICANT: Shyjan, Andrew W.
ATTLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREPOR
FILE REFERENCE: 1600.2029-001
CURRENT APPLICATION NUMBER: US/09/698,010
CURRENT FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: 60/162,358
PRIOR APPLICATION NUMBER: 60/162,358
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NUMBER OF SEQ 1D NOS: 15684
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 ; ORGANISM: Homo sapiens
US-09-522-303-1025
 ORGANISM: Homo sapiens
 US-09-522-303-1025
 US-09-698-010-14935
 SEQ ID NO 14935
LENGTH: 673
 LENGTH: 657
 TYPE: DNA
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CTCACCATCGTCTTCTGCCAGATCCTGATGGCTGAGGGGTGTGCCGGCGCCCCTGCCT 120
 CCCT1TAATCTGACTTCGGAGCCCTCGGACTACGCTCTGGACCTCAGCACTTTCCTCCAG 240
 Gaps
 1 GTCCGGCCCCAGCTGCCAGTCGAGGAACCGAACCCAAAAGGCTTCTCTTTTCTGCTG 60
 121 CCAGAGGACGCCCCTAACGCCGCATCCCTGGCGCCCACCCCTGTGTCCCCCGTCCTCGAG 180
 1 GTCCGGCGCCAGCTGCCAGTCGAACCGAACCCAGCCAAAAGGCTTCTCTTTTCTGCTG 60
 Gaps
 ..
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 .;
0
 Length 673;
 100.0%; Score 258; DB 23; Length 673; 100.0%; Pred. No. 7.7e-52; Live 0; Mismatches 0; Indels 0
 APPLICANT: HOITEMAN, Douglas A. APPLICANT: HOITEMAN, Douglas A. TITLE OF INVENTION: MOVEL NUCLEIC ACID MOLECULES AND USES; TITLE OF INVENTION: THEREFOR FILE REFERENCE: 1600.2008-001
CURRENT APPLICATION NUMBER: 02/09/699,998
CURRENT FILING DATE: 2000-10-30
PRIOR APPLICATION NUMBER: 60/162,362
PRIOR APPLICATION NUMBER: 60/162,362
PRIOR APPLICATION NUMBER: 1090-10-30
SOFTWARE: FastSEQ for Windows Version 4.0
SOFTWARE: FastSEQ for Windows Version 4.0
 Indels
Score 258; DB 23;
Pred. No. 7.76-52;
; Mismatches 0;
 509 caacacccggccgccttc
 qq
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0; Gaps

Indels

Mismat.ches

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Conservative
 ORGANISM: Homo sapiens
US-09-721-588-4548
 RESULT 13
US-09-726-787-2982
 RESULT 12
US-09-721-588-4548
 SEQ ID NO 4548
 Matches 258;
 LENGTH:
 121
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 329
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 Gaps
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 Length 673;
 sequence 2500, Application US/09716473

Sequence 2500, Application US/09716473

GENERAL INFORMATION:
APPLICANT: Williamson, Mark
APPLICANT: Williamson, Mark
TITLE OF INVENTION: THEREFOR NOVEL NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREFOR TITLE OF INVENTION: THEREFORE: 1600.2043-001

CURRENT APPLICATION NUMBER: 05/09/716,473

CURRENT FILING DATE: 2000-11-20

PRIOR FILING DATE: 1999-11-19

NUMBER OF SEO ID NOS: 2933

SOFTWARE: FastSEO for Windows Version 4.0
 Length 673;
 APPLICANT: Gearing, David P.
APPLICANT: Gearing, David P.
APPLICANT: McCarthy, Sean A.
APPLICANT: Holtzman, Douglas A.
TITLE OF INVENTION: MOVEL NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREPOR
FILE REPERENCE: 1600.2005-001
CURRENT APPLICATION NUMBER: 05/09/710,286
CURRENT FILING DATE: 2000-11-10
PRIOR APPLICATION NUMBER: 60/164,255
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4115
SOFTWARE: FESTSEQ for Windows Version 4.0
SECTION NO 3772
LENGTH: 673
 Indels
 Score 258; DB 24;
Pred. No. 7.7e-52;
 Ouery Match 100.0%; Score 258; DB 24; Best Local Similarity 100.0%; Pred. No. 7.7e-52; Matches 258; Conservative 0; Mismatches 0;
 Sequence 3772. Application US/09710286 GENERAL INFORMATION:
 100.0%;
 241 CAACACCGGCCGCCT/FC 258
 sapiens
 TYPE: DNA
GRCANISM: Homo sapiens
US-09-710-286-3772
 Query Match
Best Local Similarity
 TYPE: DNA
CRGANISM: HOMO
US-09-716-473-2500
 RESULT 11
US-09-716-473-2500
 SEQ 1D NO 2500
LENGTH: 673
 329
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121 CCAGAGGACGCCCCTAACGCCGCATCCCTGGCGCCCACCCCTGTGTCCCCCGTCCTCGAG 180
 61 CTCACCATCGTCTTCTGCCAGATCCTGATGGCTGAAGAGGGTGTGCCGGCGCCCCTGCCT 120
 240
 Gaps
CCAGAGGACGCCCTAACGCCGCATCCCTGGCGCCCCACCCCTGTGTCCCCCGTCTTCGAG
 181 CCCTTTAATCTGACTTCGGAGCCCTCGGACTACGCTCTGGACCTCAGCACTTTCTCCTCCAG
 .;
0
 100.0%; Score 258; DB 24; Longth 673; 100.0%; Pred. No. 7.7e-52; cive 0; Mismatches 0; Indels 0.
 APPLICANT: Gearing, David P.
APPLICANT: Gearing, Douglas A.
APPLICANT: HOLIZIMAN, Douglas A.
APPLICANT: Villeval, Jean-Luc
TITLE OF INVENTION: HOLEL NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.2046-001
CURRENT APPLICATION NUMBER: US/09/721,588
CURRENT FILLNC DATE: 2000-11-22
PRIOR APPLICATION NUMBER: 60/167,381
PRIOR FILING DATE: 1999-11-24
 NUMBER OF SEQ ID NOS: 5410
SOFTWARE: FastSEQ for Windows Version 4.0
 ; Sequence 4548, Application US/09721588
; GENERAL INFORMATION:
 509 caacaccggccgccttc 526
 241 CAACACCCGGCCGCCTTC 258
 509 caacacceggcegeette 526
 241 CAACACCGGCCGCCTTC 258
 Query Match
Best Local Similarity 100.0
Matches 258; Conservative
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Gaps

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CTCACCATCGTCTTCTGCCAGATCCTGATGGCTGAAGAGGGTGTGCCGGCGCCCCTGCCT 120
 121 CCAGAGGACGCCCCTAACGCCGCATCCCTGGCGCCCACCCCTGTGTCTCCCCGTCCTCGAG 180
 181 CCCTTTAATCTGACTTCGGAGCCCTCGGACTACGCTCTGGACCTCAGCACTTTCCTCCAG 240
 CTCACCATCGTCTTCTGCCAGATCCTGATGGCTGAAGAGGGTGTGCCGGCGCCCCTGCCT 120
 255 ctcaccatcgtcttctgccagatcctgatggctgaagagggtgtgccggcgccctgcct 314
 121 CCAGAGGACGCCCCTAACGCCGCATCCCTGGCGCCCACCCCTGTGTCCCCCGTCCTCGAG 180
 CCCTTTAATC/IGACTT/CGGAGCCCT/CGGACTACGCTCTGGACCT/CAGCACT/T/CCT/CCAG 240
 GTCCGGCGCCCAGCTGCCAGTCGAGGAACCGAACCCAGCCAAAAGGCTTCTTCTGCTG 60
 Length 803;
 Sequence 10469, Application US/0969998
GENERAL INFORMATION:
APPLICANT: Holtzman, Douglas A.
APPLICANT: Gearing, David P.
TITLE OF INVENTION: NOVEL NICLEIC ACID MOLECULES AND USES TITLE OF INVENTION: THEREFOR FILE REFERENCE: 1600.2008-001
CURRENT APPLICATION NUMBER: US/09/699,998
CURRENT APPLICATION NUMBER: 0500-10-30
PRIOR FILING DATE: 1999-10-29
NUMBER OF SEQ ID NOS: 10905
SOFTWAKE: Fastseo for Windows Version 4.0
 Indels
 100.0%; Score 258; DB 23;
100.0%; Pred. No. 7.8e-52;
tive 0; Mismatches 0;
 Search completed: January 30, 2001, 22:04:50 Job time: 13154 sec
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 241 CAACACCCGGCCGCCT'FC 258
 caacacccggccgcctc 441
 Conservative
 Conservative
 Query Match
Best Local Similarity
Matches 258; Conser
 ; ORGANISM: HOMO : US-09-699-998-10469
 US-09-699-998-10469
 TYPE: DNA
 61
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 181
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 CCAGAGGACGCCCCTAACGCCGCATCCCTGGCGCCCCCCTGTGTCCCCCCGTCCTCGAG 180
 CTCACCATCGTCTTCTGCCAGATCCTGATGGCTGAAGAGGGTGTGCCGGCGCCCCTGCCT 120
 ccagaygacgccctaacgccgcatccctggcgcccaccctgtgtcccccgtcctcgag 448
 1 GTCCGGCGCCAGCTGCCAGTCGAGGAACCGAACCCAACAAAGGCTTCTCTTCTTGCTG 60
 Gaps
 181 CCCTTTAATCTGACTTCGGAGCCCTCGGACTACGCTCTGGACCTCAGCACTTTCCTCCAG
 ·.
 Length 673;
 Length 706:
 Sequence 1778, Application US/0969998
GENERAL INFORMATION:
APPLICANT: HOLIZAND, Douglas A.
APPLICANT: GENERAL DOUGLAS A.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES; TITLE OF INVENTION: THEREPOR FILE REFERENCE: 1600, 2008-001
CURRENT APPLICATION NUMBER: US/09/699,998
CURRENT APPLICATION NUMBER: 60/10-30
PRIOR APPLICATION NUMBER: 60/162,362
PRIOR FILING DATE: 1999-10-29
Sequence 2982, Application US/09726787
GENERAL INFORMATION:
APPLICANT: Gearing, David P.
APPLICANT: Gearing, David P.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.2010-001
CURRENT APPLICATION NUMBER: US/09/726,787
CURRENT APPLICATION NUMBER: 60/168,132
PRIOR PELING DATE: 1999-11-30
 Indels
 Score 258; DB 55;
Pred. No. 7.7e-52;
; Mismalches 0;
 Score 258; DB 23;
Pred, No. 7.7e-52;
 NUMBER OF SEQ ID NOS: 3241
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2982
 EQ ID NOS: 10905
FastSEQ for Windows Version 4.0
 ပ
 100.0%; SC
100.0%; Pr
tive 0;
 NAME/KEY: misc_feature
| CCATION: (1)...(706)
| OTHER INFORMATION: n = A,T,C or
US-09-699-998-1778
 100.08;
 Caacaccggccgccttc 526
 241 CAACACCCGGCCGCCTTC 258
 Ouery Match
Best Local Similarity 100.
Matches 258; Conservative
 TYPE: DNA
ORGANISM: Homo sapiens
US-09-726-787-2982
 ORGANISM: Homo sapiens
 NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
 Ouery Match
Best Local Similarity
 RESULT 14
US-09-699-998-1778
 SEQ ID NO 1778
LENCTH: 706
 TYPE: DNA
 269
 61
 329
 121
 389
 449
 509
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us-08-799-910-9\_copy\_211\_468.rni

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88 ATGCCTCAACAGGCTGTGCCGGCGCCCCTGCCTCCAGAGGACGCCCCTAACGCCCGCATCC 147
 246 CCGCACTTTCACCACCACCACCTCCTTCTTTCTTTCAGCCCTTGCTAGCGCCGGGGAGCCCG 187
 148 CTGCCGCCCACCCCTGTGCCCCCGTCCTCGACCCCTTTAATCTGACTTCGGAGCCCTCG 207
 Gaps
 ADDRESSEE: Woodcock, Washburn, Kurtz, Mackicwicz & No. 5876949ris
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
 28 CCGAACCCAGCCAAAAGGCTTCTCTTTCTGCTCACCATCGTCTTCTGCCAGATCCTG 87
 APPLICANT: Martinis, Susan A.
APPLICANT: Sassanfar, Mandana
APPLICANT: Kim, Sunghoon
APPLICANT: Lee, Sang Ho
APPLICANT: Schimmel, Paul R.
TITLE OF INVENTION: RECOMBINANT MYCOBACTERIAL METHIONYL-TRNA
TITLE OF INVENTION: SYNTHETASE GENES, TESTER STRAINS AND ASSAYS
 ..
 DB 2; Length 4362;
 0; Mismatches 110; Indels
 Smith & Reynolds, P.C
 208 GACTACGCTCTGGACCTCAGCACTTTCCTCCAGCAACACC 247
 67 GCCCCCCCCTGCCCACGCCCCCCTGCAGCGCCCCTCC 28
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,073A
FILING DATE: 31-MAY-1995
 Score 32;
Pred. No.
 UPN-2201
 CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: DELUCA: Mark
REGISTRATION NUMBER: 33,229
REFRENCE/DOCKET NUMBER: UPN-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 56613100
 Sequence 3, Application US/08584226 Patent No. 5798240 GENERAL INFORMATION:
 E: Hamilton, Brook,
Two Militia Drive
 12.4%;
 TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
 LENGTH: 4362 base pairs
 Ouery Match 12.4 Best Local Similarity 49.5 Matches 109; Conservative
 nucleic acid
EDNESS: double
 NUMBER OF SEQUENCES: 2. CORRESPONDENCE ADDRESS:
 COMPUTER READABLE FORM:
 ; NAME/KEY: CDS
; LOCATION: 220..2118
US-08-455-073A-1
 linear
 Lexington
 STRANDEDNESS:
 MOLECULE TYPE:
 19103
 US-08-584-226-3/C
 ADDRESSEE:
 COUNTRY:
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531 CGCCGCGGGCGTGCCGACACACACACGCGCGAATTCCGACGTCTTCCACCGCA 472
 185 TTAATCTGACTTCGGAGCCCTCGGACTACGCTCTGGACCTCAGCACTTTCCTCCAGCAAC 244
 65 CCATCGTCTTCTGCCAGATCCTGATGGCTGAAGAGGGTGTGCCGGGGCCCCTGCCTCCAG 124
 591 CCCGCGAATTCTATCTGACGGGACGGATGAGCACGCCTGAAGGTGGCGCAGGCCGCCG 532
 125 AGGACGCCCTAACGCCGCATCCCTGGCGCCCACCCCTGTGTCCCCCGTCCTCGAGCCCT 184
 Length 599;
 Indels
 Patentin Release #1.0, Version #1.30
 0; Mismatches 97;
 DB 1;
 Score 31.8;
Pred. No. 3;
 Search completed: January 30, 2001, 21:28:34 Job time: 19996 sec
 CPI94-052
 CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/305,766
FILING DATE: 13-SEP-1994
ATTORNEY/AGENT INFORMATION:
 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,226
 ZIP: 02173-4799
COMPUTER REARABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 NAME: Brook, David E. REGISTRATION NUMBER: 22,592
 REFERENCE/DOCKET NUMBER: CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
 MOLECULE TYPE: DNA (genomic)
 Query Match 12.3%;
Best Local Similarity 48.1%;
Matches 90; Conservative
 599 base pairs
 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
 nucleic acid
EDNESS: double
Massachusetts
 linear
 411 ACGCGGC 405
 STRANDEDNESS:
 245 ACCCGGC 251
 FILING DATE:
 ENGTH:
 US-08-584-226-3
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LENGTH:
 US-07-705-490-1
 Query Match
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 94 CAAGAGGTGTGCCGGCGCCCTCCTCCAGAGGACGCCCCTAACGCCGCATCCCTGGCG 153
 154 CCCACCCTGTGTCCCCCGTCTCTCAGCCCTTTAATCTGACTTCGGAGCCCTCGGACTAC 213
 747 AGATOTOCOCOGOCOCOGIGOTOTOCOTOTIVACOTOCITOACOCOCOCOCOCOCOCOCAGAT 688
APPLICANT: Weinzierl, Robert O.J.
TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS,
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING TAFS AND METHODS OF USE
 34 CCAGCCAAAAGGCTTCTCTTTCTGCTGCTCACCATGGTCTTCTGCCAGATCCTGATGGCT
 -,
 Ouery Match 13.0%; Score 33.6; DB 1; Lenyth 1120; Best Local Similarity 51.0%; Pred. No. 1.2; Matches 104; Conservative 0; Mismatches 99; Indels 1
 ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT STREET: 4 Embarcadero Center, Suite 3400 (LTY: San Francisco STATE: California
 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
 REFERENCE/DOCKET NUMBER: A-57650-2/AJT/RAO FELECOMMUNICATION INFORMATION:
 0; Mismatches
 APPLICATION NUMBER: US/08/646,715
FILING DATE: 09-MAY-1996
CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/188,582
FILING DATE: 28-JAN-1994
ATTORNEY/AGENT INFORMATION:
 214 GCTCTGGACCTCAGCACTTTCCTC 237
 687 CCGCCGGAGC'FGCCCACGTTTTC 664
 Sequence 1, Application US/07705490 Patent No. 6107025 GENERAL INFORMATION:
 TELEPHONE: (415) 781-1189
TELEFAX: (415) 388-3249
TELEX: 910 277299
INFORMATION FOR SEQ 1D NO: 8: SEQUENCE CHARACTERISTICS: LENGTH: 1120 base pairs TYPE: nucleic acid STRANDEDNESS: double
 NAME: Osman, Richard A
REGISTRATION NUMBER: 36,627
 APPLICANT: Caskey, C. T.
APPLICANT: Nelson, David L.
APPLICANT: Pieretti, Maura
 ZIP: 9411-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
 NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
 MOLECULE TYPE: CDNA
 80..913
 linear
 USA
 ; NAME/KEY;
; LOCATION:
US-08-646-715-8
 US-07-705-490-1/c
 ropology:
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APPLICANT: Gideon Dreyfuss
APPLICANT: Mikiko C. Siomi
APPLICANT: Yan Zhang
TITLE OF INVENTION: Fragile X Related Proteins, Compositions And Methods
TITLE OF INVENTION: Of Making And Using The Same
CORRESPONDENCE ADDRESS:
 88 ATGGCTGAAGAGGGTGTGCCGGCGCCCCTCCAGAGGACGCCCCTAACGCCGCATCC 147
 148 CTGGCGCCCACCCTGTGTCCCCCGTCCTCGAGCCCTTTAATCTGACTTCGGAGCCCTCG 207
 1; Gaps
 28 CCGAACCCAGCCAAAAGGCTTCTTTTTTGCTGCTCACCATCGTCTTCTGCCAGATCCTG 87
 DB 3; Length 3765;
 Ben A.
Diagnosis of the Fragile X Syndrome
 Indels
 PatentIn Release #1.0, Version #1.25
 208 GACTACGCTCTGGACCTCAGCACTTTCCTCCAGCAACACC 247
 0; Mismatches 110;
 43 GCGCCGCGCTIGCCGCACGCCCCTIGGCACGGGGGCGCCTCC
 Score 32;
 Pred. No
 E: Thomas D. Paul
1301 McKinney, Suite 5100
 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/705,490
ELLING DATE: 19910708
CLASSIFICATION: 435
 REFERENCE/DOCKET NUMBER: D-5350
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/651-5325
 IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
 Sequence 1, Application US/08455073A Patent No. 5876949
Stephen T.
 CLASSIFICATION: 4.2.
ATTORNEY/AGENT INFORMATION:
NAME: Paul, Thomas D.
 12.4%;
 Floppy disk
 3765 base pairs
 TELEFAX: 713/651-5246
TELEX: 762029
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
 Conservative
 APPLICANT: OOSLTA, BENT
TITLE OF INVENTION: Dis
NUMBER OF SEQUENCES: 1,
CORRESPONDENCE ADDRESS:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
 single
 TYPE: NUCLEIC ACID
STRANDEDNESS: sing]
 TOPOLOGY: linear
MOLECULE TYPE: CDN.
 OPERATING SYSTEM:
 linear
 COUNTRY: U.S.A.
ZIP: 77010-3095
 Best Local Similarity
Matches 109; Conserv
 Abbar
STREET: 150-
TTTY: Houston
 GENERAL INFORMATION:
 Texas
 ANTI-SENSE: NO
 HYPOTHETICAL:
 ADDRESSEE:
 US-08-455-073A-1/c
 SOFTWARE:
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US-09-058-389A-13
 TOPOLOGY:
 COUNTRY:
 APPLICANT:
APPLICANT:
 Query Match
 Matches
 RESULT
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 GENERAL INFORMATION:
APPLICANT: Belt, Judith A.
APPLICANT: Belt, Judith A.
APPLICANT: Crawford, Charles R.
APPLICANT: Crawford, Charles R.
APPLICANT: Patel, Divyen
TITLE OF INVENTION: A NITROBENZYLMERCAPTOPURINERIBOSIDE
TITLE OF INVENTION: (NBMPR)-INSENSITIVE, EQUILIBRATIVE, NUCLEOSIDE TRANSPORT
TITLE OF INVENTION: PROTEIN, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF
TITLE OF INVENTION: USE
 ö
 116 TGCCTCCAGAGGACGCCCCTAACGCCGCATCCCTGGCGCCCCACCCCTGTGTCCCCGTCC 175
 176 TCGAGCCCTTTAATCTGACTTCGGAGCCCTCGGACTACGCTCTGGACCTCAGCACTTTCC 235
 Gaps
 0
 Score 39.4; DB 4; Length 2847;
Pred. No. 0.04;
0; Mismatches 56; Indels 0;
 /note= "HUMDAFC1 (Promotor and 5'
end of Exon 1, genomic sequence)"
 ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: US/09/058,389A
FILING DATE: APril 9, 1998
CLASSIFICATION: 800
 REFERENCE/DOCKET NUMBER: 1340-1-013N
 ; Sequence 5, Application US/09058389A ; Patent No. 6130065
 NAME: Jackson Esg., David A. REGISTRATION NUMBER: 26,742
 TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
 15.3%;
 DNA (genomic)
 INFORMATION FOR SEO ID NO: 5:
 ATTORNEY/AGENT INFORMATION:
 SEQUENCE CHARACTERISTICS:
I.ENGTH: 6354 base pairs
TYPE: nucleic acid
 NAME/KEY: misc_feature
LOCATION: 1.819
OTHER INFORMATION: /not
OTHER INFORMATION: end
 Ouery Match 15.37
Best Local Similarity 56.67
Matches 73; Conservative
 201-343-1684
 NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
 Hackensack
: New Jersey
RY: USA
 linear
 236 TCCAGCAAC 244
 625 TACTCCACC 633
 STRANDEDNESS:
 MOLECULE TYPE:
FEATURE:
NAME/KEY:
LOCATION:
 07601
 RESULT 8
US-09-058-389A-5
 US-09-058-389A-5
 PCT-US92-05920-2
 COUNTRY:
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(NBMPR)-INSENSITIVE, EQUILIHRATIVE, NUCLEOSIDE TRANSPORT PROTEIN, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF
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 100 GGTGTGCCGGCGCCCCTGCCTCCAGAGGACGCCCCTAACGCCGCATCCCTGGCGCCCACC 159
 101 GIGIGCGGCGCCCTGCCTCCAGAGGACGCCCCTAACGCCGCATCCCTGGCGCCCACCC 160
 Gaps
 .;
O
 DB 3; Length 6354;
 APPLICANT: PATEL, Divyen
TITLE OF INVENTION: A NITROBENZYLMERCAPTOPURINERIBOSIDE
TITLE OF INVENTION: (NBMPR)-INSENSITIVE, EQUILIBRATIVE,
TITLE OF INVENTION: PROTEIN, NUCLEIC ACIDS ENCODING THE
TITLE OF INVENTION: USE
NUMBER OF SEQUENCES: 22
 Indels
 Indels
 CORRESPONDENCE ADDRESS: ADDRESSEE: David A. Jackson, Esq. STREET: 411 Hackensack Ave, Continental Plaza, 4th STREET: Floor
 0.064;
29;
 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
15.0%; Score 38.6; DB 3; 165.9%; Pred. No. 0.079;
Live 0; Mismatches 29;
 14.6%; Score 37.6; DB 3; 65.5%; Pred. No. 0.064;
 0; Mismatches
 1340-1-013N
 APPLICATION NUMBER: US/09/058,389A FILING DATE: April 9, 1998
 2521 CCTGCGCCCCTGCCTCCAGCCCT 2545
 0S-09-058-389A-13

Sequence 13, Application US/09058389A

Patent No. 6130065
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "intron 3"
 160 ccrdrcrccccrccrccAGcccr 184
 ATTORNEY AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFRENCE/DOCKET NUMBER: 1340-
TELEPHONE: 201-487-5800
 161 CTGTGTCCCCGTCCTCGAGCCCT 184
 Belt, Judith A.
Crawford, Charles R.
Patel, Divyen
 61 CTGCGCCCCTGCCTCCAGCCCT 84
 LENGTH: 170 base pairs
TYPE: nucleic acid
 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
 0.uery Match
Best Local Similarity 65.9
Matches 56; Conservative
 55; Conservative
 201-343-1684
 ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
 CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
 Best Local Similarity
 linear
 GENERAL INFORMATION:
 CLASSIFICATION:
 STRANDEDNESS:
 HYPOTHETICAL:
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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 protein search, using sw model OM protein

January 30, 2001, 23:09:03 ; Search time 21.17 Seconds Run on:

(without alignments) 275.836 Million cell updates/sec

US-08-799-910-10\_COPY\_71\_156 442 1 VRROLPVEEPNPAKRLLFIL......EPSDYALDLSTFLQQHPAAF Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

195891 seqs, 67900655 residues Searched:

195891 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

pirl:\* pir2:\* pir3:\* PIR\_66;\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           | Description   |        | alreadinactor | hypothetical and | nypometical proce | grantile nacteolide | protein | ADV PLOCETT TURNS |        | f topical | tinger | id Tabuti | pectic enzyme secr | nuclear antigen EB | 9      | outc protein - Erw | platelet glycoprot | hypothetical prote | nypothetical prote | BRLFI protein - hu | probable acyl-CoA | itrate re | ~       | 1 prot | translation initia | nascent polypeptid | nypotnetical prote | cannerin I precurs | Verprolin related | protein-tyrosine-p | hypothetical prote |
|-----------|---------------|--------|---------------|------------------|-------------------|---------------------|---------|-------------------|--------|-----------|--------|-----------|--------------------|--------------------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|-----------|---------|--------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|
| SUMMARIES | g.            | 105537 | 333           | 9                | 412               | ľ                   | S       | -                 | 118344 | 100247    | 00248  | 12021     | 00070              | 130351             | 528013 | BHILL              | 75755              | D83477             | 00477              | 0.00               | 3,075             | 50719     | 00.861. | 46707  | 30806              | 08793              | THUE               | 50075              | 0,000             | > L                | 26.10              |
|           | DB            | :      |               |                  |                   |                     |         |                   |        |           |        |           |                    | , ~                |        |                    |                    |                    |                    |                    |                   |           |         |        |                    |                    |                    |                    |                   | ٠,                 | ,,                 |
|           | Length        |        |               |                  |                   |                     |         |                   |        |           |        |           |                    | 1029               |        |                    |                    |                    |                    |                    |                   |           |         |        |                    |                    |                    |                    |                   |                    |                    |
| 200       | Query         | 100.0  | 61.8          | 18.4             | æ                 | 17.6                | 17.6    | 17.2              | 17.2   | ဖ         | 9      | 9         | ·                  | 16.5               | 9      |                    |                    | 16.0               |                    |                    | ა ი               |           | ·       | · 10   | 'n                 |                    | 'n                 | 'n                 |                   | ·                  | ,                  |
|           | Score         | 442    | 273           | 81.5             | œ.                | 7.8                 | 7.8     | 76                | 76     | 74        | 74     | 73.5      | 73.5               | 73                 | 72.5   | 71.5               | 71                 | 70.5               | 70.5               | 7.0                | 7.0               | 69.5      | 69      | 69     | 69                 | 68.5               | 68.5               | 68.5               | 8 9               | 2 2                | 2                  |
|           | Result<br>No. | H      | 7             | m                | 4                 | 'n                  | ø       | 7                 | œ      | 6         | 10     | 11        | 12                 | 13                 | 14     | 15                 | 16                 | 17                 | 18                 | 19                 | 20                | 21        | 22      | 23     | 24                 | 25                 | 56                 | 27                 | 28                | 0                  | ì                  |

| hypothetical prote | hypolibetical prote | il pocuectous proce | craniosynotosis-as | translation initia | hydroxyproline-ric | hypothet toal | Critical Architect | Prophytical A process | aloid Terrierroal bloce | BPLF1 protein - hu | hypothetical prote | DODEN OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE P | wootels con carbony | מרפרסזמכומות אלטרט | probable non-ribos | יייים מיסיים פולימלחיות | probable mode proc | esd - uranoid gova | hypothetical prote |
|--------------------|---------------------|---------------------|--------------------|--------------------|--------------------|---------------|--------------------|-----------------------|-------------------------|--------------------|--------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------|--------------------|--------------------|-------------------------|--------------------|--------------------|--------------------|
| T51023             | T22216              | A 400 F B           | 000                | A44403             | 513383             | S19381        | A40701             | A72466                | 00000                   | 00000              | T46506             | C75558                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | JC5164              | 1000               | F 83340            | D70666                  | 528442             | 1000               | T43468             |
| a                  | N                   | c                   |                    | 7                  | ~                  | ~             | ٦                  | ~                     | -                       | 4 (                | v                  | N                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | 7                   | c                  | V                  | ~                       | C                  | ,                  | N                  |
| 2649               | 241                 | 267                 | 1001               | D 6 5 1            | 283                | 286           | 3566               | 169                   | 3140                    |                    | TOT                | 187                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 621                 | 0 7 1 2            | 0 L 4              | 325                     | 329                |                    | 474                |
| 15.5               | 15.4                | 15.4                | ייי                | - C                | 15.2               | 15.2          | 15.2               | 15.0                  | 150                     | 1                  | 14.9               | 14.9                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | 14.9                | 0 1                |                    | 14.8                    | 14.8               |                    | 2.<br>20           |
| 68.5               | 68                  | 89                  | a                  | ) r                | 9                  | 67            | 67                 | 66.5                  | 56                      |                    | 0                  | 99                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | 99                  | y                  | 3 .                | 65.5                    | 65.5               | 27                 | 0.00               |
| 30                 | 31                  | 32                  | 3.3                | ) •                | 3                  | S<br>S        | 36                 | 37                    | 89                      | 0 0                | J .                | 40                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | 41                  | 4.2                | • •                | 43                      | 44                 | u v                | 7                  |

differentiation-dependent protein DIF-2 - human

C:Species: Homo sapiens (man) C:Date: 02-Sep-1997 #sequence\_revision 05-Sep-1997 #text\_change 07-May-1999

C. Accession: UC5537
R. Pietzsch, A.; Buechler, C.; Aslanidis, C.; Schmitz, G.
Blochem. Biophys. Res. Commun. 235, 4-9, 1997
A.Title: Identification and characterization of a novel monocyte/macrophage differ.
A.Reference number: UC5537; MUID:97339426
A.Molecule type: mRNA
A.Molecule type: mRNA
A.Residues: 1.156 < PIE>
A.Experimental source: monocyte
A.Note: the authors translated the codon CCG for residue 106 as Arg

Gaps ö Length 156; Ouery Match
Best Local Similarity 100.0%; Pred. No. 6.2e-36;
Matches 86; Conservative 0; Mismatches 0;

ö

1 VRROLPVEEPNPAKRLLFLLLTIVFCQILMAEEGVPAPLPPEDAPNAASLAPTPVSPVLE 60

61 PFNLTSEPSDYALDLSTFLQQHPAAF q ò

131 PFNLTSEPSDYALDLSTFLQQHPAAF 156

RESULT 2
33363
91936
91996 protein - mouse
C.Species: Mus musculus (house mouse)
C.Date: 13.7an-1995 #sequence\_revision 13.7an-1995 #text\_change 16-Feb-1997
C.Accession: S33363
R.Charles, C.H.; Yoon, J.K.; Simske, J.S.; Lau, L.F.
Oncogene 8, 797-801, 1993
A.Title: Genomic structure, cDNA sequence, and expression of 91996, a growth A.Reference number: S33363 MUID:93173526
A.Status: preliminary
A.Residues: Preliminary
A.Residues: 1-153 <CHA>

and expression of gly96, a growth factor

A)Cross-references: EMBL:X67644 C;Genetics: A:Introns: 70/3 C;Keywords: transmembrane protein

Length 153; Score 273; DB 2; Pred. No. 1.3e-19; 61.8%; 68.2%; Query Match Best Local Similarity

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pectic enzyme secretion protein OutC - Erwinia chrysanthemi
C:Species: Erwinia chrysanthemi
C:Date: 24-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 16-Feb-1997
C:Accession: A47021
R:Lindeberg, M:; Collmer, A.
J. Bacteriol. 174, 7385-7397, 1992
A:Title: Analysis of eight out genes in a cluster required for pectic enzyme secret.
A:Reference number: A47021; MUID:93054355.
 Findstaumoto, K.; Ishii, N.; Yoshida, S.; Shiosaka, S.; Wanaka, A.; Tohyama, M. submitted to the EMBL Data Library, March 1998
A; Description: Molecular cloning and distinct developmental expression pattern of A; Reference.number: 214130
A; Recession: T00248
 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1561 <MAT>
A;Residues: 1-1561 <MAT>
A;Cross-references: EMBL:AB012265; NID:d1227740; PIDN:BAA32790.1; PID:d1033756
A;Experimental source: brain
C;Genetics:
A;Gene: wiz
A;Reference number: 214130
A;Accession: T00247
A;Status; prelaininary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-955 <MAT>
A;Cross-references: EMBL:AB012266; NID:d1227741; PIDN:BAA32791.1; P1D:d1033757
 zinc finger protein wizL - mouse
C;Species: wus musculus (house mouse)
C;Date: 22-Jan.1999 #sequence_revision 22-Jan-1999 #text_change 05-Nov-1999
C;Accession: T00248
 4 QLPVEEPNPAKRI, FLLI, TIVFCO---II, MAEEGVPAPI, PPEDAPNAASLAPTPVSPVLE 60
 A;Status: preliminary; not compared with conceptual translation
 A:Note: sequence extracted from NCBI backbone (NCBIP:118270) C:Reywords: transmembrane protein
 906 GSPTPKNPEDKSPQLSLSPRPTSPRAQCPQSEDEGPLNLTSGP 948
 34 GVPAPLPPEDAPNAASLAPTPVSPVLE-----PFNLTSEP
 34 GVPAPLPPEDAPNAASLAPTPVSPVLE-----PFNLTSEP
 16.6%; Score 73.5; DB 2; 30.1%; Pred. No. 4.5;
 Score 74; DB 2;
pred. No. 16;
2; Mismatches 1.
 Score 74; DB 2
Pred. No. 27;
2; Mismatches
 13; Mismatches
 16.7%;
 Match 16.7%;
Local Similarity 41.9%;
les 18; Conservative
 Best Local Similarity 30.19
Matches 22; Conservative
 Query Match
Best Local Similarity 41.9 Matches 18; Conservative
 A; Experimental source: brain C; Genetics:
 A; Molecule type: DNA
A; Residues: 1-272 <LIN>
 Query Match
 Query Match
 A; Gene: wiz
 RESULT 11
 Matches
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 8
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 R.Matsumoto, K.: Ishli, N.: Yoshida, S.: Shiosaka, S.: Wanaka, A.: Tohyama, M. submitted to the EMBL Data Library, March 1998
A.Description: Molecular cloning and distinct developmental expression pattern of splice
 A Experimental source: Serogroup B, strain MMD58
C;Genetics:
A;Gene: NMB0925
 A:Residues: 1.1677 <LAF>
A:Cross-references: EMBL:U55381; NID:g1916605; PID:g1916606; PIDN:AAB51191.1
C:Superfaṃily: human multidrug resistance prolein cMOAT2; ATP-binding cassette homology
 acyl CoA thioester hydrolase family protein NMB0925 [imported] - Neisseria meningitidis C:Species: Neisseria meningitidis C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 31-Mar-2000
 Ritetelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J. Hickey, E. K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A. ti, H.; Ohn, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M.; Science 287, 1809-1815, 2000
A.nuthors: Grandi, G.; Sun, L., Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; VA; Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58. A; Reference number: A81000; MUID:2017575
 ö
 ?
 C;Species: Leishmania tropica
C;Date: 15-Oct-1999 *sequence_revision 15-Oct-1999 *text_change 31-Jan-2000
C;Accession: T1834 S. S.; Gamarro, F.
R;Lafuente, E.; Castanys, S.; Gamarro, F.
 zinc finger protein wiz - mouse
C;Species: Mus musculus (house mouse)
C;Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 05-Nov-1999
 Gaps
 37 APLP-----PEDAPNAASLAPTPVSPVLEPFN-------LTSEPSDYALDI,ST 77
 ö
 Length 1677;
 DB 2; Length 148;
 Indels
 15;
 DB 2;
19;
 112 YLVTEAVFTYVAIDAEGNPRPIPKEGNPKLAGLLPTP 148
 A; Status: preliminary; translated from GB/EMBL/DDBJ
 54
 Score 76; DB 2
Pred. No. 1.3;
5; Mismatches
 6; Mismatches
 18 FLLLTIVFCQILMAEEGVPAPLPPEDAPNAASLAPTP
 R:Lafuente, E.; Castanys, S.; Gamarro, F. submitted to the EMBL Data Library, April 1996 A;Reference number: 218880
 Score 76;
 Pred. No.
 -glycoprotein E - Leishmania tropica
 17.2%;
 17.2%;
 Conservative
 Conservative
 | | | :|!
4657 PLVELPTEP 4665
 Query Match
Best Local Similarity
Matches 15; Conserv
 Query Match
Best Local Similarity
Matches 20; Conserv
 A; Molecule type: DNA
A; Residues: 1-148 <TET>
 Status: preliminary
 A; Molecule type: DNA
 6) PF-NLTSEP
 A; Accession: T18344
 Accession: T00247
Matsumoto, K.: Is
 Accession: A81141
 A; Accession: A81141
 C; Accession:
R; Matsumoto,
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Gaps

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15; Indels

DB 2; Length 1561: 27;

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Gaps

Indels

Length 955;

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Gaps

13;

25; Indels

Length 272;

```
A.Map position: 17pter-17p12

C.Complex: heterodimer with platelet glycoprotein Ib beta chain (NBHUIB)

C.Complex: heterodimer with platelet glycoprotein Ib alpha chain; leucine-rich alpha-2-glycoprotein Ib alpha chain; leucine-rich alpha-2-glycoprotein Ib alpha cylycoprotein; platelet membrane; tandem reper professional signal sequence status predicted <SIG>
F:116/Domain: signal sequence status predicted <SIG>
F:17-050/Product: platelet glycoprotein Ib alpha chain status predicted <MPT>
F:48-71/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F:72-93/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F:94-116/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F
 C.Comment: Glycoprotein 1b (GPIb), a surface membrane protein of platelets, participates C.Comment: Platelet activation apparently involves disruption of the macromolecular comp C.Comment: Binding sites for von Willebrand factor and thrombin (the latter site with un C.Comment: Glycocalicin, which is approximately coextensive with the extracellular part
 A. Title: Polymorphism of human glycoprotein Ib alpha results from a variable number of
 A.Molecule type: protein
A.Residues: 17-315 <TIT>
R.Hess. D.; Schaller, J.; Rickli, E.E.; Clemetson, K.J.
Eur. J. Blochem. 199, 389-393, 1991
A.Title: Identification of the disulphide bonds in human platelet glycocalicin.
A.Reference number: S16945; MUID:91301149
 10/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
(40/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
88/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
212/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
212/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
30/Region: prollne/threonine-rich 9-residue repeats
 Gaps
 (covalent) #status experimental
 A:Residues: 412-427 <RES>
A:Cross-references: GB:S34436: NID:9249176; PIDN:AAB22152.1; PID:9249177
 F:37,175/Binding site: carbonydrate (Thr) (covalent) #status experimental
 ..
6
 Length 626;
 Indels
 02-540/Domain: transmembrane #status predicted <TRM>-1-626/Domain: intracellular #status predicted <INT>
 Mismatches 11;
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 DB 1;
 A;Status: preliminary; translated from GB/EMBL/DDBJ
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Pred. No. 17;
 A:Molecule type: protein
A:Residues: 224-227:262-270;277-282 <HES>
R:Lopez, J.A.; Ludwig, E.H.; McCarthy, B.J.
J. Biol. Chem. 267, 10055-10061, 1992
 A; Cross·references: GDB:118806; OMIM:231200
A;Reference number: A94173; MUID:87289654
 A: Reference number: I55355; MUID:92250564
 16.28;
 Ouery Match 16.2
Best Local Similarity 45.0
Matches 18; Conservative
 A;Gene: GDB:GP1BA; GP1B
 preliminary
 A; Molecule type: DNA
A; Residues: 412-427
 A; Accession: 155355
 A; Note: variant D
 382
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Search completed: January 30, 2001, 23:09:04 Job time: 6029 sec

Appli Appli Appli Appli Appli Appli Appli

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Sequence 6, Appli
Sequence 6, Appli
Sequence 3, Appli
Sequence 133, Appl
Sequence 133, App
Sequence 133, App
Sequence 1, Appli
Sequence 4, Appli
Sequence 131, Appli
 Sequence 10, Application US/08826246
Patent No. 6044709
GENERAL INFORMATION:
APPLICANT: Falb, Dean
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: THE TREATMENT AND DIAGNOSIS OF
TITLE OF INVENTION: CARDIOVASCULAR DISEASE
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
 US-08-580-5458-6
US-08-22-653A-6
US-08-942-423-3
US-08-942-423-3
US-08-469-318-133
US-08-468-609A-133
US-08-469-318-131
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US-08-469-318-131
US-08-468-609A-131
US-08-468-609A-131
 US-07-935-311A-2
US-08-368-079-2
PCT-US93-07996-2
 CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/799,910
FILING DATE: 13-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/011,787
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: COLUZZI, Laura A
REGISTRATION NUMBER: 7853-078-999
TELECHONENICATION INFORMATION:
TELEFORMUNICATION INFORMATION FOR SEQ. ID NO: 10:
SEQUENCE CHARACTERISTICS:
LEGITH: 156 amino acids
 ALIGNMENTS
 PENNIE & EDMONDS LLP
1155 Avenue of the Americas
 OPERATING SYSTEM: DOS
SOFTWARE: PSESEGO Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/826,246
FILLING DATE: 28-MAR-1997
CLASSIFFCATION: 800
 IBM Compatible
 COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Common
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-826-246-10
 unknown
 TYPE: amino acid
STRANDEDNESS: unk
 New York
RESULT 1
US-08-826-246-10
 STREET:
001088888884444
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 Search time 36.91 Seconds
(without alignments)
41.840 Million cell updates/sec
 Appl
 Appli
 Sequence 3, Appl
Sequence 6, Appl
 Appl
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 Sequence 11,
 Seguence 10,
 Sequence 10
 Sequence 6,
Sequence 11
Sequence 11
 Description
 442
1 VRRQLPVEEPNPAKRLLFLL......EPSDYALDLSTFLQQHPAAF
 Sequence
 Sequence
Sequence
Sequence
 Sequence
Sequence
Sequence
Sequence
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 Sequence
 Sequence
 Sequence
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Compugen Ltd
 US-07-821-7178-6
US-08-119-2628-6
US-08-13-2628-11
US-08-234-265A-11
US-09-035-648-24
US-08-237-919-2
 US-08-641-356-2
US-08-545-860D-55
PCT-US94-04496-55
US-08-651-818A-2
 Total number of hits satisfying chosen parameters:
 PCT-US95-05518-2
US-08-854-585-2
 US-08-944-495-10
US-09-126-640-11
US-09-356-952-3
 PCT-US95-05512-2
 -08-164-292B-2
 US-08-641-356-3
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 JS-08-382-184-3
 -08-530-165-2
 -08-530-165-3
 174772 segs, 17957048 residues
 US-08-799-910-10_COPY_71_156
 SUMMARIES
 GenCore version
Copyright (c) 1993 - 2000
 2001, 22:06:25
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

 protein search, using sw model

 BLOSUM62
Gapop 10.0 , Gapext 0.5
 Issued_Patents_AA:*
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Maximum DB seq length: 200000000
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 January 30,
 Length
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Match
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Perfect score:
 Scoring table:
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 Searched:
 Database
 : 00
 Result
No.
 Run
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ZIP: 14603
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
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 NAME: Timain, Sudan J.
REGISTRATION NUMBER: 34,10.
REFERENCE/DOCKET NUMBER: 2
TELECOMMUNICATION INFORMATION
TELEPHONE: (716) 263-1636
 Lopez, Jose A.
Chung, Dominic W.
 TELEPHONE: (716) 263-1636
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
 Fujikawa, Kazuo
 610 amino acida
 MOLECULE TYPE: protein
PUBLICATION INFORMATION
 amino acid
 TOPOLOGY: linear
 CITY: Rochester
STATE: New York
 5615-5619
 GENERAL INFORMATION:
FILING DATE:
 STRANDEDNESS
 ADDRESSEE:
 TITLE: Ĭe
JOURNAL:
VOLUME: 8
 COUNTRY:
 AUTHORS:
AUTHORS:
 STREET:
 AUTHORS:
 AUTHORS
 AUTHORS
 g
 AUTHORS: Houghten, Richard A. AUTHORS: Vincete AUTHORS: Vincete, Vincete AUTHORS: Vincete, Vincete TITLE: Proteolytic fragments and synthetic TITLE: Peptides that block the binding of von Willebrand factor to the DOCUMENT NUMBER: EP 0 317 278 A2
 platelet glycoprotein Ib: A transmembrane protein with homology to leucheritch alpha-2-glycoprotein
 APPLICANT: Miller, Jonathan L.
APPLICANT: Cunningham, David
APPLICANT: Lyle, Vicki A.
APPLICANT: Lyle, Vicki A.
TITLE OF INVENTION: MUTATIONS RENDERING PLATELET
TITLE OF INVENTION: GLYCOPROTEIN ID ALPHA LESS REACTIVE
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle
STREET: Clinton Square, P.O. Box 1051
 1478 TSPLTPAMSPMSPNIPSHPVESTSSYAHOLRMROOQOOTHPALY 1523
 54 -- PVSPVLEPF--NLTSEP----SDYALDLSTFLQQ----HPAAF 86
 ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NOMBER: US/07/821,717B
FILING DATE: 15-JAN-1992
CLASSIFICATION: 424
 RELEVANT RESIDUES IN SEQ ID NO: 6: FROM 0 TO 610
 AUTHORS: Lopez, Jose A.
AUTHORS: Chung, Dominic W.
AUTHORS: Fujikawa, Kazuo
AUTHORS: Hagen, Frederick S.
AUTHORS: Papayannopoulou, Thalia
AUTHORS: Roth, Gerald J.
TITLE: Cloning of the alpha chain of human
 Proc. Natl. Acad. Sci. U.S.A
 AUTHORS: Zimmerman, Theodore S. AUTHORS: Ruggeri, Zaverio M.
 Sequence 6, Application US/07821717B Patent No. 5298239 GENERAL INFORMATION:
 NAME: Timain, Susan J.
REGISTATION UNDRER: 34,103
REFERENCE/DOCKET NUMBER: 2088
TELECOMMUNICATION INFORMATION:
TELEFAN: (716) 263-1636
TELEFAN: (716) 263-1606
INFORMATION FOR SEQ ID NO: 6:
 CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
 SEQUENCE CHARACTERISTICS:
LENGTH: 610 amino acids
TYPE: amino acid
STRANDEDNESS:
 PUBLICATION INFORMATION:
 MOLECULE TYPE: protein
 TOPOLOGY: linear
 5615-5619
AUG-1987
 CITY: Rochester
STATE: New York
 JOURNAL: VOLUME: 6
 COUNTRY:
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with hom
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6
 Ouery Match
Best Local Similarity 45.0%; Pred. No. 2.7;
Matches 18; Conservative 2; Mismatches 11; Indels
 APPLICANT: Miller, Jonathan L.
APPLICANT: Cunningham, David
APPLICANT: Cunningham, David
APPLICANT: Lyle, Vicki A.
APPLICANT: Finch, Clara N.
TITLE OF INVENTION: MUTATIONS RENDERING PLATELET
TITLE OF INVENTION: GLYCOPROTEIN ID ALPHA LESS REACTIVE
NUMBER OF SEQUENCES:
COPRESPONDENCE ADDRESS:
 glycoprotein Ib: A transmembrane protein leucine-rich alpha-2-glycoprotein protein proces. Natl and a second protein a second protein and a second protein and a second protein and a second protein and a second protein and a second protein a second pro
 6: FROM 0 TO 293
 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/119,262B FILING DATE: 09-SEP-1993 CLASSIFICATION: 424
 366 PIPSPITSEPVPEPAPNMTILEPIPSPITPEP---TSEPA 402
 36 PAPLP-----PEDAPNAASLAPTPVSPVLEPFNLTSEPS 69
 E: Nixon, Hargrave, Devans & Doyle Clinton Square, P.O. Box 1051
 : Roth, Gerald J.
Cloning of the alpha chain of human
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/821,717
FILING DATE: 15-JAN-1992
ATTORNEY/AGENT INFORMATION:
HUBLICATION DATE: 24-MAY-1989
RELEVANT RESIDUES IN SEQ ID NO:
US-07-821-7178-6
 Hagen, Frederick S.
Papayannopoulou, Thalia
 RESULT 6
US-08-119-262B-6
; Sequence 6, Application US/08119262B
; Patent No. 5492809
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Methods and Compositions for Modulating Heterotypic E-cadherin Interactions with T Lymphocytes
 1 VRRQLPVEEPNPAKRLLFLLLTIVFC-----51LMAEEGVPAPLPPEDAPNAASLA--- 51
 Length 878;
 DB 1; Length 878;
 31; Indels
 631 VPNWTIQYNDPTQESIILKP-KMALEVGDYKINLKLMDNQN 670
 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
 -- PTPVSPVLEPFNLTSEPSDYALDLSTFLOOH 82
 DB 4;
 TITLE OF INVENTION: Methods and Composition IIILE OF INVENTION: E-cadherin Interaction: NUMBER OF SEQUENCES: 8 CORRESPONDENCE ADDRESS: ADDRESSEE: Wolf, Greenfield & Sacks P.C. STREET: 600 Atlantic Avenue
 Mismatches
 Score 68.5;
Pred. No. 9;
 15.5%; Score 68.5; 25.7%; Pred. No. 9;
 APPLICATION NUMBER: PCT/US95/05518
FILING DATE: herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/237,919
FILING DATE: 3 May 1994
ATTORNEY/AGENT INFORMATION:
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 Sequence 2, Application PC/TUS9505518 GENERAL INFORMATION:
 NAME: Plumer, Elizabeth R
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B08
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
 NAME: Plumer, Elizabeth R
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: BD
TELECOMMUNICATION INFORMATION:
 15.5%;
25.7%;
 TOPOLOGY: 1.1.
 : 878 amino acids
amino acid
 ATTORNEY/AGENT INFORMATION
 Conservative
 ZIP: USA
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Flore:
 TELEFAX: 617-720-2441
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
 617-720-244]
 INFORMATION FOR SEQ ID NO SEQUENCE CHARACTERISTICS
 MOLECULE TYPE: protein US-08-237-919-2
 Ouery Match
Best Local Similarity
Matches 26; Conserva
 Ouery Match
Best Local Similarity
 Boston
 TELEPHONE:
 CITY: BOS
STATE: MA
COUNTRY:
 PCT-US95-05518-2
 RESULT
 qq
 ô
 APPLICANT: Brenner, Michael B
APPLICANT: Brenner, Michael B
APPLICANT: Cepek, Karyn L
TITLE OF INVENTION: Methods and Compositions for
TITLE OF INVENTION: Modulating Heterotypic E-cadherin Interactions with T lymphocy
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks P.C.
STREET: 600 Atlantic Avenue
 Gaps
 ;;
 Length 739;
 Indels
 391 FMOSSSAKOKTPPPVAPKPAVKSSSSOPVTPVSPVWSPGVAPTOP 435
 25 FCQILMAEEGVPAPLPPEDAPNAASLAP-TPVSPVLEPFNLTSEP 68
 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/237,919
 19;
 ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: JBM COMPALIADE
OPERATING SYSTEM: Windows95
SOFTWARE: Fastes0 for Windows Version 2.0
APPLICATION NUMBER: US/09/035,648
 Score 69.5; D
Pred, No. 5.6;
 8; Mismatches
 07334/003001
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
 ATTORNEY/AGENT INFORMATION:
NAME: Metklejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
 PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/818,829
 Sequence 2, Application US/08237919
Patent No. 5610281
 REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
 TELEX: 200154
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 37.8%;
Matches 17; Conservative
 LENGTH: 739 amino acids
TYPE: amino acid
 MOLECULE TYPE: protein FRAGMENT TYPE: internal
 COUNTRY: USA 21P: 02210 COMPUTER READABLE FORM:
 CLASSIFICATION: 424
 linear
 GENERAL INFORMATION:
 CLASSIFICATION:
 FILING DATE:
 FILING DATE
 STATE: MA
COUNTRY: U
 TOPOLOGY:
 US-09-035-648-24
 US-08-237-919-2
 CITY:
STATE:
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DB 2; Length 286; Indels

Score 65.5; DE Pred. No. 5; 3; Mismatches

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29 LMAEEGVPAPL,PPEDAP---NAASLAPTPVSP 57
 Search completed: January 30, 2001, 22:06:26
Job time: 9705 sec
 Ouery Match
Best Local Similarity 46.9%;
Matches 15; Conservative
 MICROBACTERIAL PROTEINS, MICROORGANISMS PRODUCING THEM AND THEIR USE FOR VACCINES AND FOR THE DETECTION OF TUBERCULOSIS
 ä
 Indels
 COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPENATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/641,356
 STREET: 1755 S. Jefferson Davis Highway, Suite 400
 OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
 DB 1;
 Score 65.5; DB Pred, No. 5; 3; Mismatches
 247 LVAPPPAPAPAPAEPAPAPAGEVAPTFTTP 278
 29 LMAEEGVPAPLPPEDAP---NAASLAPTPVSP 57
 PRICE APPLICATION DATA:
APPLICATION NUMBER: US/08/382,184
FILING BATE: 01-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: OBLON. NORMAN F
REGISTATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 22640720
TELECOMMUNICATION INFORMATION:
 2640720
 Sequence 3, Application US/08641356 Patent No. 5866130
 NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 22
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
 Ouery Match
Best Local Similarity 46.9%;
Matches 15; Conservative
 TELEFAX: 703-413-220
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
ATTORNEY/AGENT INFORMATION:
 LENGTH: 286 amino acids
TYPE: amino acid
STRANDEDNESS:
 LENGTH: 286 amino acids
 GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: MICI
TITLE OF INVENTION: MICI
TITLE OF INVENTION: AND
NUMBER OF SEQUENCES: 3
CORRESPONDENCES: 3
 TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
 TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
 FILING DATE:
CLASSIFICATION: 536
 STATE: Virginia
COUNTRY: U.S.A.
 Arlington
 ADDRESSEE:
ADDRESSEE:
 TELEPHONE:
 LENGTH:
 US-08-382-184-3
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huDEP-1 Homo sap Mammalian Ena (Men Mouse neural Mena+ Mouse neural Mena+ Mouse neural Mena+ Secreted protein A Human secreted pro

Streptococcus p Mycobacterium t Mycobacterium t Mycobacterium t

Sequence:

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Database

Result õ

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genes differentially expressed in cardiovascular disease - used diagnosis, drug screening and treatment of cardiovascular
 Fchd605 gene: differential expression; monocyte; human; foam cell; cardiovascular disease; atherosclerosis; ischaemia; reperfusion; hypertension; restenosis; arterial inflammation; therapy; diagnosis; drug screening; marker.
 ALIGNMENTS
 W64322
Y39083
Y38945
Y17067
Y39225
Y39082
W81746
 R66460
W36984
 R60799
W14584
 Y32063
Y39224
 W27646
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 Y68748
 Y39176
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 W32418
 Y49151
 W36006 standard; Protein; 156 AA
 (MILL-) MILLENNIUM PHARM INC
 97US-0799910,
 97WO-US02291
 Human Fchd605 gene product.
 03-MAR-1998 (first entry)
 WPI; 1997-424966/39

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 N-PSDB; T94471.
 Homo sapiens.
 WO9730065-A1.
 14-FEB-1997;
 13-FEB-1997;
16-FEB-1996;
 21-AUG-1997
68.5
68.5
67
67
 64.5
64.5
64.5
 Falb DA;
 W36006;
 New
RESULT
 M3600
 Mutant platelet gl
Mutated platelet g
Platelet glycoprot
Gene 036 product d
 Protein encoded by
Amino acid sequenc
Platelet glycoprot
 Streptococcus pneu
Human PRO1431 (UNO
Sequence of human
 Human E-cadherin p
 Human Fchd605 gene
 / Search time 54.97 Seconds
(without alignments)
53.496 Million cell updates/sec
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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 GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
 Total number of hits satisfying chosen parameters:
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 US-08-799-910-10_COPY_71_156
 442
1 VRRQLPVEEPNPAKRLLFLL.....
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Maximum Match 100%
Listing first 45 summaries
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 OM protein - protein search, using sw model
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Y68821
R51116
R56664
R89436
W18201
W25790
W25790
W25790
R85660
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 length: 0
length: .2000000000
 DB
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 Length
 Query
Match
 100.0
 442
79.5
71.5
71.5
71.5
71.5
69.5
68.5
68.5
68.5
 Minimum DB seq
Maximum DB seq
 Score
 Title:
Perfect score:
 Scoring table:
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Rape abscission/de Streptococcus pneu Amino acid sequenc

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610 AA;

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Sequence
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 1423 irrnsaiekraaatsgpngaaagpisttlvtvsgavatdeplplplsp----aassstl 1477
 (pro) urokinase, streptokinase, anisoylated plasminogen-streptokinase activator complex, tPA analogues or a protease, allowing localisation of the thrombolytic agent to a thrombus.
three-dimensional coordinates obtained from the crystals, is useful for identifying an agent that stabilizes the Ras-Sos complex. The crystals are also useful for identifying agents that inhibit the formation of Ras-Sos complex. Rs and Sos fragments are useful for prowing a crystal of a protein-ligand complex. Agents that stabilize or inhibit the formation of Ras-Sos complex are useful in the treatment of cancer. The present sequence represents a Drosophila
 Gaps
 1 VRRQLPVE------EPNPAKRLLFLLLTIVFCQILMAEEGVPAPLPPEDAPNAASLAPT 53
 and
 Platelet; glycoprotein; imaging; thrombolytic agent; tissue plasminogen activator; tPA; pro-urokinase; urokinase; streptokinase; Bernard-Soulier disease; thrombus; aggregation; anisoylated plasminogen-streptokinase activator complex; adhesion;
 A substitution in platelet glycoprotein ib alpha (Leucine 57 to Phenylalanine) underlies a form of Bernard-Soulier disease. The mutated glycoprotein can be used in compositions to inhibit platelet aggregation/adhesion. The glycoprotein may be labelled used as an imaging agent and may also be bound to a thrombolytic agent, preferably tissue plasminogen activator (tPA),
 Platclet glycoprotein Ib alpha with an amino acid substn at position 57 - has reduced reactivity with Yon Willebrand factor, and can be used to inhibit platelet aggregation and inhibition
 25;
 DB 21; Length 1596;
 37; Indels
 1478 tspltpamspmspnipshpvestsssyahqlrmrqqqqqthpaiy 1523
 54 -- PVSPVLEPF--NLTSEP----SDYALDLSTFLQQ----HPAAF 86
 Lyle VA, Miller JL;
 18.0%; Score 79.5; Di
28.3%; Pred. No. 4.2;
iive 14; Mismatches
 (UYNY) UNIV NEW YORK STATE RES FOUND.
 Claim 1; Columns 3-8; 20pp; English.
 R51116 standard; protein; 610 AA
 Platelet glycoprotein Ib alpha.
 91US-0770968.
 91US-0770968
 (first entry)
 Ouery Match
Best Local Similarity 28.3%
Matches 30, Conservative
 Finch CN,
 WPI; 1994-100287/12.
 1596 AA;
 Cunningham D,
 Homo sapiens
 07-0CT-1991;
 23-SEP-1994
 07-OCT-1991;
 15-JAN-1992;
 US5298239-A.
 Sos protien
 29-MAR-1994
 inhibition.
 Seguence
 R51116;
 R51116
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A substitution in platelet glycoprotein Ib alpha (Leucine 57 to Phenylalanine) underlies a form of Bernard-Soulier disease. The mutated glycoprotein can be used in compositions to. Inhibit the platelet aggregation/adhesion. The glycoprotein may be labelled and used as an imaging agent and may also be bound to a thrombolytic agent, preferably tissue plasminogen activator (tPA), (Pro) urokinase, streptokinase, anisoylated plasminogen-streptokinase activator complex, tPA analoques or a protease, allowing localisation of the thrombolytic agent to a thrombus.
 Gaps
 Gaps
 Platelet; glycoprotein; imaging; thrombolytic agent; tissue plasminogen activator; tPA; pro-urokinase; urokinase; streptokinase; Bernard-Soulier disease; thrombus; aggregation; anisoylated plasminogen-streptokinase activator complex; adhesion;
 Platelet glycoprotein Ib alpha with an amino acid substn at position 57 - has reduced reactivity with Yon Willebrand factor, and can be used to inhibit platelet aggregation and inhibition
 6
 9
 Length 610;
 Length 610;
 Indels
 Indels
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Pred. No. 9.5;
2; Mismatches 11;
 ---tsepa 402
 DB 15;
 366 ptpspttsepvpepapnmttleptpspttpep---tsepa 402
 36 PAPLP-----PEDAPNAASLAPTPVSPVLEPFNLTSEPS 69
 69
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 36 PAPLP----PEDAPNAASLAPTPVSPVLEPFNLTSEPS
 16.2%; Score 71.5; DF
llarity 45.0%; Pred. No. 9.5;
Conservative 2; Mismatches
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 Mutant platelet glycoprotein Ib alpha.
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 16.2%;
 91US-0770968
 91US-0770968
 92US-0821717
 (first entry)
 Conservative
 Claim 1; ; 20pp; English.
 Finch CN,
 =
 WPI; 1994-100287/12.
 Local Similarity
nes 18; Conserv
 Best Local Similarity
Matches 18; Conserv
 610 AA;
 Cunningham D,
 Homo sapiens
 07-OCT-1991;
 07-OCT-1991;
 15-JAN-1992;
 23-SEP-1994
 US5298239-A.
 29-MAR-1994
 Inhibition.
Query Match
Best Local S.
Matches 18
 Sequence
 Query Match
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2

us-08-799-910-10\_copy\_71\_156.rag

pneumococcal surface protein; vaccine; otitis media;

Streptococcus pneumoniae strain Rct123

meningitis; bacteraemia; pneumonia.

PspA;

Streptococcus pneumoniae PspA central region

(first entry)

28-OCT-1997

W14578 standard; Protein; 204 AA

/note= "unidentified amino acid" /note= "unidentified amino acid"

Location/Qualifiers

Misc-difference Misc-difference

```
ä
 This protein is encoded by gene 036 (see T91708), which was identified by differential display analysis as being expressed at a higher level in normal colon tissues than in cancercus colon tissues. Gene 036 is a candidate tumeur suppressor gene. A correlation was found between an increase in the expression level of gene 036 and a decrease in a colon cell's tumour potential. Hence, methods that increase the level of expression of gene 036 may inhibit or slow the progression to tumours and cancer, e.g. colon cancer. The 036 protein is used in claimed methods for treating a patient suffering from a disorder associated with insufficient expression of gene 036 protein, and for identifying compounds that modulate 036 protein activity. Such compounds are useful in the diagnosis, prevention and treatment of tumours and
 Gaps
 Gene 036 product differentially expressed in colon tumour cells.
 .
6
 Colon tumour; colon cancer; differential expression; gene 036; human; diagnosis; gene therapy; tumour suppressor.
 Gene 036 with reduced or amplified expression in tumour cells used, optionally with genes 097, 030 and 056 or their protein products, for diagnosis and treatment of colonic cancer
 Indels
 36 PAPLP-----PEDAPNAASLAPTPVSPVLEPFNLTSEPS 69
 Pred. No. 9.5; Hismatches
 standard; Protein; 739 AA.
 English
Best Local Similarity 45.0%;
Matches 18; Conservative
 97WO-US04191
 11-MAR-1998 (first entry)
 (MILL-) MILLENNIUM PHARM.
 Claim 38; Fig 2; 117pp;
 WPI; 1997-470615/43.
N-PSDB; T91708.
 AA;
 WO9733551-A2
 14-MAR-1997;
 15-MAR-1996;
 Homo sapiens
 18-SEP-1997
 Shyjan AW;
 Sequence
 W25790;
 W25790
 ò
```

Streptococcus pneumoniae surface protein PspC and truncated PspA used in vaccines for protecting animals against S.pneumoniae infection

Example 6; Fig 13; 296pp; English.

ŝ

Hollingshead J;

Briles DE, Brooks-Walter A, Crain MJ, McDaniel LS, Swiatlo E, Tart R, Yother

WPI; 1997-202002/18.

(UABR-) UAB RES FOUND

96WO-US14819

16-SEP-1996; 15-SEP-1995;

20-MAR-1997.

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of the alpha helix region and some of the proline-rich region, of pneumococcal surface protein A (PspA) of Streptococcus pneumoniae strain Rc123. Comparison of the N-reminal and central regions (W1453-57 and W14562-91) of PspA polypeptides from different pneumococcal strains can be used to divide the strains into several families based on sequence homologies. PspA polypeptides, or fragments of them can be used in vaccines to protect animals against S. pneumoniae infection and hence for the prevention of diseases such as otitis media, meningitis, bacteraemia and pneumonia. The sequence of the 3' half of the PspA alpha -halical region and the immediate 5' tip of the coding sequence are likely to be the critical sequences for predicting PspA cross-reactions and vaccine
 Gaps
 This sequence shows the central portion, including the C-terminus
 19
 6 PVEEPNPAKRLLFLLLTIVFCQILMAEEGVPAPLPPEDAPNAASLAPTPVSPVLEP
 Length 204;
 Indels
 DB 18;
 22;
 Score 68.5; DI
Pred, No. 5.4;
 Mismatches
 Ä
 ۳
ش
 Y99428 standard; Protein; 370
 15.5%;
ilarity 32.1%;
Conservative
 Query Match
Best Local Similarity
Matches 18; Conserv
 103 papqpapape---
 204 AA;
 Seguence
 Y99428;
 RESULT 10
 QQ
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Gaps

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FCQILMAEEGVPAPLPPEDAPNAASLAP-TPVSPVLEPFNLTSEP 68

Length 739;

DB 18;

Score 69.5; D Pred. No. 19; 8; Mismatches

15.7%; ilarity 37.8%; Conservative

Ouery Match Best Local Similarity Matches 17; Conserv

22

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RESULT W14578

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2

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R85487;
 Peptide
 RESULT 12
R85487
 Domain
 Domain
 Domain
 888888
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 ä
 A37022 to A37144 encode the new isolated human transmembrane, receptor or secreted PRO polypeptides given in Y99340 to Y99462. The transmembrane and receptor PRO proteins can be used for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interactions. The polypeptides and nucleotide sequences encoding then have various industrial applications, including uses as pharmaceutical and diagnostic agents. A37145 to A37330 represent PCR primers and hybridisation probes used in the isolation of the PRO polypeptides from the present invention.
secreted PRO polypeptides, useful for screening of potential peptide or
small molecule inhibitors of the relevant receptor/ligand interactions
 Gaps
 E-cadherin is a.cell adhesion molecule that is also known as uvomorulin, L-CAM and Cell CAM 120/80. The DNA encoding hEC was obtd. by screening normal human liver and hepatocellular carcinoma ciNA libraries and a colonic epithelial cell cDNA library. The following sequences are specifically claimed: AAS 1-878; 151-878; 30 sequential AAS from AAS 108-878; AAS 1-150; AAS 178-289; AAS 290-401; AAS 402-513; AAS 178-513; AAS 151-703; AAS 1703-788; 181-401; AAS 104-878; 1050-513; ABS 105-510; AAS 105
 Human epithelial-cadherin; E-cadherin; cell adhesion molecule; CAM;
 used to
prophylaxis
 ..
6
 Length 370;
 32 EEGVPAPLPPEDAPNA-ASLAPTPVSPVLEPFNLTSEPSDYALDLSTFL 79
 Indels
 Purified human E-cadherin protein and nucleic acid develop prods. for diagnosis, prognosis, therapy and of t-cadherin disorders, e.g. malignancies
 15.5%; Score 68.5; DB 21;
38.8%; Pred. No. 11;
Live 6; Mismatches 15;
 Sequence of human liver E-cadherin
 uvomorulin; L-CAM; Cell CAM 120/80
 Claim 12; Fig 178; 773pp; English.
 Claim 1; Page 59-63; 97pp; English
 Ä.
 R55060 standard; Protein; 878
 92US-0978897
 93WO-US11097
 (first entry)
 Conservative
 Rimm DL;
 WPI; 1994-183426/22.
N-PSDB; Q65487.
 Ouery Match
Best Local Similarity
Matches 19; Conserv
 (UYYA) UNIV YALE.
 370 AA;
 Homo sapiens
 16-NOV-1993;
 17-NOV-1992;
 08-NOV-1994
 WO9411401-A.
 26-MAY-1994.
 Morrow JS,
 Seguence
 Π
 RESULT
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Gaps
 1. VRRQLPVEEPNPAKRLLFLLTIVFC-----51LMAEEGVPAPLPPEDAPNAASLA--- 51
1705-2204; 2458-2775; DNA encoding at least 30 AAs selected from AAs 308-878. The prods. can be used in the diagnosis, prognosis, therapy and prophylaxis of conditions involving improper E-cadherin expression, Sultable dosages for i.v. admin. of a protein are
 151...702 ---. .
//abel- Extracellular_domain (amino acids 1-552
/note- "the extracellular domain (amino acids 1-552
 Inhibiting adhesion of T lymphocytes with E-cadherin - useful for isolating agents to treat auto-immune diseases e.g. Crohn's disease, psoriasis, etc
 E-cadherin: T-lymphocyte; alpha-E,beta-7 integrin; cell adhesion; autoimmune disease; Crohn disease; psoriasis.
 of the mature protein) is the preferred region for generation of peptides of the invention"
 33;
 ģ
 Length 878;
 The human E-cadherin protein precursor (R85487) is expressed
 Indels
 631 vpnwtigyndptgesiilkp-kmalevgdyklnlklmdngn 670
 PTPVSPVLEPFNL,TSEPSDYALDLSTFLQQH 82
 31;
 DB 15;
 /label- Transmembrane_domain 727..876 /label- Cytoplasmic_domain
 Score 68.5; DB
Pred. No. 30;
1; Mismatches
 Disclosure; Page 70-75; 103pp; English.
 1..150
/label-_Sig_peptide
 Location/Qualifiers
 (BGHM) BRIGHAM & WOMENS HOSPITAL.
 R85487 standard; Protein; 878 AA
 11;
 15.5%; 25.7%; 1
 95WO-US05518.
 Human E-cadherin precursor.
 18-MAR-1996 (first entry)
 Conservative
 ..726
 20-500 mcg/kg body wt.
 Brenner MB, Cepek KL;
 WPI; 1995-392921/50.
N-PSDB; T05764.
 Local Similarity
les 26; Conserv
 878 AA;
 Homo sapiens
 WO9529693-A1
 03-MAY-1995;
 03-MAY-1994;
 09-NOV-1995
 Query Match
Best Local Si
Matches 26;
 Sequence
```

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Search completed: January 30, 2001, 22:05:37
Job time: 11886 sec
 FNLTSEP
 Sequence
 62
 g
 ô
 793 ittvscgkmaaptrntcttgitdppppdgspnitsvshnsvkvkfsgfeashgpikayav 852
LTIVFCQILMA-----EEGVPAPLPPEDAPNAASLAPTPVSPVLEPFNLTSEP-SDYAL 73.
 Detection of modulators of Mena and Ena-VASP-like genes and proteins - used in control of cytoskeletal dynamic events in normal and abnormal cell morphology, adhesion, motility, growth and
 protein: mammalian Ena; Enabled; Ev1 protein; cytoskeleton; morphology; cell adhesion; cell differentiation; cell growth;
 This polypeptide comprises murine Mena (mammalian Ena) that sh significant amino acid similarity to Drosophila Ena and which exhibits a broad pattern of tissue distribution in neurons,
 "Ena-VASP homology domain 1 (EVH1)"
 305..310
/note= "mediates binding to profilin"
 /note- "mediates binding to profilin"
 Wehland J;
 (GBFB) GES BIOTECHNOLOGISCHE FORSCHUNG MBH (HUTC-) HUTCHINSON CANCER RES CENT FRED.
 'note- "O-phosphorylated"
 ..175
 "LERER repeat"
 "LERER repeat"
 "LERER repeat"
 "LERER repeat"
 'note- "LERER repeat"
 Example 1; Page 54-56; 77pp; English.
 Soriano P,
 Cocation/Qualifiers
 W37148 standard; Protein; 541 AA.
 97WO-US11669
 96US-0675815
 06-JUL-1998 (first entry)
 /note= "Li
176..180
/note= "Li
 .170
 56..160
 . 203
 207..211
 316..321
 Gertler FB, Niebuhr K,
 /note=
 'note=
 'note-
 note-
 853 ilttgeaghpsa 864
 cell motility; mouse.
 Mammalian Ena (Mena).
 74 DLSTFLOQHPAA 85
 WPI: 1998-101197/09.
N-PSDB: V02996.
 differentiation
 Mena protein;
 Modified-site
 Mus musculus.
 Binding-site
 Binding-site
 WO9801755-A1
 03-JUL-1997;
 05-JUL-1996;
 15-JAN-1998
 Peptide
 Pept 1de
 Peptide
 Peptide
 Peptide
 Peptide
 W37148;
 Domain
 15
 21
 RESULT
W37148
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Gaps
 6 PVEEPNPAKRLLFLLLTIVFCQILMAEEGVPAPLPPEDAPN----AASLAPTPVSPVLEP 61
 haematopoletic ceils. Its amino acid sequence was deduced from a cDNA clone (see V02996) obtained from a mouse embryonic stem cell. CDNA library.

(EVI, see V02997), encoding novel proteins Mena and Ena-VASP-like (EVI, see V02997), encoding novel proteins Mena and EVI (see W37149) are disclosed. Mena and EVI proteins have a discrete, EVII functional domain responsible for Mena binding to Listerie, and to the cytoskeletal proteins 2yxin and vinculin. The EVII domain of Mena is also responsible and sufficient for targeting localisation of Mena and Mena-based fusion proteins to focal adhesions, and to the surface of Listeria cells at the polar site of induction of actin comet tail formation. Based on the disclosed Mena and EVI promation, a variety of methods and compositions are provided for screening, isolating and characterising endogenous and
 exogenous factors, drugs and therapeutic agents useful to evaluate and/or control cytoskeletal dynamic events involved in normal and abnormal cell morphology, adhesion, motility, growth and/or differentiation. A method of detecting a modulator of Mena activity/expression is claimed.
 Length 541;
 Indels
fibroblasts, kidney epithelium, muscle, neural crest and
haematopoietic cells. Its amino acid sequence was deduce
 23;
 15.2%; Score 67; DB 19;
ilarity 29.9%; Pred. No. 25;
Conservative 4; Mismatches 23;
 268 paesptpqglvl--
 Query Match
Best Local Similarity
Matches 20; Conserv
 541 AA;
 312 lpstgpp 318
```

5

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09y4f5 homo sapien 09ymx0 lymantria d P89920 oat blue dw 091570 streptococc 09y729 drosophila 039492 chlamydomon 089370 paramecium 091567 streptococc 091ay streptococc 091ay streptococc 091ay streptococc 09y728 drosophila 08231 drosophila 095x31 arabidopsis 089037 rattus norv 084465 paramecium 062537 drosophila 095x31 arabidopsis 089037 rattus norv 084465 paramecium 091az1 streptococc 091ay streptococc
 091570
099729
039492
089370
091567
 Q9L565
P74745
Q96716
 045522
084565
062537.
091569
090728
095X31
 Q9Y4F5
Q9YMX0
 084465
Q9LA21
 09LAY4
09ROT4
09NP71
P70433
 P89920
 Q9LAY2
Q9LAY0
 106.5
106
106
105.5
105
105
 104.5
104.5
104.5
104.5
 104
103
102.5
102.5
 101
101.5
101.1
101
101
101
101
101
101
 January 30, 2001, 22:04:55; Search time 64.84 Seconds (without alignments) 281.993 Million cell updates/sec
 1 MCHSRSCHPTMTILQAPTPA......EPSDYALDLSTFLQQHPAAF 156
 GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
 Total number of hits satisfying chosen parameters:
 374700 segs, 117207915 residues
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 OM protein - protein search, using sw model
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 US-08-799-910-10
823
 Minimum DB seq length: 0
Maximum DB seq length: 200000000
```

Title: Perfect score:

Run on:

Scoring table: Sequence:

Searched:

## ALIGNMENTS

| ALIGNMENTS                                 | RESULT 1 075353                   | ID 075353 PRELIMINARY; PRT; 193 AA.   | AC 075353;<br>D7 01-NOV-1998 /TFEMBITE 009 CTOSTOCK | 01-NOV-1998 (TrEMBLrel. 08,      | DT 01-MAY-1999 (TEMBLE). 10, Last annotation update) | OF TEXT PROPER. | OS Homo sapiens (Human). | Eukaryota, Metazoa, Chordata, | OC Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. OX NCBI_TaxID=9606; |                                                                  | 35                                                          | RT "IEX-1L, an apoptosis inhibitor involved in NF-kappaB-mediated cell | DR EMBL: AF039067: AAC32558 1. | DR EMBL; AF071596; AAC72344.1;           |                     |                   | 03 74, 52522 771 5, 52,         | Rest Total Similarity 70 ps. 2001e //1.5; UB 4; Length 193; | /o.os; Fied. NO. 8.le-04;<br>/ative 1: Mismatches 3: Indole 27. |               | OY 1 MCHSRSCHPTMT1LQAPTPAPSTIPGPRRGSGPEIFTFDPLPEPAAPAGRPSASRGHRK 60 | DD ) WCHSCHOPWRTIOD DESTINATION OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERT | ı                                | Qy 61 RSRRVLYPR         |                    | UD OI KSKRVSLESSGEIKKSGHSKCALPWSHWGTIRLOSLDLICLLFCLFLVRRQLPVEEPNPA 120 | Qy 84 KRLLFLLTIVFCOILMAEEGVPAPLPPEDAPNAASLAPTPVSPVLEPFNITSEPSDVAI 143 |                | UD 121 KKLLFLLTIVFCQILMAEEGVPAPLPPEDAPNAASLAPTPVSPVLEPFNLTSEPSDYAL 180 | Oy 144 DLSTFLQQHPAAF 156 |
|--------------------------------------------|-----------------------------------|---------------------------------------|-----------------------------------------------------|----------------------------------|------------------------------------------------------|-----------------|--------------------------|-------------------------------|-----------------------------------------------------------------------------------|------------------------------------------------------------------|-------------------------------------------------------------|------------------------------------------------------------------------|--------------------------------|------------------------------------------|---------------------|-------------------|---------------------------------|-------------------------------------------------------------|-----------------------------------------------------------------|---------------|---------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------|-------------------------|--------------------|------------------------------------------------------------------------|-----------------------------------------------------------------------|----------------|------------------------------------------------------------------------|--------------------------|
| Database : SPTREMBL_15:*<br>1: SP_archea:* | 2: sp_bacteria:*<br>3: sp_fungi:* | 4. Sp_luman:*<br>5. sp_invertebrate.* | 6: Sp_mammal: *                                     | 7: sp_mhc:*<br>8: sp_organelle:* |                                                      |                 | 12. uV_L_Cump            | 13: sp_vertebrate:*           |                                                                                   | Pred. No. is the number of results predicted by chance to have a | and is derived by analysis of the total score distribution. | SUMMARIES                                                              | Ouery                          | NO. SCORE MATCH LENGTH DB ID Description | 5 93.7 193 4 075353 | 14.9 423 4 O9NXH8 | 114.5 13.9 1668 4 015026 015026 | 114.5 13.9 2971 4 Q9Y5L9 Q9y51                              | 114 13.9 3247 12 065553                                         | 1011 3 000084 | 109.5 13.3 552 10                                                   | 109.5 13.3 1315 10 Q9SPMO                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | 109 13.2 285 3 P78977 Parrowia 1 | 109 13.2 3325 12 OGTRMG | 108.5 13.2 233 2 C | 107.5 13.1 203 2 Q9RCX9                                                | 581 5 Q20517 Q20517                                                   | 107 13.0 426 2 | 12 098457 09845                                                        |                          |

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RAM Adams M.D., Celulares S.E., Li P.W., Hoskins R.A., Galle R.F.
Amanatides D.G., Scherar S.E., Li P.W., Hoskins R.A., Galle R.F.
Amanatides D.G., Scherar S.E., Li P.W., Hoskins R.A., Galle R.F.
George R.A., Levis S.E., R. Richards S., Ashburnar M., Henderson S.N.,
R.A. Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeliffer B.D.,
R.A. Andrews Pfannkoch C., Baldwin D.
Ballew R.M., Basu A., Baxendale D., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Beenos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Baltew R.M., Basu A., Baxendale D., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Burtis K.C., Bucam D.A., Bartler H. Gadleu E., Center A., Chandre I.,
R.A. Burtis K.C., Bucam D.A., Bartler H. Gadleu E., Center A., Chandre I.,
R.A. Dolcher A., Dong Z., Gurskseln P., Brottler P., Brottler P.,
R.A. Dolcher A., Dong C.C., Ferraz C., Ferriars S., Dunn P.,
R.A. Dolcher A., Dong C.C., Ferraz C., Ferras C., Ferriars S., Pleischman W.,
R.A. Dolcher A., Havey D., Helman T.J., Hernendez J.R., Houck J.,
R.A. Hurtis N.L., Havey D., Helman T.J., Herner W. M., Glasser K.,
Allali M., Kalush F., Rarpen G.H., Rez J., Kenlp D., Lai Z.,
Lasko P., Lei Y., Levistsky A.A., Li J., Li J., Lin X.,
Allali M., Moy M., Murphy B., Murphy D., Muslon D.L.,
R.A. Barzolo M. P., Hartei B., McInton K.J., Percent D., Percent J.,
Shue B.C., Siden-Klamos I., Simpson M., Strong R., Sun R.,
Shue B.C., Siden-Klamos J., Simpson M., Strong R., Sun R.,
R. Jeng X., Wassarman D.A., Wellbr G.M., Welssenben J.,
R. Walles R., Wochage T., Wolley K.C., Wu D., Yang G., Zhon X.,
R. Wassarman D.A., Welnsch C., Wence E., Wang X.,
R. Wassarman D.A., Welnsch C., Scheeler F., Shen H.,
Shue B.C., Siden-Klamos J., Simpson M., Strong S., Yao Q.A.,
R. Yen R., Wessarman D.A., Wellsch G.M., Welssenben J.,
R. Yang R., Woodage T., Wolley R., Wolley S., Yao Q.A.,
R. Yen R., Wessarman D.A., Wolley S., Yao Q., Zhon G., Schence 287:2185-2195(2000)
B. Will. Angere B., Shong S., Polley S., Song C., Schence 287:2185-2195(2000)
B
 Drosophila melanogaster (Fruit fly).
Eukaryote: Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
 342 TIEVLDSIPETPAP---PPPPKTAPPELPVLKPTEEDPPTPDLRRTLSDNEHRKSRRVTR 398
 68 P-----TIVFCQILMAEEGVPAP 108
 399 PLSQLETFKDMLLVNAQLYIKENVPHPPKILIGRLKDEDPEEHT-----VLJIPQSPKPSP 453
 10 TMIILQA---PTPAPSTIPGPRRGSGPEIFTFDPLPEPAAAPAGRPSASRGHRKRSRRVLY 67
 109 LPPEDAPNAASLAPTPVSPVLEPFNLTSEPSDY-----ALDLSTFLQQHPAAF 156
 DB 5; Length 649;
 13.7%; Score 112.5; DB 5; Length (25.8%; Pred. No. 0.013;
Live 26; Mismatches 67; Indels
 FBGn0034279; CG18635.
649 AA; 74414 MW; 6471AC52B49F9AE9 CRC64;
 STRAIN-BERKELEY;
MEDLINE-20196006; Pubmed-10731132;
 Query Match 13.79
Best Local Similarity 25.89
Matches 46; Conservative
 PRELIMINARY;
 SEQUENCE FROM N.A.
 FLYBASE;
 SEQUENCE
 09P944
 454
 RESULT
09P944
ID 099
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 2760 -GARKSLPAAQPR--ORLL-----RSRSPASVPAPGSELVPP---PSGGALGSPP 2803
 2705 PITVLVPAPVPAPAPIPAPAPIPAPAPIPAPPLPPP--APDGAMGALSAIRRPIRRA--- 2759
 69 RVVRRQLPVEEPNPAKRLLFLLLTIVFCQILMAEEGVPAP----LPPEDAPNAASLAPTP 124
 PTMTILQAPTPAPSTIPGPRRGSGPEIFTFDPLPEPAAAPAGRPSASRGHRKRSRRVLYP 68
 STRAIN*JURA;
Schwyzer M., Vlcek C., Lowery D.E., Bello L.J., Meyer G., Misra V.;
Submitted (NoV-1997) to the EMBL/GenBank/DDBJ databases.
 G., Misra V.,
 Schwyzer M., Styger D., Vogt B., Lowery D.E., Simard C., LaBoissiere S., Misra V., Vlcek C., Paces V.; "Gene contents in a 31-kb segment at the left genome end of bovine herpesvirus-1:";
 13.9%; Score 114; DB 12; Length 3247; 31.1%; Pred. No. 0.045; Live 12; Mismatches 49; Indels 30
 Schwyzer M.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; Z78205; CAB01605.1; -.
EMBL; AJ004801; CAA06097.1; -.
SEQUENCE 3247 AA; 332190 WW; 3AEAA72F8F001F6A CRC64;
 Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
 Thiry E., Paces V . Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases
 :
ن
 Schwyzer M., Styger D., Vogt B., Lowery D.E., Simard LaBoisslere S., Misra V., Vlcek C., Paces V.; Vet. Microbiol. 0:0-0(1996).
 Bovine herpesvirus 1.
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Varicellovirus.
NCBI_TaxID=10320;
 Created)
Last sequence update)
Last annotation update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 Schwyzer M., Vlcek C., Lowery D.E., Bello L.J.,
 PRT;
 MEDLINE-97164286; Pubmed-9010999;
 Vet. Microbiol. 53:67-77(1996).
 09V884 PRELIMINARY;
09V884;
01-MAY-2000 (TrEMBLrel. 13, C;
01-MAY-2000 (TrEMBLrel. 13, L6
01-3UN-2000 (TrEMBLrel. 14, L6
CG18635 PROTEIN,
 SEQUENCE OF 1-179 FROM N.A.
 SEQUENCE OF 1-179 FROM N.A.
 Conservative
 2804 SFVPSRPPSLEP 2815
 125 V----SPVLEP 131
 Ouery Match
Best Local Similarity
Matches 41; Conserv
 SEQUENCE FROM N.A.
 [3]
SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 STRAIN-COOPER;
 STRAIN-COOPER;
 STRAIN-COOPER;
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 STRAIN-JURA;
 STRAIN-JURA;
 41;
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39;

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RESULT Q9V884

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 60 KRSRRVLYPRVVRRQLP-VEEPNPAKRLLFLLTIVFCQILMAEEGVPAPLPPEDAPNAA 118
 MEDLINE-97127825; Pubmed-8972576; Ramon A., Gil R., Burgal M., Sentandreu R., Valentin E.; "A novel cell wall protein specific to the mycelial form of Yarrowia 'lipolytica."; 'lipolytica."; Yeast 12:1535-1548(1996).
 Nagase T., Ishikawa K., Nakajima D., Ohira M., Seki N., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
"Prediction of the coding sequences of unidentified human genes. VII. The complete sequences of 100 new cDNA clones from brain which can DNA Res. 4:111-150(1997).
EMBL: AB00237; BAA20797.2;
 66 LYPRVVRRQLPVEEPNPAKR------LLFLL------LT1VFCQILMAEEGVPAPLPP 111
 1 MCHSRSCHPTMfillQAPTPAP-STIPGPRRGSGPETFTFDPLPEPAAAPAGRPSASRGHR 59
 6 SCHPTMTILQAPTPAPSTIPGPRRGSGPEIFTFDPLPEPAAAPAGRPSASRGHRKRSRRV 65
 Gaps
 Homo sapiens (Human).
UsufaryOta: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
 28;
 13.2%; Score 109; DB 4; Length 1709; 32.6%; Pred. No. 0.069; tive 10; Mismatches 53; Indels 2
 Ouery Match
13.2%; Score 109; DB 3; Length 285;
Best Local Similarity 28.4%; Pred. No. 0.012;
Matches 40; Conservative 11; Mismatches 62; Indels
 DCF2E0FF716B672C CRC64;
 POTENTIAL.
0BA7FF1C515CD57D CRC64;
 01-JAN-1998 (TrEMBLrel. 05, Created)
U-JAN-2000 (TrEMBLrel. 13, Last sequence update)
01-CCT-2000 (TrEMBLrel. 15, Last annotation update)
KIAAQ339 PROTEIN (FRAGMENT).
 PRT; 1709 AA
 POTENTIAL.
 1709 AA; 186231 MW;
 119 SLAPTPVSPVLEPFNLTSEPS 139
 219 SLRS---SPSLPPLPLPPSPS 236
 PRINTS; PRO1217; PRICHEXTENSN.
NON_TER 1 1 1 SEQUENCE 1709 AA; 186231 MW.
 30036 MW;
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 285 AA;
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INTERPRO; IPR002965,
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 76 PVEEPNPAKRLLFLLTIVFCQILMAEEGVPAPLPPEDAPNAASLAPTP----VSPV 128
 Gaps
 16 APTPAPSTIPGPRRGSGPEIFTFDPLPEPAAPAGRPSASRGHRKRSRRVLYPRVVRRQL 75
 STRAIN-GA; MEDLINE-9233304; PubMed-1315048; J. Tillotson J.K.; Jones D., Lee L., Liu J.L.; Kung H.J.; Tillotson J.K.; Marek disease virus encodes a basic-leucine zipper gene resembling the fos/jun oncogenes that is highly expressed in lymphoblastoid
 Streptococcus pneumoniae.
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
 Lee L.F., Wu P., Sui D., Ren D., Kung H.J.;
"The Complete UL Sequence of Serotype I Marek's Disease Virus.";
Proc. Natl. Acad. Sci. U.S.A. 0:0-0(2000).
EMBL, AF17806, AAF6771.1;
SEQUENCE 3325 AA; 365698 MW; 5D4A84EF719BB9FD CRC64;
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 from multiresistant pneumococci."; to the EMBL/GenBank/DDBJ databases
 RNA stage; Herpesviridae.
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NCBI_TaxID=10390;
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112 EDAPNAASLAPTPVS 126
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A.Accession: 533363
A.Status: preliminary
A.Molecule type: mRNA
A.Residues: 1-153 ACHA-
A.Cross references: EMBL:X67644
C.Genetics: 70/3
A.Introns: 70/3
C.Keywords: transmembrane protein
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1 MCHISRSCHPIMIILQAPTPA.......EPSDYALDLSTFLQQHPAAF 156
 Description
 195891
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
 Total number of hits satisfying chosen parameters:
 195891 segs, 67900655 residues
 SUMMARIES
 OM protein - protein search, using sw model
 January 30, 2001, 21:28:35
 Post-processing: Minimum Match 0%
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Listing first 45 summaries
 BIOSUM62
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| A75588<br>A46611<br>A10532<br>A10532<br>A100964<br>A48018<br>A89295<br>A79295<br>A792953<br>A792953<br>T12920<br>T12920                                                                                                                                                                      | ALIGNMENTS  DIF-2 - human  Lision 05.Sep-1997  Hanidis, C.; Schmit  Scar 4-9; 1997  Scar 4-9; 1997  Activated of a n  197339426  ne codon CCG for re  Score 819; DB 2;  Pred. No. 1.2e-58                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | Ttches 1; PEIFTFDPLPEPA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
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|                                                                                                                                                                                                                                                                                              | nntiation-depende<br>6s: Homo sapiens<br>02.5ep-1997 Rse<br>Ssion, JG597 Rse<br>1. Biophys. Rss.<br>1. Identification<br>ence number: JG587<br>1. Sion: JG587<br>1. Sion: JG587<br>1. Sion: JG587<br>1. Match<br>watch<br>watch<br>Local Similarity                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | MCHSRSCHPTMTILQAPT MCHSRSCHPTMTILQAPT MCHSRSCHPTMTILQAPT RSRRVLYPRVVRROLPVE RSRRVLYPRVVRROLPVE APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRNLTSEP APTPVSPVLEPRN                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
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C;Species: Lymantria dispar nuclear polyhedrosis virus. LdNNPV
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Dates: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T30351
R;Kuzio, J; Pearson, M.N.; Harwood, S.H.; Funk, C.J.; Evans, J.T.; Slavicek, J.M.;
Virology 253, 17-34, 1999
A;Title: Sequence and analysis of the genome of a baculovirus pathogenic for Lymant: A;Accession: T30351
 C: Species: Chlamydomonas eugametos
C: Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jul-2000
C: Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jul-2000
C: Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jul-2000
C: Accession: S50754
R: Woessner, 3.7 P.: Molendik, A.J.; van Egmond, P.; Klis, F.M.; Goodenough, U.W.; Plant Mol. Biol. 26, 947-960, 1994
A: Title: Domain conservation in several volvocalean cell wall proteins.
A: Reference number: S50754; MUID: 95093034
A: Status: preliminary
A: Molecule type: mRNA
 A;Cross-references: EMBL:AB006622; NID:dl170675; PIDN:BAA22953.1; PID:dlC23829
A;Experimental source: brain
C;Genetics:
A;Note: KIAA0284
 PRVVRRQLPVEEPNPAKRLLFLLTIVFCQILMAEEGVPAPLPPEDAPNAASLAPTPVSP 127
 47 APAGRPSASRGHRKRSRRVLYPRVVRRQLPVEEPNPAKRLLFLLLTIVFCQILMAEEGVP 106
 368 HSPSGDPKADKRRGPTPADRDRPSVPAPVQAGGRSSGPQRAGSLKREKTEERLGSPSPAS 427
 Gaps
 Gaps
 3 HSRSCHPTMTILQAPTPA-----PSTIPGPRRGSGPEIF----TFDPL--PEPAA 46
 APTPAPSTIPGPRRGSGP-FIFTF-----DPLPEPAAAPAGRPSASRGHRKRSRRVLY 67
 64;
 128 VLEPFNLTSE------PSDYALDL-----STF-----LQQHPAA 155
 726 ALEPGESTAEAASELAVERPAOPAPDLTSDSAVESTFGHKSTVASELAARPAA 778
 Length 1323;
 Length 1029;
 mucin-like protein - Lymantria dispar nuclear polyhedrosis virus
 428 RTPARPFGSVGRRSRLAQDFMAQCLRESSPAARPSPEK------------
 107 APLPPEDAPNAASLA:-PTPVSPVLEPFNLT----SEPSDYALDLSTF 148
 468 PVLPAPLTPHGTSPVGPPTPPPAPTDP-QLTKARKQEEDDSLSDAGTY 514
 52; Indels
 DB 2;
 67;
 Score 106; DB 2;
Pred. No. 0.46;
6; Mismatches 52
 A. Status: preliminary: translated from GB/EMBL/DDBJ
 preliminary; translated from GB/EMBL/DDBJ
 A; Cross-references: EMBL: AF081810; PIDN: AAC70189.1
 hypothetical protein WP6 - Chlamydomonas eugametos
 12.9%; Score 106.5; DE
26.8%; Pred. No. 0.54;
tive 13; Mismatches
 12.9%;
llarity 29.5%;
Conservative
 Conservative
 A; Molecule type: mRNA
A; Residues: 1-1323 <OHA>
 <KU2>
 Query Match
Best Local Similarity
Matches 51; Conserv
 Local Similarity
ses 45; Conserv
 A; Molecule type: DNA
A; Residues: 1-1029 <k
 Query Match
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 Infect. Immun. 61, 109-116, 1993
A;Title: Complete nucleotide sequence of the Actinomyces viscosus T14V sialidase gene:
A;Reference number: A49227; MUID:93114861
 ż
 C.Accession: T00037
R.Ohara, O.; Nagase, T.; Ishikawa, K.; Nakajima, D.; Ohira, M.; Seki, N.; Nomura, Submitted to the EMBL Data Library, August 1997
A.Description: Prediction of the coding sequences of unidentified human genes.
A.Reference number: 214073
A.Accession: T00037
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 Species: Actinomyces viscosus
Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 22-Oct-1999
 hypothetical protein KIAA0284 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 05-Nov-1999
 A.Cross-references: GB:LO6898; NID:9289087; PIDN:AAA21932.1; PID:9141852
A:Note: sequence extracted from NCBI backbone (NCBIN:121598, NCBIP:121599)
 RVVRRQL.PVEEPNPAKR--LI.FLLLTIVFCQILMA--EEGVP----APLPPEDAPNAASI, 120
 ----PAPKPAPKPAPKPAPKPAPKPASTGPELLPVP 226
 16 APTPAPSTIPGPRRGSGPEIFTFOPLPEPAAAPAGRPSASRGHRKRSKRVLYPRVVRRQL 75
 Gaps
 9 PTMT.LQAPTPAPSTIPGPRRGSGPEIFTFIDPLPEPAAAPAGRPSASRGHRKRSRRVLYP 68
 76 PVEEPNPAKRLLFLLTIVFCQILMAEEGVPAPLP-----PEDAPNAASLAP----
 27;
 Length 901;
 ; Score 107; DB 2; Length 496;
; Pred. No. 0.19;
20; Mismatches 57; Indels
 A;Molecule type: DNA
A;Residues: 1-496 <GRA>
A;Residues: 1-496 <GRA>
A;Cross-references: EMBL:U42580; NID:g4028896; PIDN:AAC96773.1
A;Experimental source: specific host Chlorella strain NC64A
C;Genetics: A405R
 Indels
 123 ----TPVSPVLE-----PFNLTSEPSDYALDLSTFLQ 150
 Ouery Match 12.9%; Score 106.5; DB 2; Best Local Similarity 29.0%; Pred. No. 0.37; Matches 45; Conservative 19; Mismatches 64;
preliminary; translated from GB/EMBL/DDBJ
 121 APTPVSPVLEPFNLTSEPSDYALDLSTFLQQHPAA 155
 13.08;
22.8%;
 sialidase - Actinomyces viscosus
 A; Molecule type: nucleic acid
A; Residues: 1-901 <YEU>
 Conservative
 181 PKPAPKPAPK----
 Query Match
Best Local Similarity
 A;Status: preliminary
 C;Date: 19-Dec-1993
C;Accession: A49227
R;Yeung, M.K.
 A; Accession: A49227
 Contents: T14V
 37;
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 227
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Search completed: January 30, 2001, 23:09:03 Job time: 6028 sec

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A:Molecule Lype: mRNA
A:Residues: 1-815 <ZHO>
A:Cross-references: GB:U25278; NID:g837260; PIDN:AAA81381.1; PID:g837261
C:Suporfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homold
C:Keywords: ATP
F:52-315/Domain: protein kinase homology <KIN>
F:60-68/Region: protein kinase ATP-binding motif
 7;
 10;
A;"Itle: Components of a new human protein kinase signal transduction pathway. A; Reference number: A56708; MUID:95279403 A;Accession: B56708 A;Status: preliminary
 A;Cross-references: EMBL:283227; PIDN:CAB05726.2; GSPDB:GN00028; CESP:F4588.3
A;Experimental source: clone F4588
 hypothetical protein F4588.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct.1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
 59 RKRSRRVLYPRVVRRQLPVEEPNPAKRLLFLLTIVFCQILMAEEGVPAPLPPEDAPNAA 118
 49 AG---RPSASRGHRKKSRRVLYPRVVRRQLPVEEPNPAKRLLFLLLTIVFCQILMAEEGV 105
 ----PVPAPPQIATSTSLLAAQSLVPPPGL 674
 106 PAP-----VSPVLEP-FNLTSE 137
 77 SPSCCPYVPPAPLPPPPPASPCCGPSPVPAP --- CCPPPPAPAPCCPPPPPFPS--- 130
 Gaps
 4. SRSCHPTWIILQAPTPAPSTIPGP------RRGSGPEI----F"FDPL,PEPAAAP 48
 4 SRSCHPTMT1LQAPTPAPST1P--GPRRGSGPEIFTFDPLPEPAA---APAGRPSASRGH 58
 70;
 Query Match
12.6%; Score 104; DB 2; Length 815; Best Local Similarity 24.2%; Pred. No. 0.53; Matches 48; Conservative 23; Mismatches 57; Indels
 Score 103; DB 2; Length 241; Pred. No. 0.19;
 48; Indels
 A; Status: preliminary; translated from GB/EMBL/DDBJ
 C;Accession: T22216
R;Percy, C
submitted to the EMB; Data Library, December 1996
A;Reference number: 219531
A;Accession: T22216
 6; Mismatches
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Best Local Similarity 30.8%;
Matches 41; Conservative
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 138 PS----DYALDLSTFLQQ 151
 A;Gene: CESP:F45B8.3
A;Map position: X
A;Introns: 21/3; 68/3; 211/2
 || | :| :|
164 VAAPVPINPCCQP 176
 119 SLAPTPVSPVLEP 131
 A; Molecule type: DNA
A; Residues: 1-241 <WIL>
 635 PGPAPHPTGPPG-
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Homo sapiens (Human)
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Copyright (c) 1993 - 2000 Compugen Ltd.
 Total number of hits satisfying chosen parameters:
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TEGU_EBV
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 102.5
102.5
101.5
 94.5
94.5
94.5
 Perfect score:
 Scoring table:
 93
 9 9 9
 93.
 OM protein
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0B
 Database :
 Searched:
 Sequence:
 Minimum
 Maximum
 Run on:
 Result
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| POB588 homo sapien 003209 autographa 00878 mus musculu 043426 homo sapien P56720 rattus norv P28925 equine herp P06487 herpes simp 0994h2 homo sapien P4179 autographa P07359 homo sapien 014957 homo sapien 014957 homo sapien                                                                                           |
|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| BIAR_HUMAN<br>VP61_NPVAC<br>MYT_MOUSE<br>SYJT_HUMAN<br>P300_HUMAN<br>SRE1_RAT<br>ICP4_HSVEB<br>VGLI_HSV11<br>IRS2_HUMAN<br>Y 091_NPVAC<br>GPBA_HUMAN<br>NME3_HUMAN                                                                                                                                                        |
| 24.77 1 1 1 2 2 2 4 1 1 1 2 2 2 4 1 1 1 2 2 2 4 1 1 1 2 2 2 4 1 1 1 2 2 2 4 1 1 1 2 2 2 4 1 1 1 2 2 2 4 1 1 1 2 2 2 4 1 1 1 2 2 2 4 1 1 1 2 2 2 4 1 1 1 2 2 2 4 1 1 1 2 2 2 4 1 1 1 2 2 2 4 1 1 1 2 2 2 4 1 1 1 2 2 2 4 1 1 1 2 2 2 4 1 1 1 2 2 2 4 1 1 1 2 2 2 4 1 1 1 2 2 2 4 1 1 1 2 2 2 4 1 1 1 2 2 2 4 1 1 1 2 2 2 2 |
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| 88<br>                                                                                                                                                                                                                                                                                                                    |
| WWWWWW44444444400VWVWWWWWWWW                                                                                                                                                                                                                                                                                              |

## ALIGNMENTS

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ن
 MEDLINE-84270667: PubMed-6087149;
Back K., Bankier A.T., Biggin M.D., Deininger P.L., Farrell P.J.,
Cibson T.J., Hatfull G., Hudson G.S., Satchwell S.C., Seguin C.,
Tuffnell P.S., Barrell B.G.,
"DNA Sequence and expression of the B95-8 Epstein-Barr virus genome.";
Nature 310:207-211(1984).
 72 PTYTPSPKPTPPPATPKPTPPTYTPSPKPKSPVYPPPRASTPPTYTPSPKP-PATKPPT 130
 51 RPSASRGHRKRSRRVLY-----PRVVRRQLPVEEPNPAKRLLFELLTIVFCQILM 100
 Gaps
 Gaps
 PTMT1LQAPTPAPS----TIPGPRRG-SGPEIFTFDP1.PEPAAAPAGRPSASRGHRKRS 62
 SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL36, EHV-1 24, EBV BPLF1, HVS-1 64, VYV 22, AND HCMV UL48.
 484 PVSTIAPSVIPSPRLPLQIPIPLPQAAPSNPKIPLIIPSPSPTAAAA--PTIT-----
 535 -- TLSPPPYQQQPPQSAAPAPSPLLPQQQPTPS-------AAPAPSP
 41;
 58;
 109 -LPPEDAPNAASLAPTPVSPVLEPFNLTS---EPSDYALDLSTFLQ---QHPAA 155
 101 AEEGVPAPLPPEDAPNAASLAPTPVSPVLEPFNLTSEPSDYALDLSTFLQQHP 153
 1.9 PPIHTPSPKPPTSKPTPPVXTPSPKPPKPSPPTYTPTPKPPATKPPTHP 231
 Length 283;
 DB 1; Length 3149; 0.95;
 Indels
 51; Indels
 Epstein-barr virus (strain B95-8) (Human herpesvirus 4).
Viruses; dsDNA viruses, no RNA stage: Herpesviridae;
Gammaherpesvirinae; Lymphocryptovirus.
 3149 AA; 337954 MW; 3DD0C576587313D8 CRC64;
 EXTENSIN,
8D7FCD0DA8ED2D90 CRC64;
 ä
 81;
 DB
 Score 112.5; DB
Pred. No. 0.022;
9; Mismatches 8
 21-JUL-1986 (Rel. 01, Last sequence update) 01-APR-1993 (Rel. 25, Last annotation update)
 3149 AA.
 12.8%; Score 105; DB 25.3%; Pred. No. 0.95; ive 21; Mismatches
 POTENTIAL.
24 PC
283 EX
29593 MW;
 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last seq
 13.78; 24.38;
 EMBL; V01555; CAA24839.1; -.
 Local Similarity 24.3
hes 42; Conservative
 44; Conservative
 STANDARD;
 LARGE TEGUMENT PROTEIN.
 1
25
283 AA;
 Query Match
Best Local Similarity
 SEQUENCE FROM N.A.
 PIR; A03747; QQBE8
PIR; S32993; S3299
 CHAIN
SEQUENCE
 TEGU_EBV
P03186;
 PIR; S329
SEQUENCE
 Query Match
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 (EXTRACELLULAR SIGNAL-
 DOMAIN: THE SECOND PROLINE-RICH REGION MAY INTERACT WITH ACTIN TARGETING THE KINASE TO A SPECIFIC LOCATION IN THE CELL. PTM: AUTOPHOSPHORYLATED ON THREONINE AND TYROSINE RESIDUES, WHEN THE C-TERMINAL PART OF THE KINASE, WHICH COULD HAVE A REGULATORY
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutelcostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
 -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. MAP KINASE FAMILY.
SEQUENCE FROM N.A.
TISSUB-FETAL BRAIN;
MEDLINE-95279403; Pubmed-7759517;
Zhou G., Bao Z.Q., Dixon J.E.;
"Components of a new human protein kinase signal transduction
 MKOTHUMAN STANDARD; PRT; 615 AA. U13164; Q16634; Q1-NOV-1997 (Rel. 35, Last sequence update) O1-NOV-1997 (Rel. 35, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update) MITOGEN-ACTIVATED PROTEIN KINNSE 7 (EC 2.7 1.-) REGULATED KINASE 5) (ERK4) (BMK1 KINASE), MAPK7 OR PKKM7 OR ERK5 OR ERK4.
 pathway.";
J. Biol. Chem. 270:12665-12669(1995).
 MEDLINE-95374539; PubMed-7646528;
 EMBL; U25278; AAA81381.1; -. EMBL; U29725; AAA82931.1; -.
 U29727; AAA82933.1;
 U29726; AAA82932.1
 Homo sapiens (Human)
 IS ABSENT
 SEQUENCE FROM N.A.
 P24941; 1AQ1
 TISSUE-PLACENTA;
 IN LIVER.
 RESULT 5
MK07_HUMAN
 EMBL;
 EMBL;
 g
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Transferase; Serine/threonine-protein kinase; ATP-binding; Cell cycle;

PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1. PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1. PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.

PFAM; PF00069; pkinase; 1. PROSITE; PS01351; MAPK; 1.

PS00107;

INTERPRO; IPR000719; -.

IPR002290; -

NTERPRO:

ATP (BY SIMILARITY).
ATP (BY SIMILARITY). PROTEIN KINASE

346 68 83

NP\_BIND BINDING

Phosphorylation

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Μ
 28668
 Ouery Match 12.3
Best Local Similarity 28.3
Matches 41; Conservative
 STANDARD;
 22
268
27
145
 620
73
73
242
242
520
 268 AA;
 SEQUENCE FROM N.A.
 70
2229
2239
236
205
 MAIN ROOT
 EXTN_TOBAC
P13983;
 SEQUENCE
 CHAIN DOMAIN
 DOMAIN
REPEAT
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 .;
8
 1129 TSVKSPLEPAQKAAPPPREEPAPKKSSSEPPPRKPVEEKSEEGGAPAPAPAPEPKQVSAP 1188
 1189 ASRKSSKQVSQPAAV---VPPQPPSTAP------OKKEAPKAVPSEPKKKQPPP 1233
 Proto-oncogene; Chromosomal translocation; DNA-binding;
Nuclear protein; Zinc-finger; Metal-binding; Transcription regulation;
 SEQUENCE FROM N.A.
STRAIN-CV. JENALONG;
MEDLINE-99187258; Pubmed-9526510;
Greene E.A., Brard M., Dedicu A., Barker D.G.;
"MtENOD16 and 20 are members of a family of phytocyanin-related early
 57 GHRKRSRRVLYPRVVRRQLPVEEPNPAKRLLFLLLTIVFCQILMAEEGVPA-----PLP 110
 Gaps
 56
 Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
Fabales; Fabaceae; Papillonoideae; Medicago.
 12 TILGAP-TPAPSTIPGPRRGSGPEIFTFDPLPE-------PAAAPAGRPS--ASR
 45;
 DB 1; Length 3866;
 Indels
 ADFC55E14E806F1D CRC64;
 SIMILARITY).
SIMILARITY).
SIMILARITY).
 Plant Mol. Biol, 36:775-783(1998).
-!- SIMILARITY: CONTAINS ONE PLASTOCYANIN-LIKE DOMAIN.
 BROMODOMAIN (DIVERGENT). SET DOMAIN.
 MISSING (IN ISOFORM 2)
 Last annotation update)
 Score 102.5; [Pred. No. 1.8;
 1234 PEPGPEQSKOKKVAPLPSIPVKO-----KPKD 1260
 268 AA
 Last sequence update)
 Mismatches
 111 PEDAPNAA---SLAPTPVSPVLEPFNLTSEPSD 140
 A.T HOOK (
A.T HOOK (
A.T HOOK (
 POLY-GLU.
POLY-GLU.
 POLY - PRO
 PRO-RICH
 Polymorphism.
 PHD 2.
PHD 3.
 PRT;
 15-DEC-1998 (Rel. 37, Last sequence
15-JUL-1999 (Rel. 38, Last annotat.
EARLY NODULIN 20 PRECURSOR (N-20).
 Medicago truncatula (Barrel medic)
 ٨
 PHD
 19;
 15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequ
15-JUL-1999 (Rel. 38, Last anno
 12.5%;
26.8%;
 EMBL; X99467; CAA67830.1; -. Nodulation; Signal.
 420976
 41; Conservative
 STANDARD;
 469
1238
3536
3697
1505
 1497
 Alternative splicing;
 AA:
 Query Match
Best Local Similarity
 NO20_MEDTR
P93329;
 Plant Mol.
 DNA_BIND
DNA_BIND
DNA_BIND
 VARIANT
SEQUENCE
 nodulins
 DOMAIN
 RESULT 8
NO20_MEDTR
 Matches
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ره
 Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I;
Solanales; Solanaceae; Nicotiana.
 SUBCELLULAR LOCATION: EXTRACELLULAR MATRIX.
THE STRENSINS CONTAIN A CHARACTERISTIC REPEAT OF THE PENTAPEPTIDE SER-PRO(4). THE PROLINE RESIDUE IS HYDROXYLATED AND THEN GLYCOSYLATED
 H-A-P-P.
H-A-P-P. '
2 X 7 AA TANDEM REPEATS OF T-H-R-H-A-P-P.
 65 VLYPRVVRRQLPVEEPNPAKRLIFLLLTIVFCQILMAEEGVPAPLP-----PEDAPNA 117
 -----SPASPSPSLSKSPSESP-- 211
 Gaps
 13 ILQAPTPAPS-----TIPGPRRGSGPEIFTFDPLPEPAAAPAGRPSASRGHRKRSRR 64
 132 VLSSPPPPPSPPTPRSSTPIPHPPRRSLPS----PPSPSPSPSPSPSPSPS-----
 Keller B., Lamb C.J.;
"Specific expression of a novel cell wall hydroxyproline-rich
glycoprolein gene in lateral root initiation.";
Genes Dev. 3:1639-1646(1989)
-i- FUNCTION: HAS A SPECIALIZED STRUCTURAL FUNCTION, POSSIBLY IN
THE MECHANICAL, PENETRATION OF THE CORTEX AND EPIDERMIS OF THE
 01-0AN-1990 (Rcl. 13, Created)
01-0AN-1990 (Rcl. 13, Last sequence update)
01-MAR-1992 (Rcl. 21, Last annotation update)
EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).
 61;
 Length 268;
 EMBL; X138B5; CAA32090.1; -PIR; S06733; S06733.
Repeat; Cell wall; Glycoprotein; Signal; Structural protein; Hydroxylation. 1 ?
 CONTAINS THE SER-PRO(4) REPEATS
 Indels
 6FA29C5798C75F91 CRC64;
 31;
 DB 1;
BY SIMILARITY.
EARLY NODULIN 20.
PLASTOCYANIN-LIKE.
 12.3%; Score 101.5; DE 28.3%; Pred. No. 0.15; ive 12; Mismatches
 EXTENSIN.
 POLY - PRO
 -----PRSTPI--PHPRKR------
 212 -SLAPSPSDSVASLAP---SSSPSD 232
 PRT;
 118 ASLAPTPVSPV--LEPFNLTSEPSD 140
 Nicotiana tabacum (Common tobacco)
 STRAIN+CV. XANTHI; TISSUE-LEAF;
MEDLINE-90128263; Pubmed-2612909;
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 -1. SUBCELLUIAR LOCATION: SECRETED.
-1. ALTERNATIVE PRODUCTS: AT LEAST TWO FORMS OF THE PROTEINS ARE PRODUCED BY ALTERNATIVE SPLICING. THE APEG FORM INCLUDES A LARGE DOMAIN WITH 33 SEQUENCE REPEATS.
-1. TISSUE SPECIFICITY: SKIN.
-1. SIMILARITY: CONTAINS 2 P-TYPE (FREFOIL) DOMAINS.
-1. CAUTION: REF. 2 SEQUENCE DIFFERS FROM THAT SHOWN FROM POSITION 392 ONWARD AND IS SHORTER (418 AA) DUE TO A FRAMESHIFT.
 "xP2, a new member of the P-domain peptide family of potential growth factors, is synthesized in Xenopus laevis skin.";
J. Biol. Chem. 267:14451-14455(1992).
 71 VRRQLPVE-----EPNPAKRLLFLLLTIVFCQILMAEEGVPAPLPPEDAPNAASLAPTP 124
 --- FUNCTION: MAY ACT AS A GROWTH FACTOR IN THE GERMINAL LAYER OF THE EPIDERMIS. MAY ALSO BE INVOLVED IN GROWTH OF REGENERATING GLANDS AND IN PROTECTION OF THE SKIN FROM THE EXTERNAL ENVIRONMENT.
 15 QAPTPAP----STIPGPRRGSGPEIFTFDPLPEPAAAPAGRPSASRGHRKRSRRVLYPRV 70
 Gmachl M.; Berger H., Thalhammer J., Kreil G.;
"Dermal glands of Xenopus laevis contain a polypeptide with a highly
 SKIN SECRETORY PROTEIN XP2.
PYRROLIDONE CARBOXYLIC ACID (PROBABLE
33 X REPEATS OF G-[GE]-[AP](2,4)-A-E.
 DB 1; Length 439;
 Score 95; DB 1; Length 439
Pred. No. 0.8;
6; Mismatches 57; Indels
 MISSING (IN ISOFORM XP2).
 38C4A4B57CBAE778 CRC64;
 P-TYPE 1.
P-TYPE 2.
BY SIMILARITY.
 EMBL; X51394; CAA35759.1; ALT_FRAME.
PIR; S07498; SKXLAG.
PIR; A37331; A37331.
 ^ ^
 repetitive amino acid sequence.";
FEBS Lett. 260:145-148(1990).
 41173 MW;
 SEQUENCE OF 3-439 FROM N.A.
 EMBL; M90095; AAA50001.1;
 VSPVLE-----PFNLT 135
 Local Similarity 25,7
nes 35; Conservative
 HSSP; P04155; 1PS2.
INTERPRO; IPR000519;
 18
439 AA;
 TISSUE-SKIN;
MEDLINE-90127399;
 CONFLICT
 DISULFID
 Query Match
 CONFLICT
 DOMAIN
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 ŝ
 protein) reveals extensive homology with MyBP-C (C-protein) with conserved immunoglobulin C2 and fibronectin type III motifs.";
J. Biol. Chem. 268:3670-3676(1993).
-!- FUNCTION: BINDS TO MYOSIN; PROBABLY INVOLVED IN INTERACTION WITH THICK MYOFILAMENTS IN THE A DAND.
-!- TISSUE SPECIFICITY: SKELFTAL MUSCLE. SEEMS TO BE ALSO EXPRESSED IN THE SLOW TONIC ALD MUSCLE. NOT DETECTED IN GIZZARD OR HEART.
-!- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
-!- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
-!- SIMILARITY: CONTAINS 2 THRONECTIN TYPE III-LIKE DOMAINS.
 Molecular cloning of chicken myosin-binding protein (MyBP) H (86-kDa
 fmmunoglobulin domain; Cell adhesion; Muscle protein; Thick filament;
 69 RYVRRQLPVEEPNPAKRLLFLLLTIVFCQILMAEEGVPAPLPPEDAPNAASLAPTPVSPV 128
 Gaps
 9 PTMTILQAPTPAPSTIPGPRRGSGPEIFTFUPLPEPAAAPAGRPSASRGHRKRSRRVLYP 68
 38 РТРКЕСНАРТРКЕЕНАРРРКЕЕНАР-----РРКЕЕНАРАРАНЕТРРАРЕНРРДАЕОРААР 92
 XP2_XENLA STANDARD; PRT; 439 AA.
P17437; Q08944;
01-AUG-1990 (Rel. 15, Last sequence update)
01-FEB-1995 (Rel. 39, Last annotation update)
30-MAY-2000 (Rel. 39, Last annotation update)
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEC PROTEIN).
Xenopus laevis (African Clawed frog).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 ch 11.6%; Score 95.5; DB 1; Length 537; 1 Similarity 27.5%; Pred, No. 0.89; 38; Conservative 6; Mismatches 61; Indels 3:
 61; Indels
 T -> G (IN AA SEQUENCE):
A -> P (IN AA SEQUENCE).
A -> K (IN AA SEQUENCE).
O6C4CF0EFEIDD233 CRC64
 IG-LIKE C2-TYPE DOMAIN.
FIBRONECTIN TYPE-III.
IG-LIKE C2-TYPE DOMAIN.
 FIBRONECTIN TYPE-III.
 SEQUENCE OF 1-25 AND 344-439 FROM N.A. MEDLINE-92332564; PubMed-1629230; Hauser F., Roeben C., Hoffmann W.;
 PFAM; PF00047; ig; 2,
PRINTS; PR00014; FNTYPEIII.
PRINTS; PR01217; PRICHEXTENSN.
 EMBL; L05605; AAA21418.1; -.
 129 LEPFNLTSEPSDYALDLS 146
 126 - EPEKPKEEPPSVPLSLA 142
 INTERPRO; IPR001777; -. INTERPRO; IPR003965; -. INTERPRO; IPR003006; -.
 PFAM; PF00041; fn3; 2.
PFAM; PF00047; iq; 2.
 Xenupodinae; Xenopus.
 Best Local Similarity
Matches 38; Conserv
 CONFLICT
 Query Match
 Repeat
 DOMAIN
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(PROBABLE).

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C2H2-TYPE. A -> P. V -> M. AD74802EB856ACD7 CRC64;

757 C2 437 A 649 V 83113 MW;

ZN\_FING VARIANT VARIANT SEQUENCE

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FT
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Nelson D.L.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Sylfskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstcock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q.A.,
RA Chops R.A., Myers E.W., Rubin G.M., Venter J.C.
RA Globs R.A., Myers E.W., Rubin G.M., Venter J.C.
R. The genome sequence of Drosophila melanogaster.";
L. Science 287:2185-2195(2000).
 Tautz D., Nigro L.;
"Microevolutionary divergence pattern of the segmentation gene
hunchback in Drosophila.";
Mol. Biol. Evol. 15:1403-1411(1998).
- PUNCTION: GAP CLASS SEGMENTATION PROTEIN THAT CONTROLS DEVELOPMENT
OF HEAD STRUCTURES.
 -1- SUBCELLULAR LOCATION NUCLEAR.
-1- TISSUE SPECIFICITY: IN EMBRYO, EXPRESSION OF MATERNAL TRANSCRIPT
IS HIGHEST IN ANTERIOR REGION. ZYGOTIC TRANSCRIPT IS EXPRESSED IN ANTERNOR REGION UNTIL THE BEGINNING OF GASTRULATION AND IN POSTBRIOR REGION UNTIL EARLY GASTRULATION. AFTER THIS, IT IS EXPRESSED IN DEVELOPING NERVOUS SYSTEM.
 -!- DEVELOPMENTAL STAGE: EXPRESSED MATERNALLY AND ZYGOTICALLY.
EXPRESSION OF THE MATERNAL TRANSCRIPT DECREASES UNTIL EMBRYONIC
STAGE 14, ZYGOTIC TRANSCRIPT IS FIRST DETECTED AT STAGE 11.
-!- SIMILARITY: BELONGS TO THE HUNCHBACK FAMILY OF C2H2-TYPE ZINC-FINGER PROTEINS.
 [5]
SEQUENCE OF 281-349 FROM N.A.
MEDLINE-93066327; PubMed-1438276;
Sommer R.J. Retzlaff M., Goerlich K., Sander K., Tautz D.;
"Evolutionary conservation pattern of zinc-finger domains of
 Drosophila segmentation genes.";
Proc. Natl. Acad. Sci. U.S.A. 89:10782-10786(1992).
 POLY MORPH I SM
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EMBL: AE003660; AAB50232.1; -- PIR; A29253; A29253. EMBL; Y00274; CAA68377.1; -.

; T00395; -FBgn0001180; hb.

TRANSFAC,
FLYRAKE; FERDO001150.,
INTERPRO: IPRO000822: PFAM; PF00096; zf-C2H2; 6.
PRINTS: PR000048; ZINCFINGER.
PROSTE; PS00028; ZINC\_FINGER\_C2H2; 3.
PROSTE; PS000028; ZINC\_FINGER\_C2H2; 3.
Developmental protein; Gap; Zinc\_finger; Metal-binding; DNA-binding;
Repeat; Nuclear protein; Polymorphism.
Repeat: Nuclear protein; Polymorphism.
Z40 349; ZINC\_FINGERS I.
Z10 FINGERS II.

C2H2-TYPE. C2H2-TYPE. C2H2-TYPE. C2H2-TYPE. POLY-GLN. C2H2-TYPE.

ZN\_FING ZN\_FING ZN\_FING ZN\_FING DOMAIN

DOMAIN ZN\_FING

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52 PSASRGHRKRSRRVLYPRVVRRQLPVEEPNPAKRLLFLLLTIVFCQILMAEEGVP---- 106
 2 CHSRSCH-----PTMTILOAPTPAPS---TIPGPRRGSGPEIFTFDPLPEPAAAPAGR 51
 107 -----APLPPEDAPNAASLAPTPVSPVLEPFNLTSEPSDYALDLSTFLQQH 152
 SAPPAASPVLPLPASPAKSVASVEQTPSLP-----SPANLLPPLASLLQQN 478
 57;
.ch 11.5%; Score 94.5; DB 1; Length 758; 1 Similarity 24.6%; Pred. No. 1.5; 43; Conservative 19; Mismatches 56; Indels 5:
 Search completed: January 30, 2001, 23:12:24
Job time: 4005 sec
Query Match
Best Local 3
 Matches
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January 30, 2001, 23:12:24 ; Search time 43.61 Seconds (without alignments) 63:685 Million cell updates/sec
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442
1 VRROLPVEEPNPAKRLIFLL......EPSDYALDLSTFLQQHPAAF 86
 88757
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
 Total number of hits satisfying chosen parameters:
 88757 seqs, 32294092 residues
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 OM protein - protein search, using sw model
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 Minimum DB seq length: 0
Maximum DB seq length: 200000000
 SwissProt_39:*
 Title:
Perfect score:
Sequence:
 Scoring table:
 Database :
 Searched:
 Run on:
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|           | Description   | ÷, |            | Enu        | dro       | ery        | erw        | hom        | epstei   | Ogumn6 homo sapien | P19097 saccharomyc | oryct      | Q9y426 homo sapien | homod      | homo       | turn      |            | sorg       | sacchar    |            | epstein  |            |            |                                               |        | epste    | ğ          | homod      | es           | ğ           | bos tal    | gallus     | P54258 rattus norv | glycine | Q01101 homo sapien |
|-----------|---------------|----|------------|------------|-----------|------------|------------|------------|----------|--------------------|--------------------|------------|--------------------|------------|------------|-----------|------------|------------|------------|------------|----------|------------|------------|-----------------------------------------------|--------|----------|------------|------------|--------------|-------------|------------|------------|--------------------|---------|--------------------|
| SUMMARIES | ΙD            |    | IEXI_HUMAN | IEX1_MOUSE | SOS_DROME | GSPC_ERWCH | GSQC_ERWCH | GPBA_HUMAN | BRL1_EBV | TRX2_HUMAN         | FAS2_YEAST         | IF4G_RABIT | C210_HUMAN         | CAD1_HUMAN | PTPJ_HUMAN | POLR_TYMV | IF4G_HUMAN | EXTN_SORBI | LRE1_YEAST | TENX_HUMAN | TEGU_EBV | ILVB_MYCAV | MODD_MYCBO | MODD_MYCTU                                    | - 4    | EBN3_EBV | AF17_HUMAN | CXX1_HUMAN | ZIPA_ECOLI   | 댎           | P85B_BOVIN | MYBB_CHICK | RPI                | 33      | IA1_HUMAN          |
|           | DB            | :  | ٠,         | -1         | -         | -          | ٦          | ٦          | П        | ~                  | ٦                  | -          | -                  |            | ~          | -         | -4         | н          | -          | -          | -        | ~          |            | <b>,</b>                                      | -      | 7        | ~          | -          | -            | -           | -          | -4         | 7                  | -       | -                  |
|           |               |    | n i        | 13         | an a      | $\sim$     | $\sim$     | $\sim$     | 0        | ~                  | 83                 | 40         | æ                  | 88         | m          | 84        | 33         | B          | 58         | 8          | 7,       | ~          | ~          | $\sim$                                        | $\sim$ | 8        | σ          | 0          | $\sim$       | $^{\prime}$ | ~          | æ          | 1183               | ~       | ~                  |
|           | $r_{y}$       |    |            |            |           |            | -          |            |          |                    |                    |            |                    | •          | •          |           | •          |            |            | •          |          | •          | •          | •                                             | •      | •        | •          | •          | •            | •           | •          |            | 4.6                | •       | ٠.<br>د            |
| 9         | M.O.          |    | 5          | ف          | -         | Ä          | Ä          | Ä          | Ξ        | Ä                  | ä                  | H          | Ä                  | 7          | =          | H         | Ä          | =          | 7          | <b>≓</b>   | 7        | Ä          | Ä          | <u>, , , , , , , , , , , , , , , , , , , </u> | -      | _        | 1          |            | <del>,</del> | -1          |            | ~          | 7                  | -       | -                  |
|           | Score         |    | 442        | 27         | ω.        | m.         | ć.         | Ë,         | ö        | 70.5               | ę.                 | ဖ          | 68.5               | œ.         | œ.         | 8         | 68         | 67         | 67         | φ          | 9.99     | 9          | 65.5       | 'n.                                           | S.     | ō.       | 'n         | 65         | 65           | 65          | ω          | 64.5       |                    | 64      | 64                 |
|           | Result<br>No. |    | <b>-</b> ; | ~          | ო         | 7          | Ŋ          | 9          | 7        | ω                  | 6                  | 10         | 11                 | 12         | 13         | 14        | 15         | 16         | 17         | 18         | 19       | 20         | 21         | 22                                            | 23     | 24       | 25         | 26         | 27           | 28          | 29         | 30         | 31                 | 32      | 33                 |

| P54829 homo saplen P54830 mus musculu P30327 rhizobiuum m P14922 saccharomyc Q43365 homo saplen P752877 chinip yell P20127 ononis yell P22875 mus musculu P52875 mus musculu P16018 haloarcula P22736 homo saplen TS | IEXILHUMAN STANDARD: PRT: 156 AA.  D EXALHUMAN STANDARD: PRT: 156 AA.  D EXALHUMAN STANDARD: Created)  D 10.100.1995 (Rel. 36, Last sequence update)  E RADIATION:INDICIEE PRINTER. RESPONSE 3 PROTEIN! (PACAP-RESPONSIVE EARLY RESPONSE)  D 20.100.100.100.100.100.100.100.100.100.1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| PTNS_HUMAN<br>PTNS_MOUSE<br>FT21_RHIME<br>SSN6_YEASH<br>HXA3_HUMAN<br>NUSA_MYCPN<br>OOLF_NEUCR<br>POLR_OYMV<br>POLR_TYMVC<br>POLR_TYMVC<br>PF27_MOUSE<br>EF1A_HALMA<br>NR41_HUMAN                                    | 15. 15. 15. 15. 15. 15. 15. 15. 15. 15.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
| PTNS_H<br>PTNS_M<br>FT21_R<br>SSN6_Y<br>SSN6_Y<br>NAA3_H<br>NOA1F_N<br>POLR_O<br>POLR_T<br>PF27_M<br>RF1_H<br>NR41_H                                                                                                 | PRT;  year of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of  |
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| 537<br>590<br>966<br>966<br>980<br>177<br>181<br>184<br>182<br>183<br>184<br>185<br>185<br>185<br>185<br>185<br>185<br>185<br>185<br>185<br>185                                                                      | ANDARD 32, 0, 332, 1, 1, 2, 2, 2, 3, 2, 1, 3, 2, 1, 3, 2, 1, 2, 3, 2, 1, 2, 3, 2, 2, 3, 2, 2, 3, 2, 2, 3, 2, 2, 2, 3, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
| νινινικακακαι                                                                                                                                                                                                        | XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
|                                                                                                                                                                                                                      | PARTICLE AND COLLETT OF STREET OF ST |
| ΦΦΦΦΦ<br>Ψωμεω<br>ΦΦΦΦ····ΦΦΦ<br>44444ννηνννωμω                                                                                                                                                                      | HUMAN  HUMAN  P46655, 093044,  15-JUL-1998 (Re.  15-JUL-1998 (Re.  RADIATION-1995 (Re.  RADIATION-1995 (Re.  RADIATION-1000 (Re.  RADIATION-1000 (Re.  RADIATION-1000 (Re.  RADIATION-1000 (Re.  RADIATION-1000 (Re.  RADIATION-1000 (Re.  RADIATION-1000 (Re.  RADIATION-1000 (Re.  RADIATION-1000 (Re.  RENARYOTA, MA.  TISSUE-PLACENTA  MEDLINE-961313 (Re.  RENARYOTA, A.D.  "Identification of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the sween the sween the sween the sween picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of the picture of th |
| 88888884444<br>48864864444                                                                                                                                                                                           | 1   D                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
|                                                                                                                                                                                                                      | 00000000000000000000000000000000000000                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
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MEDLINE-93086427; Pubmed-1453958;
 PRINTS; PRO0810; BCTERIALGSPC.
PROSITE; PS01141; T2SP_C; 1.
 272 AA; 30301 MW;
 EMBL; X65265; CAA46369.1; -.
 STANDARD;
 FIR; S28013; S28013.
INTERPRO; IPR001478; ...
INTERPRO; IPR001639; ...
 INTERPRO; IPR001478; -. INTERPRO; IPR001639; -. PFAM; PF00595; PDZ; 1.
 61 PFNLTSEPSDYAL 73
 59 PVTL----NDFTL 67
 Erwinia chrysanthemi.
 PEAM; PF00595; PDZ;
 PIR; A47021; A47021
 SEQUENCE FROM N.A.
 Pectobacterium.
 GSQC_ERWCH
Q01564;
 ransport:
 DOMAIN
SEQUENCE
 DOMAIN
SEQUENCE
 FRANSMEM
 GSQC_ERWCH
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 9:
 STAIN=ECL6;
MEDLINE=9054355; Pubmed=1429461;
Lindeberg M., Collmer A.;
"Analysis of eight out genes in a cluster required for pectic enzyme secretion by Erwinia chrysanthemi; sequence comparison with secretion genes from other gram-negative bacteria.";
J. Bacteriol 174:7385-7397(1992).
-: FUNCTION: INVOLVED IN A GENERAL SECRETION PATHWAY (GSP) FOR THE EXPORT OF PROTEINS. REQUIRED FOR THE TRANSLOCATION OF THE MULTIPLE PECTIC ENZYMES.

MULTIPLE PECTIC ENZYMES.
 GSPC_ERWCH STANDARD; PRT; 272 AA.
P31698;
01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-NUV-1995 (Rel. 32, Last annotation update)
GENERAL SECRETION PATHWAY PROTEIN C (PECTIC ENZYMES SECRETION PROTEIN
 Gaps
 1 VRRQLPVE-----EPNPAKRLLFLLLTIVFCQILMAEEGVPAPLPPEDAPNAASLAPT 53
 Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 25;
 DB 1; Length 1595;
 GLN-RICH.
HIS-RICH.
TSCPVPCHFPRS -> HILPSPLSLPAQR
 37; Indels
 (IN REF. 2).
V -> P (IN REF. 2).
W; 33AE31F0767A219F CRC64;
 1477 TSPLTPAMSPMSPNIPSHPVESTSSSYAHQLRMRQQQQQTHPAIY 1522
 54 -- PVSPVLEPF--NLTSEP----SDYALDLSTFLQQ----HPAAF 86
 -!- SUBCELLULAR LOCATION: INNER MEMBRANE (PROBABLE).
 factor; Neurogenesis.
 Ouery Match
17.8%; Score 78.5; De
Best Local Similarity 28.3%; Pred. No. 3.9;
Matches 30; Conservative 14; Mismatches
 GLY-RICH.
 INTERPRO: IPR000219; ...
INTERPRO: IPR000519; ...
INTERPRO: IPR001691; ...
INTERPRO: IPR001895; ...
INTERPRO: IPR001895; ...
PFAM; PF00169; PH: 1.
PFAM; PF00617; RasGEF; 1.
PFAM; PF00621; RASGEF; 1.
PROSITE: PS00720; GBS_CDC25; 1.
PROSITE: PS500720; PH-DOMAIN; 1.
Guanine-nucleotide releasing facto
 EMBL; L02214; AAA24830.1; -.
 1462
AA; 177837
 Erwinia chrysanthemi.
 SEQUENCE FROM N.A.
 Pectobacterium.
 CONFLICT
SEQUENCE
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GSPC_ERWCH
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 Condemine G.; Dorel C., Hugowvieux-Cotte-Pattat N., Robert-Baudouy J.; "Some of the out genes involved in the secretion of pectate Lyases in Erwinia chrysanthemi are regulated by kdgR."; Mol. Microbiol. 6:3199-3211(1992).
-: FUNCTION: INVOLVED IN A GENERAL SECRETION PATHWAY (GSP) FOR THE EXPORT OF PROTEINS. REQUIRED FOR THE TRANSLOCATION OF THE MULTIPLE PECTIC ENZYMES.
 01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-JUL-1993 (Rel. 32, Last annotation update)
GENERAL SECRETION PATHWAY PROTEIN C (PECTIC ENZYMES SECRETION PROTEIN
 4 OLPVEEPNPAKRLFLLLTIVFCQ---ILMAEEGVPAPLPPEDAPNAASLAPTPVSPVLE 60
 25; Indels 13; Gaps
 Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 Query Match
16.6%; Score 73.5; DB 1; Length 272;
Best Local Similarity 30.1%; Pred. No. 1.7;
Matches 22; Conservative 13: Mismatches 25; Indels 1:
 Trainsmembrane: Inner membrane.
Trainsmembrane: Information (Potential).
17 35 POTENTIAL).
36 272 PERIPUASMIC (POTENTIAL).
272 AA: 30162 MW: 0E2CIA952B426D5A CRC64;
PERIPLASMIC (POTENTIAL).
064C7311F9714405 CRC64;
 -!- SUBCELLULAR LOCATION: INNER MEMBRANE (PROBABLE).
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 SEQUENCE FROM N.A.
MEDLINE-84270665; PubMed-6087149;
MEDLINE-84270665; PubMed-6087149;
Baser R., Bantler A.T., Biggin M.D., Deininger P.L., Farrell P.J.,
Glbson T.J., Hatfull G., Hudson G.S., Satchwell S.C., Seguin C.,
Tuffnell P.S., Barrell B.G.;
"DNA sequence and expression of the B95-8 Epstein-Barr virus genome.";
"Nature 310.207-211(1984).
"IFUNCTION: TRANSCRIPTION ACTIVATION.
"INCCELLANBOUS: BRLF1 PROTEIN IS AN EARLY OR IMMEDIATE EARLY
 Gaps
 Gaps
 TRX2_HUMAN STANDARD; PRT; 2715 AA.
09UMN6; 09UK25; 095836; 09Y669; 015022;
01-0CT-2000 (Rel. 40, Created)
01-0CT-2000 (Rel. 40, Last annotation update)
01-0CT-2000 (Rel. 40, Last annotation update)
TRITHORAX HOMOLOG 2 (MIXED LINEAGE LEUKEMIA GENE HOMOLOG 2 PROTEIN)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Iranscription regulation; Activator; DNA-binding; Early protein.
SEQUENCE 605 AA; 66594 MW; B5B7DF0593FADB08 CRC64;
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 ..
o
 Score 70.5; DB 1; Length 605;
 Indels
 Indels
 Epstein-barr virus (strain B95-8) (Human herpesvirus 4).
Viruses; dSDNA viruses, no RNA stage: Herpesviridae;
Gammaherpesvirinae; Lymphocryptovirus.
 18;
 PAPLP-----PEDAPNAASLAPTPVSPVLEPFNLTSEPS 69
 36 PAPLPPEDAPNAASLAPTPVSPVLEPF-NLTSEPSDYALD 74
 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
TRANSCRIPTION ACTIVATOR BRLFI.
 605 AA
 Pred. No. 8.2;
 Mismatches
 Pred. No. 6.8;
2; Mismatches
 -1- SIMILARITY: TO HVS-1 EDRF1 (GENE 50).
 PRT;
 [1]
SEQUENCE FROM N.A. (LONG ISOFORM).
 .;
?
 16.0%;
 EMBL; V01555; CAA24814.1; -. PIR; A03771; OQBE29. PIR; S33019; S33019.
 45.0%;
 Conservative
 Conservative
 STANDARD;
 (KIAA0340).
TRX2 OR HRX2 OR MLL2.
 Homo sapiens (Human)
 Best Local Similarity
Matches 18; Conserv
 Best Local Similarity
Matches 19; Conserv
 FRANSFAC; T00710;
 BRL1_EBV
 SEQUENCE
 Query Match
 7
 FRX2_HUMAN
 36
 BRL1_EBV
 RESULT
 RESULT
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 g
 RECOCEETTE
 õ
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 M.T., 7620, 170000372; ...
INTERRO: IPRO00483; ...
INTERRO: IPRO10611; ...
PFAM; PF001660; LRRCT; 1.
PFAM; PF01463; LRRCT; 1.
PFAM; PF01461; LRRCT; 1.
PRINTS; PR00019; LEURICHRPT.
Platelet; Transmembrane; Glycoprotein; Hemostasis; Blood coagulation; Repeat; Leucine-repeat; Signal; Coll adhesion; Disease mutation; Solpmorphism; von Willebrand disease; Bernard Soulier syndrome.
 MISCELLANGOUS: BINDING SITES FOR VON WILLEBRAND FACTOR AND THROWBIN (THE LATTER SITE WITH UNKNOWN FUNCTION) ARE IN THE AMINO-TERMINAL PART OF THE MOLECULE.
SIMILARITY: THE REPEATED LEUCINE-RICH (LRR) SEGMENT IS FOUND IN MANY PROTEINS. NUMBER IN THIS PROTEIN: 8
 PLATELET GLYCOPROTEIN IB ALPHA CHAIN.
 L -> F (IN BSS).

/FTId=VR_002256.

T -> M (IN ALLOANTIGEN SIBA(+)).

/FTId=VR_005257.

A -> V (IN BSS).

/FTId=VAR_005258.
 Length 626;
 EXTRACELLULAR (POTENTIAL)
 19514119845DF573 CRC64;
 CYTOPLASMIC (POTENTIAL),
 /FTId-VAR_005261.
M -> V (IN PSEUDO-VWD).
/FTId-VAR_005262.
 /FTId=VAR_005259.
C -> S (IN BSS).
/FTId=VAR_005260.
G -> V (IN PSEUDO-VWD).
 LEUCINE-RICH REPEATS
 DB 1;
 N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
 MISSING (IN BSS)
 THR/PRO-RICH
THR/PRO-RICH
 THR/PRO-RICH,
 THR/PRO-RICH
 THR/PRO-RICH
 Score 71.5;
 POTENTIAL
 LERR
LERR
LERR
LERR
LERR
 68955 MW;
 EMBL; J02940; AAA52595.1; -. EMBL; M2403; AAA55596.1; -. PIR; A27075; NBHUIA. MIM; 231200; -.
 16.28;
ACTIN-BINDING PROTEIN.
 249
 255
 626
 626
224
60
60
108
131
179
 195
 225
 430
 161
 626 AA;
 17
17
506
327
39
 195
 225
 249
 255
 161
 DOMAIN
TRANSMEM
 REPEAT
DISULFID
 SEQUENCE
 DISULFID
 DISULFID
 CARBOHYD
 CARBOHYD
 CARBOHYD
 Query Match
 VARIANT
 VARIANT
 VARIANT
 VARIANT
 VARIANT
 VARIANT
 VARIANT
 REPEAT
REPEAT
 DOMAIN
 REPEAT
 REPEAT
 REPEAT
 REPEAT
 CHAIN
 REPEAT
 REPEAT
 EPEAT
 REPEAT
 CHAIN
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Q.

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 Amino acid sequence of the human protein synthesis initiation factor eIF-4 gamma.";
 MRNA TO THE RIBOSOME.
--- SIMILARITY: COWTAINS! RNA RECOGNITION MOTIF (RRM).
--- SIMILARITY: THE C-TERMINAL REGION IS SIMILAR TO THE N-TERMINAL REGION OF WHEAT EUKARYOTIC INITIATION FACTOR (ISO)4F SUBUNIT P02.
 100 QMPVEEPAPISR-------EAGEPYCLSPE-----PIPLAEPILEVE 134
 4 QLPVEEPNPAKRLLFLLLTIVFCQILMAEEGVPAPLPPEDAPNAASLAPTPVS-PVLEPF 62
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
 synthesis initiation factor
 -:- FUNCTION: COMPONENT OF THE PROTEIN COMPLEX EIF-4, WHICH IS INVOLVED IN THE RECOGNITION OF THE MRNA CAP, ATP-DEPENDENT UNMINDING OF 5'-TERMINAL SECONDARY STRUCTURE AND RECRUITMENT
 RNA-BINDING (RNP2) (BY SIMILARITY).
RNA-BINDING (RNP1) (BY SIMILARITY).
 Koehrer K., Beyer A., Mewes H.-W., Gassenhuber J., Wiemann S., Submitted (MAY-1999) to the EMBL/GenBank/DDHJ databases.
 "Mapping the cleavage site in protein synthesis initiation far
eIF-4 gamma of the 2A proteases from human Coxsackievirus and
 DB 1; Length 1402;
29;
 PFAN, PF02020; IF5_eIF4_eIF2; 1.
PROSITE; PS00030; RRM_RNP_1; FALSE_NEG.
Initiation factor; Protein biosynthesis; Phosphorylation;
 21; Indels
 7FD85D7E30519230 CRC64;
 Etchison D., Rhoads R.E.;
 30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
 15.6%; Score 69; DB 1
30.2%; Pred. No. 29;
tive 7; Mismatches
 181 AA
 or send an email to license@isb-sib.ch)
 POLY - PRO
 POLY-GLU
 POLY-GLU
 J. Biol. Chem. 267:23226-23231(1992)
 Biol. Chem. 268:19200-19203(1993)
 135 VTLSKPVPVSEFSSSPIQVLTPLASH 160
 PRT;
 63 NLTSEP-----SDYALDLSTFLQQH 82
 PARTIAL SEQUENCE.
MEDLINE-93054654; PubMed-1429670;
 262 275 POLY-602 607 RNA-1698 706 1393 1398 POLY-1402 AA; 154050 MW;
 EMBL; L22090; AAA31242.1; -.
 PROTEIN C210RF25 (FRAGMENT).
 Query Match 15.6
Best Local Similarity 30.2
Matches 26; Conservative
 STANDARD;
 Homo sapiens (Human)
 IPR000504;
 Yan R., Rychlik W.,
 SEQUENCE FROM N.A.
 TISSUE-UTERUS
 RNA-binding.
 C210_HUMAN
Q9Y426;
 rhinovirus.
 SEQUENCE
 C210RF25
 DOMAIN
 DOMAIN
 DOMAIN
 DOMAIN
 DOMAIN
 RESULT 11
C210_HUMAN
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 ij
 CATALYTIC ACTIVITY: (3R)-3-HYDROXYACYL-[ACYL-CARRIER PROTEIN] + NADP(+) = 3-OXOACYL-[ACYL-CARRIER PROTEIN] + NADP(+) = 3-OXOACYL-[ACYL-CARRIER PROTEIN] + NADPH.
SUBUNIT: FATTY ACID SYNTHETASE ARE (ALPHA(6)BETA(6)] HEXAMERS OF TWO MULTIFUNCTIONAL SUBUNITS (ALPHA & BETA).
SIMILARITY: TO THE FATTY ACID SYNTHETASE, SUBUNIT ALPHA FROM OTHER PUNGI.
LONG-CHAIN FATTY ACIDS FROM ACETYL-COA, MALONYL-COA AND NADPH.

THE ALPHA SUBUNIT CONTAINS DOMAINS FOR: ACYL CARRIER PROTEIN,

3-OXOACYL-[ACYL-CARRIER PROTEIN]

CARRIER-PROTEIN] SYMPHASE, THIS SUBUNIT COORDINATES THE BINDING

OF THE SIX BETA SUBUNITS TO THE ENZYME COMPLEX.

CATALYTIC ACTIVITY: ACETYL-COA + N MALONYL-COA + ZN NADPH -

LONG-CHAIN FATTY ACID + (N+1) COA + N CO(2) + 2N NADP(+).

CATALYTIC ACTIVITY: ACYL-PCYL-CARRIER PROTEIN] + MALONYL-(ACYL-CARRIER PROTEIN) + MALONYL-(ACYL-CARRIER PROTEIN) + CO(2) +
 PHOSPHOPANTETHEINE (BY SIMILARITY).
BETA-KETOACYL SYNTHASE (BY SIMILARITY).
G->S: CERULENIN-RESISTANCE.
 Gaps
 01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
EUKARYOTIC TRANSLATION INITIATION FACTOR 4 GAMMA (EIF-4-GAMMA) (EIF-
 Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae: Oryctolagus.
 PROSITE; PS00012; PHOSPHOPANTETHEINE; 1.
PROSITE; PS00606; B_KETOACYL_SYNTHASE; 1.
Fatty acid biosynthesis; Multifunctional enzyme; Oxidoreductase; Transferase; NADP; Phosphopantetheine.
 ۳,
 DB 1; Length 1894;
 18; Indels
 SEQUENCE FROM N.A., AND SEQUENCE OF 479-500.
STRAIN-NEW ZEALAND WHITE: TISSUE-BRAIN:
MEDLINE-93374895: Pubmed-8396129.
Lamphear B.J., Yan R., Yang F., Waters D., Liebig H.-D.,
Klump H., Kuechler E., Skern T., Rhoads R.E.;
 AECC0B2269DEE833 CRC64,
 ACYL CARRIER.
BETA-KETOACYL REDUCTASE.
BETA-KETOACYL SYNTHASE.
 31 AEEGVPAPLPPEDAPNAASLAPTPV---SPVLEPFNLTSEP
 Score 69.5; DB
Pred, No. 36;
4; Mismatches
 PRT; 1402 AA.
 15.7%;
39.0%;
 EMBL; J03936; AAA34601.1; -.
 1312 1312
1257 1257
1894 AA; 208098 1
 [ACYL-CARRIER PROTEIN]
 16; Conservative
 STANDARD;
 PIR; A31107; A31107.
SGD; S0006152; FAS2.
INTERPRO; IPR000255; -.
 IPR002582; -.
 INTERPRO; IPR000794; -.
 PFAM: PF01648: ACPS: 1
 Query Match
Best Local Similarity
 180
 682
 IF4G_RABIT
P41110;
 ACT_SITE
MUTAGEN
SEQUENCE
 INTERPRO
 BINDING
 IF4G_RABIT
 Matches
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 g
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4

32; Gaps

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or send an email to license@isb-sib.ch).
 OF
 ं
 /ride*vak_ou8/12.
MISSING (IN GASTRIC ADENOCARCINOMA).
/FTIde*VAR_001308.
N -> S (IN LOBULAR BREAST CARCINOMA).
 MISSING (IN GASTRIC CARCINOMA; LOSS HETEROZYGOSITY).
 N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
H->- Y (IN DIFFUSE GASTRIC CANCER).
T->- P (IN DIFFUSE GASTRIC CANCER).
 PRINTS; PR00205; CADHERIN.
PROSITE; PS00212; CADHERIN.1; 3.
Cell adhesion; Glycoprotein; Phosphorylation; Transmembrane;
Calcium-binding; Repeat; Signal; Disease mutation; Polymorphism.
 /FTId-var_001310.
D -> A (IN DIFFUSE GASTRIC CANCER).
/FTId-var_001311.
 T -> L (IN DIFFUSE GASTRIC CANCER).

(FILG=VAR_001316.

V -> N (IN DIFFUSE GASTRIC CANCER).

FILG=VAR_001317.

V -> A (IN DIFFUSE GASTRIC CANCER).
 /FTId-VAR_001318.
R -> Q (IN DIFFUSE GASTRIC CANCER).
 /FTId-VAR_001307,
D -> G (IN DIFFUSE GASTRIC CANCER).
/FTId-VAR_008712,
 Q (1N DIFFUSE GASTRIC CANCER)
 MISSING (IN GASTRIC CARCINOMA). /FTId-VAR_001313.
 /FIId=VAR_008713.
A -> T (IN THYROID CANCER)
 EPITHELIAL-CADHERIN.
EXTRACELLULAR (POTENTIAL).
 POTENTIAL, CYTOPLASMIC (POTENTIAL).
 /FTId-VAR_001314.
 /FTId-VAR_001309
 /FTId=VAR_001315
 /FTId=VAR_001312
 CADHERIN 4.
 CADHERIN 1
 CADHERIN 2
 CADHERIN 3
 POTENTIAL
 INTERPRO: IPRO00233; -.
INTERRO: PRO02126; -.
PFAH; PF01049; Cadherin_C_term; 1.
PFAH; PF00028; cadherin; 5.
 ?
 EMBL, 213009, CAA78353.1, -...
EMBL, 218923, CAA79356.1, -...
EMBL, X12790, CAA31279.1, -...
EMBL, L34545, AAA21764.1; -...
 882
707
731
882
375
375
375
697
697
637
123
 193
 244
 277
 315
 336
 370
 400
 423
 463
 470
 470
 473
 487
 592
 598
 617
 PIR, S25141; IJHUCE.
PIR, S37654; S37654.
HSSP; P09803; ISUH.
MIM; 192090; -.
 537
 193
 315
 336
 370
 418
 463
 470
 470
 473
 244
 274
 100
 187
 592
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 617
 DOMAIN
TRANSMEM
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 Š
 Oestman A., Yang Q., Tonks N.K.;
"Expression of DEP-1, a receptor-like protein-tyrosine-phosphatase,
is enhanced with increasing cell density.";
Proc. Natl. Acad. Sci. U.S.A. 91:9680-9684(1994).
-:- FUNCTION: MAY CONTRIBUTE TO THE MECHANISM OF CONTACT INHIBITION OF
CELL GROWTH.
 Gaps
 588 VNDNAPIPEPR-----TIFFCERNPKPQVINI---IDADLPPNTSPFTAELTHGA 634
 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
PROTEIN-TYROSINE PHOSPHATASE ETA PRECURSOR (EC 3.1.3.48) (R-PTP-ETA)
CDENSITY ENHANCED PHOSPHATASE-1) (DEP-1) (CD148 ANTIGEN).
 VRRQLPVEEPNPAKRLLFLLLTIVFC-----QILMAEEGVPAPLPPEDAPNAASLA--- 51
 Eukaryota, Melazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 -:- CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)0 - PROTEIN TYROSINE + ORTHOPHOSPHATE.
-:- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-:- PTM: N - AND O-CATION: TYPE I MEMBRANE PROTEIN.
-:- SIMILARITY: CONTAINS 1 PROTEIN TYPE III-LIKE DOMAIN.
-:- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.
-:- DATABASE: NAME-PRROW; NOTE-CD guide CDJ48 entry;
-:- MWW-"hittp://www.ncbi.nlm.nlh.gov/prow/cd/cdl48.htm".
 PFAM; PFULLS:
PROMOTI; fig; 5.
PRINTS; PROMOTI; fig; 5.
PRINTS; PROMOTI; FIG; 5.
PROSITE; PROMOTI; TYR_PHOSPHATASE_1; 1.
PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
PROSITE; PS50056; TYR_PHOSPHATASE_PTP; 1.
PROSITE; PS50056; TYR_PHOSPHATASE_PTP; 1.
PROSITE; PS50056; TYR_PHOSPHATASE_PTP; 1.
PROFICE PS50056; TYR_PHOSPHATASE_PTP; 1.
PROFICE PS50056; TYR_PHOSPHATASE_PTP; 1.
PROFICE PS50056; TYR_PHOSPHATASE_PTP; 1.
PROFICE PS50056; TYR_PHOSPHATASE_PTP; 1.
PROFICE PS50056; TYR_PHOSPHATASE_PTP; 1.
PROFICE PS50056; TYR_PHOSPHATASE_PTP; 1.
PROFICE PS50056; TYR_PHOSPHATASE_PTP; 1.
PROFICE PS50056; TYR_PHOSPHATASE_PTP; 1.
PROFICE PS50056; TYR_PHOSPHATASE_PTP; 1.
PROFICE PS50056; TYR_PHOSPHATASE_PTP; 1.
PROFICE PS50056; TYR_PHOSPHATASE_PTP; 1.
PROFICE PS50056; TYR_PHOSPHATASE_PTP; 1.
PROFICE PS50056; TYR_PHOSPHATASE_PTP; 1.
PROFICE PS50056; TYR_PHOSPHATASE_PTP; 1.
PROFICE PS50056; TYR_PHOSPHATASE_PTP; 1.
PROFICE PS50056; TYR_PHOSPHATASE_PTP; 1.
PROFICE PS50056; TYR_PHOSPHATASE_PTP; 1.
PROFICE PS50056; TYR_PHOSPHATASE_PTP; 1.
PROFICE PS50056; TYR_PHOSPHATASE_PTP; 1.
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PROFICE PS50056; TYR_PHOSPHATASE_PTP; 1.
PROFICE PS50056; TYR_PHOSPHATASE_PTP; 1.
PROFICE PS50056; TYR_PHOSPHATASE_PTP; 1.
PROFICE PS50056; TYR_PHOSPHATASE_PTP; 1.
PROFICE PS50056; TYR_PHOSPHATASE_PTP; 1.
PROFICE PS50056; TYR_PHOSPHATASE_PTP; 1.
PROFICE PS50056; TYR_PHOSPHATASE_PTP; 1.
PROFICE PS50056; TYR_PHOSPHATASE_PTP; 1.
PROFICE PS50056; TYR_PHOSPHATASE_PTP; 1.
PROFICE PS50056; TYR_PHOSPHATASE_PTP; 1.
PROFICE PS50056; TYR_PHOSPHATASE_PTP; 1.
PROFICE PS50056; TYR_PHOSPHATASE_PTP;
 9
 33;
L -> V (IN ENDOMETRIAL CANCER).
/FITdevAR_001321.
S -> G (IN OVARIAN CANCER; LOSS | HETEROXYGOSITY).
/FIId-VAR_001322.
 Length 882;
 Indels
 SANWIIQYNDPIQESIILKP-KMALEVGDYKINLKLMDNQN 674
 82
 DB 1;
 ------PTPVSPVLEPFNLTSEPSDYALDLSTFLQQH
 Score 68.5; DE
Pred. No. 20;
1; Mismatches
 1337 AA.
 PRT;
 SEQUENCE FROM N.A.
MEDLINE-95024024; Pubmed-7937872;
 PFAM; PF00102; Y_phosphatase; 1.
PFAM; PF00041; fn3; 5.
 11;
 15.5%;
25.7%;
 EMBL; U10886; AAB36687.1; -. HSSP; P18052; 1YFO.
 Conservative
 STANDARD;
 INTERPRO, IPRO00242, -.
 711
 838
 Homo sapiens (Human).
 IPR001777
 Similarity
 711
 838
 Query Match
Best Local Simi
Matches 26;
 4IM: 600925
 PTPJ_HUMAN
 NTERPRO;
 VARIANT
 VARIANT
 RESULT 13
P'IPJ_HUMAN
 52
 635
 g
 g
 FT
FT
FT
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 δ
 R -> Q (IN DIFFUSE GASTRIC CANCER).

/FILGH-VAR_001319.

A -> I (IN ENLOMETRIAL CANCER; LOSS (

HETEROZYGOSITY).

/FIId-VAR_001320.
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 Gaps
 POLY-GLU.
POLY-ALA.
RNA-BINDING (RNP2) (BY SIMILARITY).
RNA-BINDING (RNP1) (BY SIMILARITY).
PRGP -> ARGAQ (IN REF. 1).
MW; C712A09D270DF2AB CRC64;
 9
 Ouery Match
15.4%; Score 68; DB 1; Length 1395;
Best Local Similarity 43.2%; Pred. No. 36;
Matches 19; Conservative 6; Mismatches 13; Indels
 INTERPRO: IPRO00504; -
PFAM: PPO0020: IFS_eIF4_EIF2: 1.
PROSITE: PSO00303: RRM_RNP_1: FALSE_NEG.
Initiation factor; Protein biosynthesis: Phosphorylation;
 28 ILMAEEGVPAP--LPPEDAPNAASLAPTPVSPVLEPFNLTSEPS 69
 153360 MW;
 EMBL; D12686; BAA02185.1; -.
 258 27
305 30
599 60
696 70
497 50
 RNA-binding.
 DOMAIN
CONFLICT
SEQUENCE
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```

Search completed: January 30, 2001, 23:12:25 Job time: 4006 sec

:eduence:

Run on:

Searched:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 Query
Match Length DB
 em_hum5:
em_hum6:
gb_pr5:*
gb_pr7:*
gb_htg1:
gb_htg2:
 85.4 1693
79.8 1864
38.4 473
19.7 1758
17.1 203476
17.0 1898
16.4 187868
12.3 297
 .0 1938
.4 187868
 205512
 1152.2
1080.4
1080.6
1088.6
1048.6
979.8
2471
2142.4
210.6
 Score
 Result
No.
 ; Search time 1900.13 Seconds
(without alignments)
3307.456 Million cell updates/sec
 2236266
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
 1118133 segs, 2558875100 residues
 Total number of hits satisfying chosen parameters:
 January 30, 2001, 12:11:54
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 nucleic search, using sw model
 IDENTITY_NUC Gapop 10.0 , Gapext 1.0
 length: 0
length: 2000000000
 em_huml:
 em_sts:*
 em_or:*
 gb_p13:
 em_pat:
 em_ro:*
 em_un:*
 gb_ba1:*
 em_om: *
 em_sy:'
 gb_ba3
 GenEmbl:*
 Minimum DB seq
Maximum DB seq
 Perfect score:
 Scoring table:
 OM nucleic
 Database :
```

Y14551 Homo sapien 881914 IEX-1-radia AC006165 Homo sapi AB023051 Homo sapi AP000512 Homo sapi AF071596 Homo sapi AF071596 Homo sapi X96438 H.sapiens P

Description

SUMMARIES

X96437 R.norvegicu AC074150 Mus muscu AC022301 Mus muscu AC022301 Mus muscu A75448 Sequence 11 A78427 Sequence 11 A7848 Homo sapi A75468 Sequence 11 A75468 Sequence 11 A78447 Sequence 11 A78447 Sequence 11 AC026631 Homo sapi

AC026631

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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|---------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------|------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------|-----------------------------------|
| STS                                                                                                                       | STS                                                                              | E                                                                      | n<br>n                                                                                                                                     | STS                                                                                                                                                       | STS                                                                                                                                         | STS                                                                                                                                          | . STS                                                                                                                                           | STS                                                                                                              | STS                                                                                                                                            | STS                                                                   | ŭ<br>E                                                                                                                                             | , v                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | BASE COUNT                                                                                                                                                                                                                                                                               | Ouery Match<br>Best Local<br>Marches 120                                                                                                                                                                                |                                                                                                                                                                               | Oy 61 CC<br>11<br>Db 97723 CC                                                                                                                                                                                                                                                          | Oy 121 CT<br>Db 97783 CT                                                                                | 191                               |
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AFU71596 1693 bp DNA Homo sapiens apoptosis inhibitor (IEX-1L) gene, AF071596

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Kondratyev.A.D., Chung,K.N. and Jung,M.O.

Identification and characterization of a radiation-inducible glycosylated human early-response gene
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 Kumar, R., Kobayashi, T., Warner, G.M., Wu, Y., Salisbury, J.L., Lingle, W. and Pittelkow, M.R. A Novel Immediate Early Response Gene, 1Ex-1 Is Induced by Ultraviolet Radiation in Human Keratinocytes (Upublished 3) (bases 1 to 477)
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 1311 CCCGGTGCTTGA-GCGGGACCGAGGCGCACAGAGACCGAGGCGCATAGAGACCGA-GCAC 1368
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 ACTGTGTGAGACTTCGGCGGACCATTAGGAATGAGATCCGTGAGATCCTTCCATCTTCTT 1087
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 ### HITTO CONTRACT TO THE FIRST CONTRACT 1072 CCCTGTGTCCCCCGTCCTCGAGCCCTTTAATCTGACTTCGGAGCCCTCGGACTACGCTCT
 1369 AGCCCAGCT-GGGCTAGGCCCGGTGGGAAGGAGAGCGTCGTTAATTTATTGTTATTGCT
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrala; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
I (Dasas 1 to 18786)

Metaker, M. L., Lewis, L.R., Hume, J., Edwards, C., Harris, C.;
Dederich, D., Thomas, S., Okwuonu, G., Carlock, C., Garner, T.,
Addison, S., Pace, A., Williams, G., Bonnin, D., Brooks, A., Brown, J.,
Buhay, C., Burkett, C., Checko, J., Chen, G., Chen, Z.,
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Gorrell, J. H., Gunarathor, P., Haller, G., Hernandez, J., Hogues, M.,
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Worley, K., and Gibbs, R.
 AC022301 187868 bp DNA HTG 15-JUN-2000
Mus musculus clone RP23-329K24, *** SEQUENCING IN PROGRESS ***, 59
 Direct Submission
Submitted (29-JAN-2000) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
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 360 GGCGCCCACCCCTGTGTCCCCCGTCCTCGAGCCCTTTAATCTGACTTCGGAGCCCTCGGA
 Web site: http://www.hgsc.bcm.tmc.edu/
 Unpublished
2 (bases 1 to 187868)
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 LOCUS
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AC022301
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 TITLE
JOURNAL
REFERENCE
 TITLE
JOURNAL
 VERSION
KEYWORDS
SOURCE
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Chemistry: Dye-primer Bodipy: 82% of reads
Chemistry: Dye-terminator Big Dye: 10% of feads
Assembly program: Phrap: version 0.990129
Consensus quality: 133377 bases at least Q40
Consensus quality: 159061 bases at least Q30
Consensus quality: 169086 bases at least Q30
Estimated insert size: 166938; sum-of-contigs estimation
Quality coverage: 2.3x in Q20 bases; sum-of-contigs estimation
 consists of 59 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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 7154: contig of 7154
7254: gap of unknown
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66 a 117 c 61 g
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Matches 212; Conservative
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 Searched:
 Seguence:
 Database
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AC006165 Homo sapi AB023051 Homo sapi AP000612 Homo sapi S81914 IEX-1=radia X96437 R.norvegicu

HSDIF2 AF039067 AF039067 HSPRG1 HSPRG1 AB0203051 AP000512 S81914 S81914 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP000512 AP0

1223 1758 203476 1938

Y14551 Homo sapien AF039067 Homo sapi AF071596 Homo sapi H.sapiens P

AF083421 Homo sapi

AF083421

Q.

Length DB

Description

SUMMARIES

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393 c 369 9 285 t
 Eukaryota; Metazoa; Chordata; Craniaia; Verlebrata; Euleleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (basa 1 to 1309) Wu,M.X., Ao,Z., Prasad,K.V.S., Wu,R. and Schlossman,S.F. IEX.IL, an apoptosis inhibitor involved in NF-kappaB-mediated cell
 240
 61 CTCACCATCGTCTTCTGCCAGATCCTGATGGCTGAAGAGGGTGTGCCGGGGCCCCTGCCT 120
 9
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 Cost to 1309)

Ao.Z. and Wu.M.X.

Ao.Z. and Wu.M.X.

Direct Submission

Submitted (17-DEC-1997) Tumor Immunology, Dana Farber Cancer Institute, 44 Binney Street, Boston, MA 02115, USA

Location/Qualifiers

1. 1309

1. 1309

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Homo sapiens anti-death protein (IEX-1L) mRNA, complete cds.
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183. .>1230
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Matches 258
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| Matches                          | : 258; Conservative 0; Mismatches 0; Indels 0; Gaps 0;                                                                    | Small                                   |
|----------------------------------|---------------------------------------------------------------------------------------------------------------------------|-----------------------------------------|
|                                  | GTCCGCCCCCCACTCCAGCACCGAACCGAACCCACCAAAAGCTTCTCTCTTTCTGTG 60                                                              | are no<br>signif                        |
| r                                |                                                                                                                           | by das                                  |
| Oy 61<br>Db 974                  | CTCACCATGGTCTTCTGCCAGATGCTGAAGAGGGTGTGCCGGCGCCCCTGCCT 120<br>                                                             | Map (5714)                              |
| Qy 121<br>Db 1034                |                                                                                                                           | 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 |
| 181                              | 「「「「「「「」」」「「「」」」「「」」「「」」「「」」「」」「」」「「」」「」」「」」「」」「」」「」」「」」「」」「」」「」」「」」「」」「」」「」」「」」「」」「」」「」」「」」「」」「」」「                       | 1536.                                   |
|                                  | CCTTTAATCTGACTTCGGAGCCCTCGGACTTGGACCTCAGCACTTTCCTCCAG 240 CCTTTAATCTGACTTCGGAGCCCTCGGACTTCGGACCTCAGCACTTTCCTCAG 1153      | 3623.                                   |
|                                  |                                                                                                                           | 6834,                                   |
| Db 1154                          |                                                                                                                           | 11234.                                  |
| RESULT<br>ACOUG165               | 9                                                                                                                         | 762.                                    |
| LOCUS                            | AC006165 44118 bp DNA PRI 08-DEC-1998<br>N Homo sapiens clone UWGC:y54c125 from 6p21, complete sequence.                  | 2727.                                   |
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| REFERENCE                        | 1 (bases 1 to 44118)                                                                                                      | sonrce                                  |
| 2000                             |                                                                                                                           |                                         |
| TITLE<br>JOURNAL                 |                                                                                                                           |                                         |
| REMARK                           | Fred Hutchinson Cancer Research Center<br>The Clinical Research Division                                                  |                                         |
|                                  | 1100 Fairview Ave. N., P.O. Box 19024                                                                                     |                                         |
| REFERENCE                        |                                                                                                                           | repeat_region                           |
| TITLE                            |                                                                                                                           | repeat_region                           |
| JOURNAL                          | Submitted (08-DEC-1998) Human Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA                 | repeat_region                           |
| REMARK                           | University of Washington Human Genome Center<br>Box 352145, Seattle, WA 98195                                             | repeat_region                           |
| COMMENT                          | Contact: Daniel E. Geraghty (geraghty@fhcrc.org) Overlapping Sequences:                                                   | repeat_region                           |
|                                  | 5': UWGC:y54c283<br>3': UWGC:y54c222 (Genbank Accession: AC006049)                                                        | repeat_region                           |
|                                  | Sequence Quality Assessment:                                                                                              | repeat_region                           |
| ٠                                | This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.                     | repeat_region                           |
|                                  | All manually edited bases have been reduced to quality zero.<br>Quality levels above 40 are expected to have less than    | repeat_region                           |
|                                  | <pre>1 error in 10,000 bp. Base-by-base quality values are not generally visible from the</pre>                           | repeat_region                           |
|                                  | Genbank flat file format but are available as part of this entry's ASN.1 file.                                            | repeat_region                           |
|                                  |                                                                                                                           | repeat_region                           |
|                                  | DS or two chemistry coverage: 99,5% Single stranded regions: 2                                                            | repeat_region                           |
|                                  | Sequence Validation:                                                                                                      | repeat_region                           |
|                                  | This sequence has been validated by Multiple Complete Digest Mapping. Comparison of the experimentally derived map digest | repeat_region                           |
|                                  | . Tragments with sequence-predicted fragments is given below.                                                             | repeat_region                           |

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 lbost....toopop
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of PCR primers."
 between
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 181 CCCTTTAATCTGACTTCGGAGCCCTCGGACTACGCTCTGGACCTCAGCACTTTCCTCCAG
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 98225 CAACACCGGCCGCCTTC 98242
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Matches 258; Conserv
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 52458
 Query Match
 LOCUS
DEFINITION
 BASE COUNT
ORIGIN
 61
 121
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 RESULT
S81914
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/note="WI-18721;The location is between each flanking site
 Licakawa, M., Yamaguchi, H., Imai, K. and Shimada, J.
Direct Submission
Direct Clomission
Submission
Submission
Submission
Hirakawa, Japan Science and Technology Corporation (JST), Advanced
Databases Department; 5-3, Yonbancho, Chiyoda-ku, Tokyo 102-0081,
URL: http://www.alis.tokyo.jst.go.jp,
URL: http://www.alis.tokyo.jst.go.jp/, Tel:81-3-5214-8491,
 Japan Science and Technology Corporation (JST)

3.3 Vonbancyo, Chiyoda-ku, Tokyo, 102-0081 Japan
For further infomation about this sequences, please visit our sequence archive web site (http://www-alis.tokyo.jst.go.jp/HGS/top.html) or send email to webmaster@www-alis.tokyo.jst.go.jp/
 This sequence is conducted by Tokai University as a JST sequencing
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HLA Class I region,
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 Phone: +81-463-93-1121, Fax.+81-463-94-8884,
The sequence is submitted by Human Genome Sequencing in ALIS
project of JST
CTCACCATCGTCTTCTGCCAGATCCTGATGGCTGAAGAGGGTGTGCCGGCCCCCTGCCT
 CCCTTTAATCTGACTTCGGAGCCCTCGGACTACGCTCTGGACCTCAGCACTTTCCTCCAG
 Shiina, S., Tammya, G., Oka, A. and Inoko, H.
Inoo sapiens 2.229, 817bp genomic DNA of 6p21.3 HLA
Published Only in DataBase (1999) In press
(bases 1 to 200000)
Hirakawa, M., Yamaguchi, H., Imai, K. and Shimada, J.
 ... vvvjiž 200000 bp DNA IOMO sapiens genomic DNA, chromosome 6p2l.3, ap000512
 Principal Investigator: Hidetoshi Inoko Ph.D
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 AP000512
AP000512.1 G1:5926699
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 .200000
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 Homo sapiens
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 63
 61060
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TITLE
 JOURNAL
REFERENCE
AUTHORS
 TITLE
JOURNAL
 RESULT
AP000512
 ACCESSION
 VERSTON
KEYWORDS
SOURCE
 REFERENCE
 STS
 STS
 FEATURES
 STS
 COMMENT
 g
 g
 q
 g
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COMMENT

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Charles, C.H., Yoon, J.K., Simske, J.S. and Lau, L.F. Genomic structure; cDNA sequence, and expression of gly96, a growth factor-inducible immediate-early gene encoding a short-lived
 Direct Submission
Submitted (29-JUL-1992) L. Lau, University of Illinois College of
Med., Dept. of Genetics, M/C 669, 808 South Wood Street, Chicago,
IL 60612, USA
 92935 TTGGCCATCATCTTCTGCCAGATTTTGATGGCCTGAAGAGGGTGTGTCCCAGCCCCTGGCT 92994
 92995 CCGGAGGATGCTACCAGCGCCGTGACCCCATTTCTGCGCCCATTACTGCGCCC 93054
 93055 CCGGTCCTCGAGCCTTTGAACCTGACCTCGGAGTCCTCGGACTATGCGCTGGATCTTAAA 93114
 121 CCAGAGGACGCCCTAACGCCGCATCCC------TGGCGCCCACCCCTGTGTCC 168
 169 CCCGTCCTCGAGCCCTTTAATCTGACTTCGGAGCCCTCGGACTACGCTCTGGACCTCAGC 228
 61 CTCACCATCGTCTTCTGCCAGATCCTGATGGCTGAAGAGGGTGTGCCGGCGCCCCTGCCT 120
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Pred. No. 4.7e-24;
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 11-MAR-1993
 Mammalia; Eutheria;
Mus.
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1 (bases 1 to 1938)
Lau, L.
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 Óncogene 8 (3), 797-801 (1993)
93173526
 Location/Qualifiers
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75.9%;
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M.musculus gly96 mRNA
 143243:
 161164:
 29876:
 29976:
 180416:
 glycosylated protein
 X67644.1 GI:287803
 Query Match
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Matches 205; Conservative
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 129877
129977
143244
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161265
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 RESULT 12
 ACCESSION
VERSION
KEYWORDS
SOURCE
 REFERENCE
AUTHORS
 TITLE
 JOURNAL
MEDLINE
FEATURES
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TITLE
 REFERENCE
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 MMGLY96
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 Consensus quality: 139978 bases at least Q40
Consensus quality: 15603 bases at least Q30
Consensus quality: 165603 bases at least Q30
Consensus quality: 177139 bases at least Q30
Consensus quality: 177139 bases at least Q30
Estimated insert size: 183300; agarose-fp estimation
Estimated insert size: 206576; sum-of-contigs estimation
Quality coverage: 3.48 in Q20 bases; sum-of-contigs estimation
* NOTE: This is a 'working draft' sequence. It currently
* consists of 30 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
 gap of unknown length contig of 1288 bp in length
 gap of unknown length
contig of 1243 bp in length
 bp in length
length
 1175: contig of 1175 bp in length
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of 5793 b
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of 4422
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of 6556 l
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of 7772 l
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of 6648
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of 6986 l
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of 6164
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of 6977
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of 6377
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 2554
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 unknown
 Web site: http://www.jgi.doe.gov
 Center Project Name: 0
Center clone name: RPCI-23_128D3
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
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 6736:
9196:
 9606
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 Summary Statistics
 2664
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gap of unknown l
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of 1850 h
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of 2272 l
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of 2345
 contig of 3405
gap of unknown
 unknown
of 2462
 contig of 1469
gap of unknown
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 186840
 37198
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 FEATURES
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5850 others

BASE COUNT ORIGIN

source

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 1 (bases 1 to 297)
Sibson, Dr. and Gross, J.
HUMAN NUCLEIC ACID FRAGMENTS, ISOLATED FROM BRAIN ADRENAL TISSUE,
PLACENTA OR BONE NARROW
PALCENTA OR BONE NARROW
PALCENT, RES COUNCIL (1881; SIBSON DAVID ROSS (GB)
LOCATION/QUALIFIERS
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 19-0CT-1999
 13 CTGCCAGTCGAGGAACCGAACCCAGCCAAAAGGCTTCTCTTTTCTGCTGCTCACCATCGTC 72
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unidentified
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 62 TCACCATC 69
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Matches 193;
 VERSION
KEYWORDS
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ORGANISM
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ACCESSION
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 RESULT
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